

1859	16	0.2	24	1	ABA04737	Human alkylation D
1860	16	0.2	24	1	AA520582	Homo iGF conjugate
1861	16	0.2	24	1	ABA01588	Human neuroprotein
1862	16	0.2	24	1	AAD27206	Rat alpha1-2-fucl c
1863	16	0.2	24	1	ABA92654	Human tra oncogene
1864	16	0.2	24	1	AB861805	Analyte sorting ta
1865	16	0.2	24	1	AB862060	Analyte sorting ta
1866	16	0.2	24	1	AB190136	Capture oligonucle
1867	16	0.2	24	1	AB184908	Capture oligonucle
1868	16	0.2	24	1	AB184908	Capture oligonucle
1869	16	0.2	24	1	AB180197	Capture oligonucle
1870	16	0.2	24	1	AB859343	Human C1P4-like PC
1871	16	0.2	24	1	AB826310	Human C/EBP antise
1872	16	0.2	24	1	AB826470	Toxicologically re
1873	16	0.2	24	1	AB828494	Toxicologically re
1874	16	0.2	24	1	AB8275326	Tubedown-1 PCR pri
1875	16	0.2	24	1	AB857885	Alpha1-2-fucosyltra
1876	16	0.2	24	1	ABV93494	Bacillus thuringie
1877	16	0.2	24	1	ABV93779	B. thuringiensis t
1878	16	0.2	24	1	ADB97806	Rat hepatoma H35 c
1879	16	0.2	24	1	ADC54034	Simian virus 40 (S
1880	16	0.2	24	1	ADC54035	Simian virus 40 (S
1881	16	0.2	24	1	ADC79565	Human C18 forward
1882	16	0.2	24	1	ADB44506	Primer #1 to ampli
1883	16	0.2	24	1	ADB35077	Sox1 gene sense PC
1884	16	0.2	25	1	AAH38515	SNP specific SNPE
1885	16	0.2	28	1	AAH78855	Deoxy-A22-cagged s
1886	16	0.2	28	1	AA143065	Regulatable, catal
1887	16	0.2	28	1	ADA39569	Regulatable RNA rela
1888	15.8	0.2	19	1	AAZ70920	Human biallelic ma
1889	15.8	0.2	19	1	AB144134	Human chromosome 1
1890	15.8	0.2	19	1	ADA26006	Human REL-A short
1891	15.8	0.2	19	1	ADA26567	Human REL-A short
1892	15.8	0.2	20	1	AA039533	PCR primer #1 for
1893	15.8	0.2	20	1	AA068872	Oligonucleotide (S
1894	15.8	0.2	20	1	AA064083	NANBHV NS1/NS2 (EN
1895	15.8	0.2	20	1	AA082613	Chromosome 11 (loc
1896	15.8	0.2	20	1	AA084981	Putative NFAT bind
1897	15.8	0.2	20	1	AA086501	S-adenosylmethion
1898	15.8	0.2	20	1	AAV30369	Oligomer p2097 use
1899	15.8	0.2	20	1	AAV47686	Unmethylated Cpg d
1900	15.8	0.2	20	1	AAK14631	Triple helix chid
1901	15.8	0.2	20	1	AAV74243	CpG-N motif O-ODN
1902	15.8	0.2	20	1	AAZ04642	PCR primer used to
1903	15.8	0.2	20	1	AAZ03923	PCR primer used to
1904	15.8	0.2	20	1	AAZ29314	JNK1-specific prob
1905	15.8	0.2	20	1	AAA13122	PI3K antisense inh
1906	15.8	0.2	20	1	AA068855	Human tumour suppr
1907	15.8	0.2	20	1	AA062857	JNK antisense olig
1908	15.8	0.2	20	1	AAH57033	Human oestrogen re
1909	15.8	0.2	20	1	AAH67019	Sequencing primer
1910	15.8	0.2	20	1	AAH67018	Sequencing primer
1911	15.8	0.2	20	1	AAH65675	S. pneumoniae groE
1912	15.8	0.2	20	1	AAH15627	Human Bcl-2 protei
1913	15.8	0.2	20	1	AAH91416	Immunostimulatory
1914	15.8	0.2	20	1	AAH91454	Human inflammatory
1915	15.8	0.2	20	1	AAH67069	Maize MADS-box reg
1916	15.8	0.2	20	1	AA092665	Human Nck-2 phosph
1917	15.8	0.2	20	1	AAH85193	PCR primer used to
1918	15.8	0.2	20	1	AAH76456	Maize ZmMADS2 codi
1919	15.8	0.2	20	1	AAH05931	Human diacylglycer
1920	15.8	0.2	20	1	ABX36522	Apoptotic protease
1921	15.8	0.2	20	1	AAH46646	Human ABCG11 exon1
1922	15.8	0.2	20	1	ABK30537	Human glioma-asso
1923	15.8	0.2	20	1	ABK30537	Angiogenesis inh
1924	15.8	0.2	20	1	ABK39008	Immunostimulatory
1925	15.8	0.2	20	1	AAH43545	Human DB2 antisen
1926	15.8	0.2	20	1	AB092940	T. causchii/wheat
1927	15.8	0.2	20	1	AAH34043	HIV-1TR NF-AT bind
1928	15.8	0.2	20	1	AB096037	Tumour suppresion
1929	15.8	0.2	20	1	ABK05917	Hepatitis B virus
1930	15.8	0.2	20	1	ABK58945	Human tumour maie
1931	15.8	0.2	20	1	ABK27349	Mutant gamma-amino
1932	15.8	0.2	20	1	ABZ29930	Candida albicans G
1933	15.8	0.2	20	1	ABZ97643	probe n. Unidenti
1934	15.8	0.2	20	1	AAH30332	Human PKD1 gene mu
1935	15.8	0.2	20	1	ABZ87057	Human oligonucleot
1936	15.8	0.2	20	1	ABZ85658	Human oligonucleot
1937	15.8	0.2	20	1	ABZ92273	Human oligonucleot
1938	15.8	0.2	20	1	ABZ86043	Human oligonucleot
1939	15.8	0.2	20	1	ABZ91095	Human oligonucleot
1940	15.8	0.2	20	1	ABZ98029	Human MCP4 oligonu
1941	15.8	0.2	20	1	ABZ89014	Human oligonucleot
1942	15.8	0.2	20	1	ABZ58313	Silkworm spider dr
1943	15.8	0.2	20	1	ADA26561	Human Jun N-term
1944	15.8	0.2	20	1	ACD99549	Immunostimulatory
1945	15.8	0.2	20	1	ADA66415	NF-AT DNA binding
1946	15.8	0.2	20	1	ADA38277	Antisense oligonc
1947	15.8	0.2	20	1	ADB36618	Immunostimulatory
1948	15.8	0.2	21	1	AAK34470	Primer ampcri for
1949	15.8	0.2	21	1	AAZ88152	Mouse polyeyatic k
1950	15.8	0.2	21	1	AAZ75207	Human biallelic ma
1951	15.8	0.2	21	1	AAZ75959	Human biallelic ma
1952	15.8	0.2	21	1	AAZ73269	Human biallelic ma
1953	15.8	0.2	21	1	AAK37188	Human PRO315 forw
1954	15.8	0.2	21	1	AAK73260	SNP flanking seque
1955	15.8	0.2	21	1	AAH54275	Primer #26 used in
1956	15.8	0.2	21	1	AAH66956	SSP1 cDNA amplify
1957	15.8	0.2	21	1	ABZ60540	Human polymorphism
1958	15.8	0.2	21	1	ABZ60546	Human polymorphism
1959	15.8	0.2	21	1	ABZ60547	Human polymorphism
1960	15.8	0.2	21	1	ABZ60541	Human polymorphism
1961	15.8	0.2	21	1	ABZ30456	Candida albicans G
1962	15.8	0.2	21	1	ABZ98430	Human multidrug re
1963	15.8	0.2	21	1	ABZ94302	Human BNO1 gene ex
1964	15.8	0.2	21	1	ACD68312	Novel human secret
1965	15.8	0.2	21	1	ACH04414	Human secreted/cra
1966	15.8	0.2	21	1	ACD67958	Novel human secret
1967	15.8	0.2	21	1	ADH17974	Human PRO PCR prim
1968	15.8	0.2	21	1	ADD70620	Human secreted/cra
1969	15.8	0.2	21	1	ADD39697	Human secreted/cra
1970	15.8	0.2	21	1	ADD70143	Human secreted/cra
1971	15.8	0.2	21	1	ADD38264	Human secreted/cra
1972	15.8	0.2	21	1	ADD39220	Human secreted/cra
1973	15.8	0.2	21	1	ADD38743	Human secreted/cra
1974	15.8	0.2	21	1	ADD40174	Human secreted/cra
1975	15.8	0.2	21	1	ADH50395	Human secreted/cra
1976	15.8	0.2	21	1	ADH20007	Human secreted/cra
1977	15.8	0.2	21	1	ADH27646	Stearoyl-CoA desat
1978	15.8	0.2	21	1	ADH49918	Human secreted/cra
1979	15.8	0.2	21	1	ADH21476	Human secreted/cra
1980	15.8	0.2	22	1	AAK16571	Position Flpter 0.
1981	15.8	0.2	22	1	AAV23629	Homo sapiens 20q13
1982	15.8	0.2	22	1	AAH89363	Chromosomal bindi
1983	15.8	0.2	22	1	AAH66131	Human glaucoma-cod
1984	15.8	0.2	22	1	ABZ54658	Human p53 protein
1985	15.8	0.2	22	1	ABZ97569	Human NOV-asso
1986	15.8	0.2	22	1	ACF42636	Human ALMS1 PCR pr
1987	15.8	0.2	23	1	AAZ27024	Apolipoprotein AI
1988	15.8	0.2	23	1	AAH91823	Human inflammatory
1989	15.8	0.2	23	1	AAH18988	Human library acet
1990	15.8	0.2	23	1	ABX09377	Arterioecterois-d
1991	15.8	0.2	23	1	ABZ30886	Candida albicans G
1992	15.8	0.2	24	1	ABZ66701	Human multidrug re
1993	15.8	0.2	24	1	AAQ40413	Sequence of probe
1994	15.8	0.2	24	1	AAH59853	DELTA mitogen acti
1995	15.8	0.2	24	1	AAV35630	SHOX gene exon IV
1996	15.8	0.2	24	1	AAV30696	Telomerase reverse
1997	15.8	0.2	24	1	AAH86853	Apoptery-specific
1998	15.8	0.2	24	1	AAZ24999	Sense probe to Fra
1999	15.8	0.2	24	1	AAH99740	Immunostimulatory
2000	15.8	0.2	24	1	AAH19364	Mammalian IL-12 p4
2001	15.8	0.2	24	1	AAH169622	Human mitotic cycl
2002	15.8	0.2	24	1	ABZ91855	Methyl Cpg binding
2003	15.8	0.2	24	1	ABN81547	Olfactory receptor
2004	15.8	0.2	24	1	ABZ78461	Angiogenesis inh

c2005	15.8	0.2	24	1	AAD5840	Nuclear Localizat
c2006	15.8	0.2	24	1	ABO77631	Human Hemari prote
c2007	15.8	0.2	24	1	ABO83395	Human proteasome p
c2008	15.8	0.2	24	1	AB185134	Capture oligonucle
c2009	15.8	0.2	24	1	AB189739	Capture oligonucle
c2010	15.8	0.2	24	1	AB185135	Capture oligonucle
c2011	15.8	0.2	24	1	AB189738	Capture oligonucle
c2012	15.8	0.2	24	1	ABA97547	Cancer cell discrit
c2013	15.8	0.2	24	1	ABK67727	Novel transglutam
c2014	15.8	0.2	24	1	ABK67734	Novel transglutam
c2015	15.8	0.2	24	1	ACC42750	High mobility comp
c2016	15.8	0.2	24	1	ABX94600	Human MNE3 PCR pri
c2017	15.8	0.2	24	1	ACH03278	Immunostimulatory
c2018	15.8	0.2	24	1	ADB37242	Immunostimulatory
c2019	15.8	0.2	24	1	AAU57131	Rt-PCR primer 2 re
c2020	15.8	0.2	27	1	AAAT70281	Sequence of scisb1
c2021	15.8	0.2	27	1	AAAT70274	Sequence of scisb1
c2022	15.8	0.2	27	1	AAAG2240	SS probe MRCO46.
c2023	15.8	0.2	27	1	AAAG2247	SS probe MRCO71.
c2024	15.8	0.2	27	1	AAQ40854	DNA sequence used
c2025	15.8	0.2	27	1	AAQ99706	Immunostimulatory
c2026	15.8	0.2	27	1	ABK78427	Angiogenesis inhib
c2027	15.8	0.2	27	1	ABL39406	Immunostimulatory
c2028	15.8	0.2	27	1	ACH03245	Immunostimulatory
c2029	15.8	0.2	27	1	ADB37208	Immunostimulatory
c2030	15.8	0.2	29	1	AAV15487	PR-1 promoter prim
c2031	15.8	0.2	29	1	AAAG4315	RNA-protein fusion
c2032	15.8	0.2	29	1	AAAG0066	Synthetic branched
c2033	15.8	0.2	29	1	AAH20990	C-myc epitope puro
c2034	15.8	0.2	29	1	AAK98637	S cerevisiae alpha
c2035	15.8	0.2	29	1	AAQ79096	Tobacco PMT PCR pr
c2036	15.8	0.2	29	1	AAU4903	Triplex forming ol
c2037	15.8	0.2	29	1	AAV59216	Linear multimer pr
c2038	15.8	0.2	29	1	ADCE5873	DNA oligonucleotid
c2039	15.8	0.2	30	1	AAV48087	Oligonucleotide 30
c2040	15.8	0.2	30	1	ABL56893	Synthetic deoxyrib
c2041	15.8	0.2	30	1	ABA97617	Poly f nucleotide
c2042	15.8	0.2	30	1	ABK5890	Probe poly f for a
c2043	15.8	0.2	31	1	AAI30723	Human single nucle
c2044	15.8	0.2	32	1	AAH28290	3' untranslated re
c2045	15.8	0.2	35	1	AAV83644	Oligonucleotide us
c2046	15.8	0.2	41	1	ABZ46913	Human ATP-binding
c2047	15.8	0.2	41	1	ABZ45507	Human ATP-binding
c2048	15.6	0.2	17	1	AAV19118	Anchored oligo (T)
c2049	15.6	0.2	22	1	AAQ49241	Mouse TG mRNA anch
c2050	15.6	0.2	22	1	AAQ49245	Mouse TG mRNA anch
c2051	15.6	0.2	22	1	AAQ39499	Steroidogenesis ac
c2052	15.6	0.2	22	1	AAV93818	Antitumoral phosp
c2053	15.6	0.2	22	1	AAV58375	Biotinylated prime
c2054	15.6	0.2	22	1	AAV09726	Human biallelic po
c2055	15.6	0.2	22	1	AAV49228	rb gene antisense
c2056	15.6	0.2	22	1	AAV22316	PCR primer for CDN
c2057	15.6	0.2	22	1	AAZ22320	PCR primer for CDN
c2058	15.6	0.2	22	1	AAZ44360	Human G protein-co
c2059	15.6	0.2	22	1	AAA96617	(7)-primer for fir
c2060	15.6	0.2	22	1	AAK53416	Oligonucleotide-na
c2061	15.6	0.2	22	1	AAK53419	Oligonucleotide-na
c2062	15.6	0.2	22	1	AAK28471	Random oligonucleo
c2063	15.6	0.2	22	1	AAK28474	Random oligonucleo
c2064	15.6	0.2	22	1	AAK10359	Oligonucleotide-go
c2065	15.6	0.2	22	1	AAK10362	Oligonucleotide-go
c2066	15.6	0.2	22	1	AAK19185	Human GPCR12 cDNA
c2067	15.6	0.2	22	1	AAK62985	Human GPCR12 cDNA
c2068	15.6	0.2	22	1	AAK62985	Shrimp white spot
c2069	15.6	0.2	22	1	AAH74167	DNA chip oligonuc
c2070	15.6	0.2	22	1	AAK65681	HIV-1 detection pr
c2071	15.6	0.2	22	1	AAK65766	Canine narcolepsy
c2072	15.6	0.2	22	1	AAK14405	Human VEGF121-se
c2073	15.6	0.2	22	1	AAK543594	Cornedoesmosin PCR
c2074	15.6	0.2	22	1	AAK543596	Cornedoesmosin PCR
c2075	15.6	0.2	22	1	AAK543598	Cornedoesmosin PCR
c2076	15.6	0.2	22	1	ABK58867	Human G-protein co
c2077	15.6	0.2	22	1	ABK588982	Human G-protein co
c2078	15.6	0.2	22	1	ABK35691	Immunostimulatory
c2079	15.6	0.2	22	1	ABK65026	Nanoparticle-oligo
c2080	15.6	0.2	22	1	ABK65023	Nanoparticle-oligo
c2081	15.6	0.2	22	1	ABK65033	Nanoparticle-oligo
c2082	15.6	0.2	22	1	ABQ93639	Human DISC1/DISC2
c2083	15.6	0.2	22	1	ABK95541	Novel G-protein co
c2084	15.6	0.2	22	1	ABK95526	Novel G-protein co
c2085	15.6	0.2	22	1	ABK64664	Nucleic acid detec
c2086	15.6	0.2	22	1	ABK64691	Nucleic acid detec
c2087	15.6	0.2	22	1	ABK64661	Nucleic acid detec
c2088	15.6	0.2	22	1	ABK54436	Silver staining me
c2089	15.6	0.2	22	1	ABK30733	CP probe to determ
c2090	15.6	0.2	22	1	ABK80504	Sample DNA used to
c2091	15.6	0.2	22	1	ACD27308	Nanotechnology nuc
c2092	15.6	0.2	22	1	ACD27311	Nanotechnology nuc
c2093	15.6	0.2	22	1	ABK98146	Nucleic acid detec
c2094	15.6	0.2	22	1	ABK98149	Nucleic acid detec
c2095	15.6	0.2	22	1	ABK20620	Biological materia
c2096	15.6	0.2	22	1	ABK21572	Multiple group PC
c2097	15.6	0.2	22	1	AAK61634	Capture oligonucle
c2098	15.6	0.2	22	1	AAK61663	Oligonucleotide #2
c2099	15.6	0.2	22	1	AAK61675	Oligonucleotide #3
c2100	15.6	0.2	22	1	AAK61637	Target DNA #14 use
c2105	15.6	0.2	22	1	ACG70452	CD8e/Zns core/shel
c2106	15.6	0.2	22	1	ACD27246	Imobilised captur
c2107	15.6	0.2	22	1	ACD27243	Oligo #3 for struc
c2108	15.6	0.2	22	1	ABK80729	Nanoparticle-asso
c2109	15.6	0.2	22	1	ACD27113	Nanotechnology nuc
c2110	15.6	0.2	22	1	ACD27116	Nanotechnology nuc
c2111	15.6	0.2	22	1	ACD27376	Nanotechnology nuc
c2112	15.6	0.2	22	1	ACD27373	Nanotechnology nuc
c2113	15.6	0.2	22	1	ACD27178	Nanotechnology nuc
c2114	15.6	0.2	22	1	ACD27181	Nanotechnology nuc
c2115	15.6	0.2	22	1	ACD27051	Nanotechnology nuc
c2116	15.6	0.2	22	1	ACD27048	Nanotechnology nuc
c2117	15.6	0.2	22	1	AAK56810	T(13) bio-primer O
c2118	15.6	0.2	22	1	ACH00055	Nanotechnology nuc
c2119	15.6	0.2	22	1	ACH00055	Nanotechnology nuc
c2120	15.6	0.2	22	1	ADA06147	Nanotechnology nuc
c2121	15.6	0.2	22	1	ADA06150	Nanotechnology nuc
c2122	15.6	0.2	22	1	ADA26496	DNA nanolithograph
c2123	15.6	0.2	22	1	ACD14863	Target DNA for qua
c2124	15.6	0.2	22	1	ACD26986	Nanotechnology nuc
c2125	15.6	0.2	22	1	ACD26983	Nanotechnology nuc
c2126	15.6	0.2	22	1	ADG61353	PCR primer W1022 f
c2127	15.6	0.2	22	1	AAQ33511	Sequence of micros
c2128	15.6	0.2	23	1	AAK79433	HLA-DR typing prim
c2129	15.6	0.2	23	1	AAK79436	HLA-DR allele amp
c2130	15.6	0.2	23	1	AAK741806	Cytomegalovirus 1a
c2131	15.6	0.2	23	1	AAV05109	PCR primer SEQ ID
c2132	15.6	0.2	23	1	AAV16642	Primer DR BETA (87
c2133	15.6	0.2	23	1	AAZ01304	PCR primer for PG1
c2134	15.6	0.2	23	1	AAZ25416	Infectious pancrea
c2135	15.6	0.2	23	1	AAZ29413	Forward primer amp
c2136	15.6	0.2	23	1	AAK62742	Endoglucanase PCR
c2137	15.6	0.2	23	1	AAK62750	Endoglucanase PCR
c2138	15.6	0.2	23	1	AAK38463	Murine Notch-1 gen
c2139	15.6	0.2	23	1	AAK38462	Murine Notch-1 gen
c2140	15.6	0.2	23	1	AAK19543	Human Fc-epsilonRI
c2141	15.6	0.2	23	1	AAK99964	Human Fc-epsilonRI
c2142	15.6	0.2	23	1	ABL48583	Human GRID Genebio
c2143	15.6	0.2	23	1	ABL48583	Human GRID Genebio
c2144	15.6	0.2	23	1	ABL48595	Human GRID Genebio
c2145	15.6	0.2	23	1	ABL48571	Human GRID Genebio
c2146	15.6	0.2	23	1	AAK56136	Human SCN5A PCR-S5
c2147	15.6	0.2	23	1	AAK92703	Primer DR beta (87
c2148	15.6	0.2	23	1	AAK73876	Human signal recog
c2149	15.6	0.2	23	1	ABK66428	HIVta/gb intermed
c2150	15.6	0.2	23	1	ABL30942	Human HLA genotyp
c2151	15.6	0.2	23	1	ABL30948	Human HLA genotyp

c2151	15.6	0.2	23	1	ABX95421	Human leukocyte an	c2224	15.6	0.2	24	1	ABQ01125	Oligonucleotide ad
c2152	15.6	0.2	23	1	ABX14428	PCR primer #1 for	c2225	15.6	0.2	24	1	ABA96608	Human hexokinase p
c2153	15.6	0.2	23	1	ADCS8832	Cytokine ampliflyin	c2226	15.6	0.2	24	1	AB160935	Human nucleotide r
c2154	15.6	0.2	23	1	ADCS1352	PCR primer GAG022	c2227	15.6	0.2	24	1	ABY75518	Human tetramerised
c2155	15.6	0.2	23	1	ADCS6895	KRT14 forward qRT-	c2228	15.6	0.2	24	1	ABZ58004	Siencing element
c2156	15.6	0.2	24	1	ABZ23536	fragment of a plas	c2229	15.6	0.2	24	1	ABZ59409	Human fibronectin
c2157	15.6	0.2	24	1	ABA05517	Human Tre carcino	c2230	15.6	0.2	24	1	ABZ83122	Toxicologically re
c2158	15.6	0.2	24	1	ABA99264	Human tra oncogene	c2231	15.6	0.2	24	1	ACD40373	Peptide linker mod
c2159	15.6	0.2	24	1	AA064570	Primer for amplify	c2232	15.6	0.2	24	1	ACD40372	Peptide linker mod
c2160	15.6	0.2	24	1	AA173521	Enterovirus genom	c2233	15.6	0.2	24	1	ABR21430	Multiple group PC
c2161	15.6	0.2	24	1	AA179282	MH0677, a competi	c2234	15.6	0.2	24	1	ABR92923	Screening method r
c2162	15.6	0.2	24	1	AA176347	Human fibronectin	c2235	15.6	0.2	24	1	ABZ81458	Rat bombesin recep
c2163	15.6	0.2	24	1	AAV53719	Nucleotide sequenc	c2236	15.6	0.2	24	1	ABZ93304	Polypeptide-ankyr
c2164	15.6	0.2	24	1	AAV1632	Nucleotide sequenc	c2237	15.6	0.2	24	1	ADA00309	Human alpha-fetop
c2165	15.6	0.2	24	1	AAV1739	Nucleotide sequenc	c2238	15.6	0.2	24	1	ACD68506	Novel human secret
c2166	15.6	0.2	24	1	AAV42871	Stem loop of Bacil	c2239	15.6	0.2	24	1	ACD06888	Single chain varia
c2167	15.6	0.2	24	1	AAV22161	BH3 interacting do	c2240	15.6	0.2	24	1	ACD06887	Single chain varia
c2168	15.6	0.2	24	1	AAV04082	Oligonucleotide MH	c2241	15.6	0.2	24	1	ACH04608	Human secreted/tra
c2169	15.6	0.2	24	1	AAV21662	Human helicase gen	c2242	15.6	0.2	24	1	ACH04612	Single chain varia
c2170	15.6	0.2	24	1	AAV54149	Human fibronectin	c2243	15.6	0.2	24	1	ACD68152	Novel human secret
c2171	15.6	0.2	24	1	AAV00525	Antisense oligonuc	c2244	15.6	0.2	24	1	ACD45098	Self-antigen vacci
c2172	15.6	0.2	24	1	AAV00524	Target sequence #2	c2245	15.6	0.2	24	1	ACD45097	Self-antigen vacci
c2173	15.6	0.2	24	1	AAV33593	Low adenostine ant	c2246	15.6	0.2	24	1	AAV35700	RT-PCR primer 2 is
c2174	15.6	0.2	24	1	AAV60156	PCR primer specifi	c2247	15.6	0.2	24	1	ADB68055	G4 phosphorothioat
c2175	15.6	0.2	24	1	AAV76685	Human PRO1561 PCR	c2248	15.6	0.2	24	1	ADC02727	Ex vivo stem-cell
c2176	15.6	0.2	24	1	AAV19715	Human fibronectin	c2249	15.6	0.2	24	1	ADC18248	Human PRO PCR prim
c2177	15.6	0.2	24	1	AAV37302	Human PRO1561 forw	c2250	15.6	0.2	24	1	ADC51826	GRP8 PCR primer, S
c2178	15.6	0.2	24	1	AAV89978	PCR primer hAPexo	c2251	15.6	0.2	24	1	ADC14154	RPX1 PCR primer, S
c2179	15.6	0.2	24	1	AAV86950	PCR primer used to	c2252	15.6	0.2	24	1	ADD06134	N-acetylglactosam
c2180	15.6	0.2	24	1	AAV72353	Human RecQ4 helica	c2253	15.6	0.2	24	1	ADD24846	Human TPMT mutant
c2181	15.6	0.2	24	1	AAH19006	Forward primer use	c2254	15.6	0.2	24	1	ADD70894	Human secreted/tra
c2182	15.6	0.2	24	1	AAV02986	Human CMHR1 revers	c2255	15.6	0.2	24	1	ADD39971	Human secreted/tra
c2183	15.6	0.2	24	1	AAV54467	DNA encoding prote	c2256	15.6	0.2	24	1	ADD70417	Human secreted/tra
c2184	15.6	0.2	24	1	AAV64915	Beta-transducin 41	c2257	15.6	0.2	24	1	ADD38538	Human secreted/tra
c2185	15.6	0.2	24	1	AAV57997	Nucleic acid tripl	c2258	15.6	0.2	24	1	ADD68286	PCR primer relat
c2186	15.6	0.2	24	1	AAV57998	Nucleic acid tripl	c2259	15.6	0.2	24	1	ADD39494	Human secreted/tra
c2187	15.6	0.2	24	1	AAV57999	Nucleic acid tripl	c2260	15.6	0.2	24	1	ADD39017	Human secreted/tra
c2188	15.6	0.2	24	1	AAV58000	Nucleic acid tripl	c2261	15.6	0.2	24	1	ADD40448	Human secreted/tra
c2189	15.6	0.2	24	1	AAV57996	Nucleic acid tripl	c2262	15.6	0.2	24	1	ADD50659	Human secreted/tra
c2190	15.6	0.2	24	1	AAV58001	Nucleic acid tripl	c2263	15.6	0.2	24	1	ADD20281	Human secreted/tra
c2191	15.6	0.2	24	1	AAH42594	PCR primer used to	c2264	15.6	0.2	24	1	ADD50192	Human secreted/tra
c2192	15.6	0.2	24	1	AAH47567	Human excitatory a	c2265	15.6	0.2	24	1	ADD21750	Human secreted/tra
c2193	15.6	0.2	24	1	AAH49710	Human ATP-depend	c2266	15.6	0.2	26	1	AAV16616	Gaustic acid produ
c2194	15.6	0.2	24	1	AAV62506	Primer #5. Synthe	c2267	15.6	0.2	26	1	AAV93819	Antitumoural phosp
c2195	15.6	0.2	24	1	ABV57917	Rat VgA1/51 PCR pr	c2268	15.6	0.2	29	1	AAV74918	CD40L poly-A tract
c2196	15.6	0.2	24	1	AAH91494	Human inflammatory	c2269	15.6	0.2	29	1	AAV74907	CD40L poly-A tract
c2197	15.6	0.2	24	1	AAH46618	Synthetic oligonuc	c2270	15.6	0.2	29	1	AAV74935	CD40L poly-A tract
c2198	15.6	0.2	24	1	AAH20251	Oligonucleotide SE	c2271	15.6	0.2	29	1	AAV74921	CD40L poly-A tract
c2199	15.6	0.2	24	1	AAH20250	Oligonucleotide SE	c2272	15.6	0.2	29	1	AAV74928	CD40L poly-A tract
c2200	15.6	0.2	24	1	AAV45579	B cell lymphoma CT	c2273	15.6	0.2	30	1	AAV74908	CD40L poly-A tract
c2201	15.6	0.2	24	1	AAV45578	Human helix-describ	c2274	15.6	0.2	30	1	ABV56892	Synthetic deoxyrib
c2202	15.6	0.2	24	1	AAH73961	Human helix-describ	c2275	15.6	0.2	30	1	ABV56890	Synthetic deoxyrib
c2203	15.6	0.2	24	1	AAH56082	Human SN3A PCR-SS	c2276	15.6	0.2	30	1	ABV56889	Synthetic deoxyrib
c2204	15.6	0.2	24	1	AAH46768	Human anion-exchan	c2277	15.6	0.2	30	1	ABV97613	Poly b nucleotide
c2205	15.6	0.2	24	1	AAV67781	Hybrid RNA sequen	c2278	15.6	0.2	30	1	ABA97614	Poly c nucleotide
c2206	15.6	0.2	24	1	AAV67782	Hybrid DNA sequen	c2279	15.6	0.2	30	1	ABA97616	Poly e nucleotide
c2207	15.6	0.2	24	1	AAV57731	Human zinc finger	c2280	15.6	0.2	30	1	ABV95886	Probe poly b for a
c2208	15.6	0.2	24	1	AAV50712	Pseudomonas gluta	c2281	15.6	0.2	30	1	ABV95887	Probe poly c for a
c2209	15.6	0.2	24	1	AAV38044	4-SP4 PCR primer u	c2282	15.6	0.2	30	1	ABV95889	Probe poly e for a
c2210	15.6	0.2	24	1	ABN85224	Human translation	c2283	15.6	0.2	30	1	ADA26181	Rice semi-dwarf (s
c2211	15.6	0.2	24	1	ABO93694	Minimally cross-hy	c2284	15.6	0.2	42	1	AAV27160	Human Machado-Jose
c2212	15.6	0.2	24	1	ABL61603	Human GPR8-related	c2285	15.4	0.2	17	1	AAQ98018	PNA oligomer targ
c2213	15.6	0.2	24	1	ABO78896	Human zinc finger	c2286	15.4	0.2	17	1	AAV53745	Rat ICAM hammerhea
c2214	15.6	0.2	24	1	ABO80847	Tyrosine specific	c2287	15.4	0.2	17	1	AAV56931	HIV-1 proviral DNA
c2215	15.6	0.2	24	1	ABA05437	Human ribosome S6	c2288	15.4	0.2	17	1	AAV70134	Human fil1 VEGF re
c2216	15.6	0.2	24	1	ABA97997	Human mitochondria	c2289	15.4	0.2	17	1	AAV23093	Integrin subunit b
c2217	15.6	0.2	24	1	ABV57119	Human shear protein	c2290	15.4	0.2	17	1	AAV18371	RT-PCR primer of t
c2218	15.6	0.2	24	1	ABV68805	Human gene specifi	c2291	15.4	0.2	17	1	AAV25448	Oestrogen receptor
c2219	15.6	0.2	24	1	ABV94593	G-protein-coupled	c2292	15.4	0.2	17	1	AAV25454	Oestrogen receptor
c2220	15.6	0.2	24	1	ABA03363	B alpha1,2-fucosyl	c2293	15.4	0.2	17	1	AAV91530	DNA-RNA-DNA oligon
c2221	15.6	0.2	24	1	ABO06249	Oligonucleotide ad	c2294	15.4	0.2	17	1	ABT06124	Human light chain
c2222	15.6	0.2	24	1	ABO03462	Oligonucleotide ad	c2295	15.4	0.2	17	1	ABV56672	Human CLCA1 gene e
c2223	15.6	0.2	24	1	ABO06208	Oligonucleotide ad	c2296	15.4	0.2	17	1	AAV44151	Oligo-AT PCR prime

2297	15.4	0.2	17	1	AD504269	Human MD27 scannin	2370	15.4	0.2	20	1	AB289489	Human oligonucleot
2298	15.4	0.2	17	1	AD804878	Human MD212 scanni	2371	15.4	0.2	20	1	AB299051	Human PD34C oligon
2299	15.4	0.2	17	1	AD804877	Human MD212 scanni	2372	15.4	0.2	20	1	AB299440	Human oligonucleot
2300	15.4	0.2	17	1	ADC38428	Human AMLp1b scann	2373	15.4	0.2	20	1	AB299049	Human oligonucleot
2301	15.4	0.2	17	1	ADC37823	Human AMLp1a scann	2374	15.4	0.2	20	1	ABX12893	Human RNase III an
2302	15.4	0.2	17	1	ADC37821	Human AMLp1a scann	2375	15.4	0.2	20	1	ACCT9318	Human apretaxin mu
2303	15.4	0.2	17	1	ADC37819	Human AMLp1a scann	2376	15.4	0.2	20	1	AD444738	Antisense oligonuc
2304	15.4	0.2	17	1	ADC37818	Human AMLp1a scann	2377	15.4	0.2	20	1	ADB24516	Human CYP2D6-relat
2305	15.4	0.2	17	1	ADC37820	Human AMLp1a scann	2378	15.4	0.2	20	1	AB222802	Human heparanase p
2306	15.4	0.2	17	1	ADC38429	Human AMLp1b scann	2379	15.4	0.2	20	1	ABX11809	Canine Cmu positiv
2307	15.4	0.2	17	1	ADC37822	Human AMLp1a scann	2380	15.4	0.2	20	1	ACC45930	Human HBM STS mark
2308	15.4	0.2	18	1	AAQ20108	Cross-linking olig	2381	15.4	0.2	20	1	AB084130	HIV-1 amplificatio
2309	15.4	0.2	18	1	AAQ20108	Cross-linking olig	2382	15.4	0.2	20	1	ACD25678	Human calcium chan
2310	15.4	0.2	18	1	AAQ30446	Oligomer TNFR941 f	2383	15.4	0.2	20	1	ACD27533	Antisense oligonuc
2311	15.4	0.2	18	1	AAQ30448	Oligomer TNFR943 f	2384	15.4	0.2	20	1	ADB98628	Sequence tagged si
2312	15.4	0.2	18	1	AAQ30447	Oligomer TNFR942 f	2385	15.4	0.2	20	1	ADB68682	Microsomal triglyc
2313	15.4	0.2	18	1	AAV54170	Nucleotide sequenc	2386	15.4	0.2	20	1	ADB81657	HIV PRT antisense
2314	15.4	0.2	18	1	AAV54169	Nucleotide sequenc	2387	15.4	0.2	20	1	ADB81656	HIV PRT antisense
2315	15.4	0.2	18	1	AAV54172	Nucleotide sequenc	2388	15.4	0.2	20	1	ADB81658	HIV PRT antisense
2316	15.4	0.2	18	1	AAV54167	Nucleotide sequenc	2389	15.4	0.2	20	1	ADB81655	HIV PRT antisense
2317	15.4	0.2	18	1	AAV54175	PCR primer for Hum	2390	15.4	0.2	21	1	AAQ25453	Purine rich HIV ta
2318	15.4	0.2	18	1	AAV54168	Oligonucleotide ZC	2391	15.4	0.2	21	1	AAQ25454	Purine rich HIV ta
2319	15.4	0.2	18	1	AAV590642	Human adipose t1ss	2392	15.4	0.2	21	1	AAV14800	Primer 6 for 3' po
2320	15.4	0.2	18	1	AAV590640	Human adipose t1ss	2393	15.4	0.2	21	1	AAQ56046	5 to 1 isolat
2321	15.4	0.2	18	1	AAV590645	Human adipose t1ss	2394	15.4	0.2	21	1	AAQ70078	CYP2(487-713) prim
2322	15.4	0.2	18	1	AAV590643	Human adipose t1ss	2395	15.4	0.2	21	1	AAV422886	HIV pol start sequ
2323	15.4	0.2	18	1	AAV58495	Human adipose t1ss	2396	15.4	0.2	21	1	AAV25373	Primer F2 for H. py
2324	15.4	0.2	18	1	ACN05072	PCR primer used to	2397	15.4	0.2	21	1	AAV72523	5-Cys-encoding oli
2325	15.4	0.2	18	1	AD054040	Human TBM7alpha CD	2398	15.4	0.2	21	1	AAV00223	Human folliectatin
2326	15.4	0.2	18	1	ACD28312	Flea Ecdysone rece	2399	15.4	0.2	21	1	AAV75636	Human biallelic ma
2327	15.4	0.2	19	1	AAQ57387	Enzymatic RNA mole	2400	15.4	0.2	21	1	AAV676783	Human biallelic ma
2328	15.4	0.2	19	1	AAQ86354	Mutagenic oligo fo	2401	15.4	0.2	21	1	AAV63478	Oligodeoxynucleoti
2329	15.4	0.2	19	1	AAV48575	Human tub gene pri	2402	15.4	0.2	21	1	AAV63484	Antisense PCR pri
2330	15.4	0.2	19	1	AAV16754	Human tub gene exo	2403	15.4	0.2	21	1	ABK70314	Antisense PCR pri
2331	15.4	0.2	19	1	AAV35929	PCR primer for gra	2404	15.4	0.2	21	1	ABK70358	Synthetic antisens
2332	15.4	0.2	19	1	AAV18566	Primer for ASTH1 p	2405	15.4	0.2	21	1	AB597903	Human UDP-glucuron
2333	15.4	0.2	19	1	AAV287330	Maize cytochrome p	2406	15.4	0.2	21	1	AAV46159	Human ALADIN cDNA
2334	15.4	0.2	19	1	AAV14224	Alpaca/llama CY.M	2407	15.4	0.2	22	1	AAV05634	Primer hdi0103 use
2335	15.4	0.2	19	1	AAV81372	cdk-we-hu ribozyme	2408	15.4	0.2	22	1	AAV789376	PCR primer for Hox
2336	15.4	0.2	19	1	AAV50034	INT PR3 primer for	2409	15.4	0.2	22	1	AAV01250	PCR primer for Hox
2337	15.4	0.2	19	1	AAV80473	ASTH1 polymorphic	2410	15.4	0.2	22	1	AAV61616	Mismatch probe spe
2338	15.4	0.2	19	1	AAV58884	Cdk-we-hu ribozyme	2411	15.4	0.2	22	1	AAV523763	Primer B #16 used
2339	15.4	0.2	19	1	ABK41515	Human CTNN3 exon-	2412	15.4	0.2	22	1	AAV19569	Plasmid pYAC4 5' p
2340	15.4	0.2	19	1	ABZ81965	Microtubule associ	2413	15.4	0.2	22	1	AB559235	Human G-protein cou
2341	15.4	0.2	20	1	AAV41317	Human gene signatu	2414	15.4	0.2	22	1	ABX30787	Candida albicans G
2342	15.4	0.2	20	1	AAV71323	Primer for pUC19 D	2415	15.4	0.2	22	1	AAV183462	PCR primer 3247R u
2343	15.4	0.2	20	1	AAV200499	Human chlorodoxin	2416	15.4	0.2	22	1	ABX47143	Mouse SVO2-1-F1 fo
2344	15.4	0.2	20	1	AAV05711	NF-IL6 promoter se	2417	15.4	0.2	22	1	ABX16068	Yeast pYAC4 PCR pr
2345	15.4	0.2	20	1	AAV289058	Human nibrin PCR p	2418	15.4	0.2	22	1	AD068482	SNP typing-related
2346	15.4	0.2	20	1	AAV289102	Human nibrin PCR p	2419	15.4	0.2	22	1	AD068480	SNP typing-related
2347	15.4	0.2	20	1	AAV25034	NiJegen breakage	2420	15.4	0.2	23	1	AD066235	Human caspase-12 c
2348	15.4	0.2	20	1	AAV14233	Alpaca male-specific	2421	15.4	0.2	23	1	AAV20514	Human peptide tran
2349	15.4	0.2	20	1	AAV271992	Human biallelic ma	2422	15.4	0.2	23	1	ACC44862	Human antibody 146
2350	15.4	0.2	20	1	AAV57011	Human oestrogen re	2423	15.4	0.2	25	1	AD026500	Bacterial PNP DNA
2351	15.4	0.2	20	1	AAV98163	Human IGEBR gene p	2424	15.4	0.2	26	1	AD026899	Bacterial PNP DNA
2352	15.4	0.2	20	1	AAV16233	Human ABCG6 (MRP6)	2425	15.4	0.2	26	1	AAV39650	PolyPNP out-of-fra
2353	15.4	0.2	20	1	AAV91298	Human E2F transacti	2426	15.4	0.2	27	1	AAV43904	M. tuberculosis rpo
2354	15.4	0.2	20	1	AAV80766	Oligonucleotide hy	2427	15.4	0.2	30	1	ABV56891	Synthetic deoxyrib
2355	15.4	0.2	20	1	AAV80767	Oligonucleotide hy	2428	15.4	0.2	30	1	ABV97615	Poly d nucleotide
2356	15.4	0.2	20	1	AAV80765	Oligonucleotide hy	2429	15.4	0.2	30	1	ABV58888	Probe q1 for a
2357	15.4	0.2	20	1	AAV80765	Oligonucleotide hy	2430	15.4	0.2	16	1	AAV44149	Oligo-RT PCR prim
2358	15.4	0.2	20	1	ABV82550	Zmax1 gene region	2431	15.2	0.2	17	1	AAV18388	RT-PCR primer of t
2359	15.4	0.2	20	1	ABV52403	Mouse Flup-C chine	2432	15.2	0.2	17	1	AAV14174	Modified Poly-T pr
2360	15.4	0.2	20	1	ABV74280	Human calcium chan	2433	15.2	0.2	20	1	ABV05917	Hepatitis B virus
2361	15.4	0.2	20	1	ABV79760	Human Fas target o	2434	15.2	0.2	20	1	AAQ52607	EBV target sequenc
2362	15.4	0.2	20	1	ABV76305	Human NOVX coding	2435	15.2	0.2	20	1	AAQ50354	Platelet aggregati
2363	15.4	0.2	20	1	ABV05162	TNFR1 expression m	2436	15.2	0.2	20	1	AAQ71930	Human IL-2R gamma
2364	15.4	0.2	20	1	ABV23347	Human Zmax1 cDNA f	2437	15.2	0.2	20	1	AAQ62081	Lactobacillus 16S/r
2365	15.4	0.2	20	1	ABV74796	Human TNFR2 antis	2438	15.2	0.2	20	1	AAQ79310	Human c-rafi-1 onco
2366	15.4	0.2	20	1	ABV73453	Chimeric phospho	2439	15.2	0.2	20	1	AAQ88215	Lactobacillus sp.
2367	15.4	0.2	20	1	ABV58888	Human RecQ protei	2440	15.2	0.2	20	1	AAQ87041	HPV 18-specific ol
2368	15.4	0.2	20	1	ABV78262	Human bifunctional	2441	15.2	0.2	20	1	AAV10129	Sequence #1 used i
2369	15.4	0.2	20	1	ABZ89718	Human oligonucleot	2442	15.2	0.2	20	1	AAV29999	Human Fas ligand g

2443	15.2	0.2	20	1	AAV03702	Primer SHF-15 for	c2516	15.2	0.2	20	1	ABZ86062	Human oligonucleot
2444	15.2	0.2	20	1	AAV5872	LRPS SNP primer 58	c2517	15.2	0.2	20	1	ABZ86067	Human oligonucleot
2445	15.2	0.2	20	1	AAV58794	LRPS exon primer 5	c2518	15.2	0.2	20	1	ABZ91932	Human oligonucleot
2446	15.2	0.2	20	1	AAV4036	Maie oligonucleot	c2519	15.2	0.2	20	1	ABZ93349	Human oligonucleot
2447	15.2	0.2	20	1	AAZ24530	Human SR-BI gene e	c2520	15.2	0.2	20	1	ABZ85670	Human oligonucleot
2448	15.2	0.2	20	1	AAZ24510	MSH2 gene specific	c2521	15.2	0.2	20	1	ABZ87733	Human oligonucleot
2449	15.2	0.2	20	1	AAZ06123	PCR primer used to	c2522	15.2	0.2	20	1	ABZ86077	Human oligonucleot
2450	15.2	0.2	20	1	AAZ05811	PCR primer used to	c2523	15.2	0.2	20	1	ABZ98588	Human oligonucleot
2451	15.2	0.2	20	1	AAZ05492	PCR primer used to	c2524	15.2	0.2	20	1	ABZ86408	Human oligonucleot
2452	15.2	0.2	20	1	AAZ04381	PCR primer used to	c2525	15.2	0.2	20	1	ABZ88781	Human oligonucleot
2453	15.2	0.2	20	1	AAZ03998	PCR primer used to	c2526	15.2	0.2	20	1	ABZ89873	Human oligonucleot
2454	15.2	0.2	20	1	AAZ00497	Human chlorodoxin	c2527	15.2	0.2	20	1	ABZ97370	Human IL4-R oligon
2455	15.2	0.2	20	1	AAZ93090	PCR primer used to	c2528	15.2	0.2	20	1	ABZ98753	Human tryptase b o
2456	15.2	0.2	20	1	AAZ95676	PCR primer used to	c2529	15.2	0.2	20	1	ABZ90024	Human oligonucleot
2457	15.2	0.2	20	1	AAZ96459	PCR primer used to	c2530	15.2	0.2	20	1	ABZ98885	Human PDE3A oligon
2458	15.2	0.2	20	1	AAZ97516	Primer used to amp	c2531	15.2	0.2	20	1	ABZ86072	Human oligonucleot
2459	15.2	0.2	20	1	AAZ97150	PCR primer used to	c2532	15.2	0.2	20	1	ABZ93216	Human oligonucleot
2460	15.2	0.2	20	1	AAZ93652	PCR primer used to	c2533	15.2	0.2	20	1	ADA19180	Human IL4-R oligon
2461	15.2	0.2	20	1	AAZ24622	Human SR-BI gene e	c2534	15.2	0.2	20	1	ADA66526	Human oligonucleot
2462	15.2	0.2	20	1	AAZ03540	Reverse PCR primer	c2535	15.2	0.2	20	1	ABZ84008	Toxicologically re
2463	15.2	0.2	20	1	AAZ48058	Human IGF-II anti	c2536	15.2	0.2	20	1	ABZ95028	Human bcr-abl gene
2464	15.2	0.2	20	1	AAZ09630	Oligonucleotide Ne	c2537	15.2	0.2	20	1	ABZ10388	Haematopoietic cel
2465	15.2	0.2	20	1	AAZ40047	PCR primer VO3 to	c2538	15.2	0.2	20	1	ABZ43156	Neuroblastoma-rela
2466	15.2	0.2	20	1	AAZ29103	Human mcl-1 anti-a	c2539	15.2	0.2	20	1	ACC80146	VEGFR-2 antisense
2467	15.2	0.2	20	1	AAZ11835	Human MDMX antisen	c2540	15.2	0.2	20	1	ACC80120	VEGFR-2 antisense
2468	15.2	0.2	20	1	AAZ14764	PCR primer used to	c2541	15.2	0.2	20	1	AAZ53968	PCR mutation detec
2469	15.2	0.2	20	1	AAZ87140	Human TRAP100 PCR	c2542	15.2	0.2	20	1	AAZ52676	PCR primer #1 used
2470	15.2	0.2	20	1	AAZ76123	Anti-human Fas ant	c2543	15.2	0.2	20	1	ABZ32311	Neuroblastoma-rela
2471	15.2	0.2	20	1	AAZ56181	Oligonucleotide Al	c2544	15.2	0.2	20	1	ABZ12687	Human IL4/IL-13 r
2472	15.2	0.2	20	1	AAZ62074	Reverse primer use	c2545	15.2	0.2	20	1	ADA45251	Human MSH2 gene PC
2473	15.2	0.2	20	1	AAZ80268	Reverse primer #96	c2546	15.2	0.2	20	1	ACD99727	Immunostimulatory
2474	15.2	0.2	20	1	AAZ56744	Sequence of an oli	c2547	15.2	0.2	20	1	ACD44983	Human SR-BI gene P
2475	15.2	0.2	20	1	AAZ95232	Human cDNA clone-s	c2548	15.2	0.2	20	1	AAZ58181	Cytokine ampliflyin
2476	15.2	0.2	20	1	AAZ15338	Human glycogen syn	c2549	15.2	0.2	20	1	ADB36804	Immunostimulatory
2477	15.2	0.2	20	1	AAZ59877	Human protein kina	c2550	15.2	0.2	20	1	ADB70394	Human CTRBP PCR pr
2478	15.2	0.2	20	1	AAZ77978	PCR primer for a m	c2551	15.2	0.2	20	1	ADB99933	Vitamin D nuclear
2479	15.2	0.2	20	1	AAZ99302	Immunostimulatory	c2552	15.2	0.2	20	1	ADB99933	Baeyer-Villiger re
2480	15.2	0.2	20	1	AAZ28352	DNA oligomer #2.	c2553	15.2	0.2	20	1	ADB61221	Mouse mdm2 antisen
2481	15.2	0.2	20	1	AAZ98984	Pol primer PCRT1 t	c2554	15.2	0.2	20	1	ADB81663	HIV PRT antisense
2482	15.2	0.2	20	1	AAZ982913	Human beta-actin d	c2555	15.2	0.2	20	1	ADB81661	HIV PRT antisense
2483	15.2	0.2	20	1	AAZ98247	C neofortmans stral	c2556	15.2	0.2	20	1	ADB81660	HIV PRT antisense
2484	15.2	0.2	20	1	AAZ99947	Synthetic oligonc	c2557	15.2	0.2	20	1	ADB81659	HIV PRT antisense
2485	15.2	0.2	20	1	AAZ99949	Synthetic oligonc	c2558	15.2	0.2	20	1	ADB80858	ESB gene SNP prime
2486	15.2	0.2	20	1	AAZ80769	Oligonucleotide hy	c2559	15.2	0.2	20	1	ADB43461	Human SNGC sequenc
2487	15.2	0.2	20	1	AAZ80772	Oligonucleotide hy	c2560	15.2	0.2	21	1	AAQ299595	Pol 67/70 region s
2488	15.2	0.2	20	1	AAZ80770	Oligonucleotide hy	c2561	15.2	0.2	21	1	AAQ79231	Guanosine rich oli
2489	15.2	0.2	20	1	AAZ80768	Oligonucleotide hy	c2562	15.2	0.2	21	1	AAZ16460	PCR primer, p53-PP
2490	15.2	0.2	20	1	AAZ98556	Human g protein-co	c2563	15.2	0.2	21	1	AAZ51629	Vital integrase in
2491	15.2	0.2	20	1	AAZ91537	DNA oligonucleotid	c2564	15.2	0.2	21	1	AAZ74344	Oligo for use in p
2492	15.2	0.2	20	1	AAZ06590	Human Her-1 antis	c2565	15.2	0.2	21	1	AAZ95441	Primer for breast
2493	15.2	0.2	20	1	ABK30536	Human glioma-asnoc	c2566	15.2	0.2	21	1	AAZ80147	Immunoglobulin sig
2494	15.2	0.2	20	1	ABK37119	Human lysophosphol	c2567	15.2	0.2	21	1	AAZ79218	Oligonucleotide #1
2495	15.2	0.2	20	1	ABZ77947	Angiogenesis inhbi	c2568	15.2	0.2	21	1	AAZ26573	Human polymorphic
2496	15.2	0.2	20	1	ABZ07450	Rat protein phosph	c2569	15.2	0.2	21	1	AAZ26268	Human polymorphic
2497	15.2	0.2	20	1	ABZ93308	Immunostimulatory	c2570	15.2	0.2	21	1	AAZ26511	Human polymorphic
2498	15.2	0.2	20	1	ABZ99738	Human clusterin in	c2571	15.2	0.2	21	1	AAZ26572	Human polymorphic
2499	15.2	0.2	20	1	ABZ72241	Antisense oligonc	c2572	15.2	0.2	21	1	AAZ26485	Human polymorphic
2500	15.2	0.2	20	1	ABZ31037	Candida albicans G	c2573	15.2	0.2	21	1	AAZ20460	Forward PCR primer
2501	15.2	0.2	20	1	ABZ97649	probe c. Unidenti	c2574	15.2	0.2	21	1	AAZ00040	afGP PCR antisense
2502	15.2	0.2	20	1	ABZ97648	probe s. Unidenti	c2575	15.2	0.2	21	1	AAZ95022	prostate cancer di
2503	15.2	0.2	20	1	ABZ89176	Human JAZF1/JAZ1	c2576	15.2	0.2	21	1	AAZ46283	PCR primer for int
2504	15.2	0.2	20	1	ABZ44428	Human HPK/GCK-like	c2577	15.2	0.2	21	1	AAZ75280	Human biallelic ma
2505	15.2	0.2	20	1	ABZ08503	Bovine leukocyte a	c2578	15.2	0.2	21	1	AAZ72608	Human biallelic ma
2506	15.2	0.2	20	1	AAZ42516	Alpha-V integrin-s	c2579	15.2	0.2	21	1	AAZ76610	Human biallelic ma
2507	15.2	0.2	20	1	ABZ70669	Human hepatocellul	c2580	15.2	0.2	21	1	AAZ60966	Human biallelic ma
2508	15.2	0.2	20	1	ABZ195391	Capture oligonucle	c2581	15.2	0.2	21	1	AAZ80269	Tumour necrosis fa
2509	15.2	0.2	20	1	ABZ194169	Capture oligonucle	c2582	15.2	0.2	21	1	AAZ95320	Reverse primer #97
2510	15.2	0.2	20	1	ABZ023390	Human Trp8 gene am	c2583	15.2	0.2	21	1	AAZ95430	Human gene single
2511	15.2	0.2	20	1	ABZ78238	Human bifunctional	c2584	15.2	0.2	21	1	AAZ96688	Human gene single
2512	15.2	0.2	20	1	ABZ690374	Human oligonucleot	c2585	15.2	0.2	21	1	AAZ22257	Placental growth f
2513	15.2	0.2	20	1	ABZ85597	Human oligonucleot	c2586	15.2	0.2	21	1	AAZ62597	CHRNA7 polymorphis
2514	15.2	0.2	20	1	ABZ88038	Human oligonucleot	c2587	15.2	0.2	21	1	AAZ62143	Solute carrier fam
2515	15.2	0.2	20	1	ABZ89084	Human oligonucleot	c2588	15.2	0.2	21	1	AAZ91825	Human inflammatory

2589	15.2	0.2	21	1	AAAF87033	Anchored 3' oligo	c2662	15.2	0.2	23	1	ADCC02390	Ex vivo stem cell
c2590	15.2	0.2	21	1	ABK51835	DNA probe #1 for h	c2663	15.2	0.2	23	1	ADBE27638	Steroyl-CoA desat
c2591	15.2	0.2	21	1	ABK88538	Human cholecyetoxi	c2664	15.2	0.2	23	1	AAE62506	Primer #5. Synthe
c2592	15.2	0.2	21	1	ABK16848	Human protein refo	c2665	15.2	0.2	24	1	AAH46618	Synthetic oligonuc
c2593	15.2	0.2	21	1	ABZ31311	Candida albicans G	c2666	15.2	0.2	24	1	ABBA03363	B alpha1,2-fucosyl
c2594	15.2	0.2	21	1	ABZ98398	Human multicliding re	c2667	15.2	0.2	27	1	AAAF4926	CD40L poly-A tract
c2595	15.2	0.2	21	1	ABK94358	Endothelin convert	c2668	15.2	0.2	27	1	AAAF4932	CD40L poly-A tract
c2596	15.2	0.2	21	1	ABK94357	Endothelin-1 (BDN-	c2669	15.2	0.2	27	1	AAAF4931	CD40L poly-A tract
c2597	15.2	0.2	21	1	ABK94084	Endothelin-1 (BDN-	c2670	15.2	0.2	27	1	AAAF4934	CD40L poly-A tract
c2598	15.2	0.2	21	1	ABK94083	Murine OAS gene is	c2671	15.2	0.2	28	1	AAAF4920	CD40L poly-A tract
c2599	15.2	0.2	21	1	ABV74830	Mouse BORIS identit	c2672	15.2	0.2	28	1	AAAF4916	CD40L poly-A tract
c2600	15.2	0.2	21	1	ADCT8764	Human gene expressi	c2673	15.2	0.2	28	1	AAAF4927	CD40L poly-A tract
c2601	15.2	0.2	21	1	ADD56481	Mouse beta-actin p	c2674	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2602	15.2	0.2	21	1	ADD90708	Mouse beta-actin p	c2675	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2603	15.2	0.2	21	1	AAQ27806	APP exon 17 primer	c2676	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2604	15.2	0.2	21	1	AAQ78894	Synthetic Scori-Bg	c2677	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2605	15.2	0.2	21	1	AAQ55161	Sequence of PCR pr	c2678	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2606	15.2	0.2	21	1	AAQ93086	Alpha-1,3-GalT pol	c2679	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2607	15.2	0.2	21	1	AAQ78897	Mouse Huntington's	c2680	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2608	15.2	0.2	21	1	AAQ78849	Human cyclin TI PC	c2681	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2609	15.2	0.2	21	1	AAQ99612	Maize c1p gene pr	c2682	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2610	15.2	0.2	21	1	AAQ26493	CDNA transcript re	c2683	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2611	15.2	0.2	21	1	AAZ32687	Human APP exon 17-	c2684	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2612	15.2	0.2	21	1	AAZ37259	PCR primer for AV3	c2685	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2613	15.2	0.2	21	1	AAAC61082	Primer B6K31 used	c2686	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2614	15.2	0.2	21	1	AAAZ9764	H. polymorpha TP81	c2687	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2615	15.2	0.2	21	1	AAAZ94181	Human GABAB-R1a PC	c2688	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2616	15.2	0.2	21	1	AAAC81233	Human tyrosine pho	c2689	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2617	15.2	0.2	21	1	AAAC80270	Reverse primer #98	c2690	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2618	15.2	0.2	21	1	AAH26873	Human prostate spe	c2691	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2619	15.2	0.2	21	1	AAH28299	Mouse nurse cell r	c2692	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2620	15.2	0.2	21	1	AAH28297	3' untranslated re	c2693	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2621	15.2	0.2	21	1	AAH28297	3' untranslated re	c2694	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2622	15.2	0.2	21	1	ABL35693	Immunostimulatory	c2695	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2623	15.2	0.2	21	1	ABK97546	Human LCAT gene fo	c2696	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2624	15.2	0.2	21	1	ABK40406	Probe for gene anal	c2697	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2625	15.2	0.2	21	1	AAI64493	Marmoset Type II G	c2698	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2626	15.2	0.2	21	1	ABE55000	Human lymphoma-spe	c2699	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2627	15.2	0.2	21	1	ABE67627	Mouse casein kinase	c2700	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2628	15.2	0.2	21	1	ABE45313	Human chromosome 1	c2701	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2629	15.2	0.2	21	1	ABO80518	HPB17 reverse PCR	c2702	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2630	15.2	0.2	21	1	ABSS2976	Human IGE receptor	c2703	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2631	15.2	0.2	21	1	ABE71631	T cell receptor (T	c2704	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2632	15.2	0.2	21	1	AAE67914	Human MPO-110 cDNA	c2705	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2633	15.2	0.2	21	1	ABK55618	Human NOV3a RT-PCR	c2706	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2634	15.2	0.2	21	1	ACD19520	Novel human proteol	c2707	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2635	15.2	0.2	21	1	ACF03609	Human NOV8 forward	c2708	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2636	15.2	0.2	21	1	ACCS8206	PCR primer used in	c2709	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2637	15.2	0.2	21	1	ACF57219	Human LAMB3 forward	c2710	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2638	15.2	0.2	21	1	ADB81310	PCR primer 9 used	c2711	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2639	15.2	0.2	21	1	ADC10255	Human NOVX polyep	c2712	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2640	15.2	0.2	21	1	ADB76823	Pfisteria shumway	c2713	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2641	15.2	0.2	21	1	ADE15462	T cell receptor va	c2714	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2642	15.2	0.2	21	1	AAT05666	PCR primer for nuc	c2715	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2643	15.2	0.2	21	1	AAE63128	Glutathione S-tran	c2716	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2644	15.2	0.2	21	1	AAV57842	Human chromosome 1	c2717	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2645	15.2	0.2	21	1	AAV64634	PCR primer for amp	c2718	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2646	15.2	0.2	21	1	AAV55546	PCR primer for cre	c2719	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2647	15.2	0.2	21	1	AAK00262	TNF microsatellite	c2720	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2648	15.2	0.2	21	1	AAI18542	Deleted INC carcino	c2721	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2649	15.2	0.2	21	1	AAAI3773	Deleted GST promot	c2722	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2650	15.2	0.2	21	1	AAI59333	PCR primer used to	c2723	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2651	15.2	0.2	21	1	AAH19012	Reverse primer #99	c2724	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2652	15.2	0.2	21	1	AAH19012	Forward primer use	c2725	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2653	15.2	0.2	21	1	AAI76321	Human TNFC microsa	c2726	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2654	15.2	0.2	21	1	AAI26655	Human TNFC microsa	c2727	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2655	15.2	0.2	21	1	AAH99915	Human alpha4 integ	c2728	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2656	15.2	0.2	21	1	AAH85127	R. anaerobicifera O	c2729	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2657	15.2	0.2	21	1	ABE73976	Interleukin-3 muta	c2730	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2658	15.2	0.2	21	1	ACA60764	Double TCF binding	c2731	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2659	15.2	0.2	21	1	ABT17614	Invasive detection	c2732	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2660	15.2	0.2	21	1	ABZ57960	Human respiratory	c2733	15.2	0.2	29	1	AAAF4927	C. perfringens bet
c2661	15.2	0.2	21	1	ADC03090	Ex vivo stem-cell	c2734	15.2	0.2	29	1	AAAF4927	C. perfringens bet

2735	15	0.2	15	1	AAD29506	Primer used for th
2736	15	0.2	15	1	AA022531	Reverse primer
2737	15	0.2	15	1	AB082140	Accipiter vector PH
2738	15	0.2	15	1	ABX00240	Hepatitis C virus
2739	15	0.2	15	1	ABX03406	Hepatitis C virus
2740	15	0.2	15	1	ABX57064	Hydrazide precursor
2741	15	0.2	15	1	ABX57064	Hydrazide precursor
2742	15	0.2	15	1	ABX57064	Hydrazide precursor
2743	15	0.2	15	1	ABX57064	Hydrazide precursor
2744	15	0.2	15	1	ABX57064	Hydrazide precursor
2745	15	0.2	15	1	ABX57064	Hydrazide precursor
2746	15	0.2	15	1	ABX57064	Hydrazide precursor
2747	15	0.2	15	1	ABX57064	Hydrazide precursor
2748	15	0.2	15	1	ABX57064	Hydrazide precursor
2749	15	0.2	15	1	ABX57064	Hydrazide precursor
2750	15	0.2	15	1	ABX57064	Hydrazide precursor
2751	15	0.2	15	1	ABX57064	Hydrazide precursor
2752	15	0.2	15	1	ABX57064	Hydrazide precursor
2753	15	0.2	15	1	ABX57064	Hydrazide precursor
2754	15	0.2	15	1	ABX57064	Hydrazide precursor
2755	15	0.2	15	1	ABX57064	Hydrazide precursor
2756	15	0.2	15	1	ABX57064	Hydrazide precursor
2757	15	0.2	15	1	ABX57064	Hydrazide precursor
2758	15	0.2	15	1	ABX57064	Hydrazide precursor
2759	15	0.2	15	1	ABX57064	Hydrazide precursor
2760	15	0.2	15	1	ABX57064	Hydrazide precursor
2761	15	0.2	15	1	ABX57064	Hydrazide precursor
2762	15	0.2	15	1	ABX57064	Hydrazide precursor
2763	15	0.2	15	1	ABX57064	Hydrazide precursor
2764	15	0.2	15	1	ABX57064	Hydrazide precursor
2765	15	0.2	15	1	ABX57064	Hydrazide precursor
2766	15	0.2	15	1	ABX57064	Hydrazide precursor
2767	15	0.2	15	1	ABX57064	Hydrazide precursor
2768	15	0.2	15	1	ABX57064	Hydrazide precursor
2769	15	0.2	15	1	ABX57064	Hydrazide precursor
2770	15	0.2	15	1	ABX57064	Hydrazide precursor
2771	15	0.2	15	1	ABX57064	Hydrazide precursor
2772	15	0.2	15	1	ABX57064	Hydrazide precursor
2773	15	0.2	15	1	ABX57064	Hydrazide precursor
2774	15	0.2	15	1	ABX57064	Hydrazide precursor
2775	15	0.2	15	1	ABX57064	Hydrazide precursor
2776	15	0.2	15	1	ABX57064	Hydrazide precursor
2777	15	0.2	15	1	ABX57064	Hydrazide precursor
2778	15	0.2	15	1	ABX57064	Hydrazide precursor
2779	15	0.2	15	1	ABX57064	Hydrazide precursor
2780	15	0.2	15	1	ABX57064	Hydrazide precursor
2781	15	0.2	15	1	ABX57064	Hydrazide precursor
2782	15	0.2	15	1	ABX57064	Hydrazide precursor
2783	15	0.2	15	1	ABX57064	Hydrazide precursor
2784	15	0.2	15	1	ABX57064	Hydrazide precursor
2785	15	0.2	15	1	ABX57064	Hydrazide precursor
2786	15	0.2	15	1	ABX57064	Hydrazide precursor
2787	15	0.2	15	1	ABX57064	Hydrazide precursor
2788	15	0.2	15	1	ABX57064	Hydrazide precursor
2789	15	0.2	15	1	ABX57064	Hydrazide precursor
2790	15	0.2	15	1	ABX57064	Hydrazide precursor
2791	15	0.2	15	1	ABX57064	Hydrazide precursor
2792	15	0.2	15	1	ABX57064	Hydrazide precursor
2793	15	0.2	15	1	ABX57064	Hydrazide precursor
2794	15	0.2	15	1	ABX57064	Hydrazide precursor
2795	15	0.2	15	1	ABX57064	Hydrazide precursor
2796	15	0.2	15	1	ABX57064	Hydrazide precursor
2797	15	0.2	15	1	ABX57064	Hydrazide precursor
2798	15	0.2	15	1	ABX57064	Hydrazide precursor
2799	15	0.2	15	1	ABX57064	Hydrazide precursor
2800	15	0.2	15	1	ABX57064	Hydrazide precursor
2801	15	0.2	15	1	ABX57064	Hydrazide precursor
2802	15	0.2	15	1	ABX57064	Hydrazide precursor
2803	15	0.2	15	1	ABX57064	Hydrazide precursor
2804	15	0.2	15	1	ABX57064	Hydrazide precursor
2805	15	0.2	15	1	ABX57064	Hydrazide precursor
2806	15	0.2	15	1	ABX57064	Hydrazide precursor
2807	15	0.2	15	1	ABX57064	Hydrazide precursor

2881	15	0.2	23	1	ABK52683	Human GPCR promotr	c2954	14.8	0.2	19	1	AA065640	Human APLP primer
c2882	15	0.2	23	1	ABK68382	Tomato senescence-	2955	14.8	0.2	19	1	AA542915	Human G protein-Co
c2883	15	0.2	23	1	ABK95525	Novel G-protein co	2956	14.8	0.2	19	1	AA083562	DNA synthesis meth
c2884	15	0.2	23	1	ABK95525	Novel G-protein co	2957	14.8	0.2	19	1	AA083562	Cdc25 hs ribozyme
c2885	15	0.2	23	1	ABK95525	Novel G-protein co	2958	14.8	0.2	19	1	AA083562	Cell-cycle depende
c2886	15	0.2	23	1	ABK67730	Novel transglutami	2959	14.8	0.2	19	1	AA083562	Cdc25 hs ribozyme
c2887	15	0.2	23	1	ABK95525	Novel G-protein co	2960	14.8	0.2	19	1	AA083562	PCR primer P4 used
c2888	15	0.2	23	1	ABK95525	Novel G-protein co	2961	14.8	0.2	19	1	AA083562	HIV-1 related bind
c2889	15	0.2	23	1	ABK95525	Novel G-protein co	2962	14.8	0.2	19	1	AA083562	Probe d. Unident
c2890	15	0.2	23	1	ABK95525	Novel G-protein co	2963	14.8	0.2	19	1	AA083562	TNF alpha PCR prim
c2891	15	0.2	23	1	ABK95525	Novel G-protein co	2964	14.8	0.2	19	1	AA083562	Human PKC-alpha sh
c2892	15	0.2	23	1	ABK95525	Novel G-protein co	2965	14.8	0.2	19	1	AA083562	Human PKC-alpha sh
c2893	15	0.2	23	1	ABK95525	Novel G-protein co	2966	14.8	0.2	19	1	AA083562	Stearyl-CoA desat
c2894	15	0.2	24	1	ABK95525	Novel G-protein co	2967	14.8	0.2	19	1	AA083562	Stearyl-CoA desat
c2895	15	0.2	24	1	ABK95525	Novel G-protein co	2968	14.8	0.2	19	1	AA083562	Probe pool Lf1 to
c2896	15	0.2	24	1	ABK95525	Novel G-protein co	2969	14.8	0.2	19	1	AA083562	Probe NN-D for use
c2897	15	0.2	24	1	ABK95525	Novel G-protein co	2970	14.8	0.2	19	1	AA083562	Probe NN-B for use
c2898	15	0.2	24	1	ABK95525	Novel G-protein co	2971	14.8	0.2	19	1	AA083562	Probe Lf-1 for CDN
c2899	15	0.2	24	1	ABK95525	Novel G-protein co	2972	14.8	0.2	19	1	AA083562	Oligonucleotide #9
c2900	15	0.2	24	1	ABK95525	Novel G-protein co	2973	14.8	0.2	19	1	AA083562	PCR primer #55 for
c2901	15	0.2	24	1	ABK95525	Novel G-protein co	2974	14.8	0.2	19	1	AA083562	NANB hepatitis vir
c2902	15	0.2	25	1	ABK95525	Novel G-protein co	2975	14.8	0.2	19	1	AA083562	NANB hepatitis vir
c2903	15	0.2	25	1	ABK95525	Novel G-protein co	2976	14.8	0.2	19	1	AA083562	NANB hepatitis vir
c2904	15	0.2	25	1	ABK95525	Novel G-protein co	2977	14.8	0.2	19	1	AA083562	Amyloid precursor
c2905	15	0.2	26	1	ABK95525	Novel G-protein co	2978	14.8	0.2	19	1	AA083562	PNA oligomer targe
c2906	15	0.2	26	1	ABK95525	Novel G-protein co	2979	14.8	0.2	19	1	AA083562	Human gene signatu
c2907	15	0.2	26	1	ABK95525	Novel G-protein co	2980	14.8	0.2	19	1	AA083562	Factor XIII subun
c2908	15	0.2	27	1	ABK95525	Novel G-protein co	2981	14.8	0.2	19	1	AA083562	Human vascular end
c2909	15	0.2	29	1	ABK95525	Novel G-protein co	2982	14.8	0.2	19	1	AA083562	Human vascular end
c2910	15	0.2	30	1	ABK95525	Novel G-protein co	2983	14.8	0.2	19	1	AA083562	Human vascular end
c2911	15	0.2	30	1	ABK95525	Novel G-protein co	2984	14.8	0.2	19	1	AA083562	Oligonucleotide H-
c2912	15	0.2	30	1	ABK95525	Novel G-protein co	2985	14.8	0.2	19	1	AA083562	Oligonucleotide E3
c2913	15	0.2	30	1	ABK95525	Novel G-protein co	2986	14.8	0.2	19	1	AA083562	Oligonucleotide E3
c2914	15	0.2	30	1	ABK95525	Novel G-protein co	2987	14.8	0.2	19	1	AA083562	LRP5 SNP primer 58
c2915	15	0.2	30	1	ABK95525	Novel G-protein co	2988	14.8	0.2	19	1	AA083562	Zea maize genome re
c2916	15	0.2	30	1	ABK95525	Novel G-protein co	2989	14.8	0.2	19	1	AA083562	Antisense MDRI oli
c2917	15	0.2	30	1	ABK95525	Novel G-protein co	2990	14.8	0.2	19	1	AA083562	Rat c-Fos protein
c2918	15	0.2	30	1	ABK95525	Novel G-protein co	2991	14.8	0.2	19	1	AA083562	Antisense oligonuc
c2919	15	0.2	30	1	ABK95525	Novel G-protein co	2992	14.8	0.2	19	1	AA083562	Human prostate can
c2920	15	0.2	30	1	ABK95525	Novel G-protein co	2993	14.8	0.2	19	1	AA083562	Prostate disease m
c2921	15	0.2	30	1	ABK95525	Novel G-protein co	2994	14.8	0.2	19	1	AA083562	Human osteopontin
c2922	15	0.2	30	1	ABK95525	Novel G-protein co	2995	14.8	0.2	19	1	AA083562	PCR primer used to
c2923	15	0.2	30	1	ABK95525	Novel G-protein co	2996	14.8	0.2	19	1	AA083562	PCR primer used to
c2924	15	0.2	30	1	ABK95525	Novel G-protein co	2997	14.8	0.2	19	1	AA083562	PCR primer used to
c2925	15	0.2	30	1	ABK95525	Novel G-protein co	2998	14.8	0.2	19	1	AA083562	PCR primer used to
c2926	15	0.2	30	1	ABK95525	Novel G-protein co	2999	14.8	0.2	19	1	AA083562	PCR primer used to
c2927	15	0.2	30	1	ABK95525	Novel G-protein co	3000	14.8	0.2	19	1	AA083562	PCR primer used to
c2928	15	0.2	30	1	ABK95525	Novel G-protein co	3001	14.8	0.2	19	1	AA083562	PCR primer used to
c2929	15	0.2	30	1	ABK95525	Novel G-protein co	3002	14.8	0.2	19	1	AA083562	Antisense oligonuc
c2930	15	0.2	30	1	ABK95525	Novel G-protein co	3003	14.8	0.2	19	1	AA083562	Human ABC1 gene ex
c2931	15	0.2	30	1	ABK95525	Novel G-protein co	3004	14.8	0.2	19	1	AA083562	PI3K antisense inh
c2932	15	0.2	30	1	ABK95525	Novel G-protein co	3005	14.8	0.2	19	1	AA083562	Primer used to amp
c2933	15	0.2	30	1	ABK95525	Novel G-protein co	3006	14.8	0.2	19	1	AA083562	Primer specific fo
c2934	15	0.2	30	1	ABK95525	Novel G-protein co	3007	14.8	0.2	19	1	AA083562	Human TRPC7 gene i
c2935	15	0.2	30	1	ABK95525	Novel G-protein co	3008	14.8	0.2	19	1	AA083562	Human biallelic ma
c2936	15	0.2	30	1	ABK95525	Novel G-protein co	3009	14.8	0.2	19	1	AA083562	Murine IL-5 antise
c2937	15	0.2	30	1	ABK95525	Novel G-protein co	3010	14.8	0.2	19	1	AA083562	Human fira-1 mRNA a
c2938	15	0.2	30	1	ABK95525	Novel G-protein co	3011	14.8	0.2	19	1	AA083562	Ribonucleotide red
c2939	15	0.2	30	1	ABK95525	Novel G-protein co	3012	14.8	0.2	19	1	AA083562	Dog genomic marker
c2940	15	0.2	30	1	ABK95525	Novel G-protein co	3013	14.8	0.2	19	1	AA083562	Dog genomic marker
c2941	15	0.2	30	1	ABK95525	Novel G-protein co	3014	14.8	0.2	19	1	AA083562	Antisense IGFBP-5
c2942	15	0.2	30	1	ABK95525	Novel G-protein co	3015	14.8	0.2	19	1	AA083562	Human alpha (1) co
c2943	15	0.2	30	1	ABK95525	Novel G-protein co	3016	14.8	0.2	19	1	AA083562	Human alpha (1) co
c2944	15	0.2	30	1	ABK95525	Novel G-protein co	3017	14.8	0.2	19	1	AA083562	Sequencing primer
c2945	15	0.2	30	1	ABK95525	Novel G-protein co	3018	14.8	0.2	19	1	AA083562	Human Bcl-2 prome
c2946	15	0.2	30	1	ABK95525	Novel G-protein co	3019	14.8	0.2	19	1	AA083562	Human interleukin-
c2947	15	0.2	30	1	ABK95525	Novel G-protein co	3020	14.8	0.2	19	1	AA083562	Human intereukin-
c2948	15	0.2	30	1	ABK95525	Novel G-protein co	3021	14.8	0.2	19	1	AA083562	Biomarker UC band
c2949	15	0.2	30	1	ABK95525	Novel G-protein co	3022	14.8	0.2	19	1	AA083562	Oligonucleotide fo
c2950	15	0.2	30	1	ABK95525	Novel G-protein co	3023	14.8	0.2	19	1	AA083562	Human E2F transcri
c2951	15	0.2	30	1	ABK95525	Novel G-protein co	3024	14.8	0.2	19	1	AA083562	Hypersensitive rea
c2952	15	0.2	30	1	ABK95525	Novel G-protein co	3025	14.8	0.2	19	1	AA083562	Human biallelic ma
c2953	15	0.2	30	1	ABK95525	Novel G-protein co	3026	14.8	0.2	19	1	AA083562	Human biallelic ma

3027	14.8	0.2	20	1	AAH46128	Human CLCA1 sequen	3100	14.8	0.2	21	1	AAT11723	Polycystic kidney
3028	14.8	0.2	20	1	AA500329	Primer c816F, used	3101	14.8	0.2	21	1	AAT86043	Primer p7 amplifie
3029	14.8	0.2	20	1	AAH80771	Oligonucleotide by	3102	14.8	0.2	21	1	AAV62909	Human galactokinase
3030	14.8	0.2	20	1	ABR85841	Murine G protein-c	3103	14.8	0.2	21	1	AAV20817	Primer for Human h
3031	14.8	0.2	20	1	ABR34887	Fat regulated gene	3104	14.8	0.2	21	1	AAZ26119	Human polymorphic
3032	14.8	0.2	20	1	AA597790	Murine SACL gene-s	3105	14.8	0.2	21	1	AAZ26693	Human polymorphic
3033	14.8	0.2	20	1	AA597594	Murine SACL gene-s	3106	14.8	0.2	21	1	AA35653	PCR primer used to
3034	14.8	0.2	20	1	AA597784	Murine SACL gene-s	3107	14.8	0.2	21	1	AA35653	PCR primer for tel
3035	14.8	0.2	20	1	AA597786	Murine SACL gene-s	3108	14.8	0.2	21	1	AA35653	Reverse primer cna
3036	14.8	0.2	20	1	ABX37182	Human lysophosphol	3109	14.8	0.2	21	1	AA228937	PCR primer hpl-629
3037	14.8	0.2	20	1	ABN83847	Insulin gene -2221	3110	14.8	0.2	21	1	AA75055	Human hpl-629
3038	14.8	0.2	20	1	AB574284	Human calcium chan	3111	14.8	0.2	21	1	AA272700	Human diallelic ma
3039	14.8	0.2	20	1	ABA50030	Oestrogen receptor	3112	14.8	0.2	21	1	AA63845	PCR primer used to
3040	14.8	0.2	20	1	AAJ36736	Human Lp-PLA2 gene	3113	14.8	0.2	21	1	AA63845	PCR primer used to
3041	14.8	0.2	20	1	ABR67644	probe o. Unidenti	3114	14.8	0.2	21	1	AA63845	Human gene single
3042	14.8	0.2	20	1	ABA97650	probe u. Unidenti	3115	14.8	0.2	21	1	AA63845	Human gene single
3043	14.8	0.2	20	1	AB516663	Human Inhibitor of	3116	14.8	0.2	21	1	AA63845	Human gene single
3044	14.8	0.2	20	1	ABL94386	Mouse c/EBP beta p	3117	14.8	0.2	21	1	AA63845	Human gene single
3045	14.8	0.2	20	1	AB193710	Capture oligonucle	3118	14.8	0.2	21	1	AA63845	Human gene single
3046	14.8	0.2	20	1	AB194356	Capture oligonucle	3119	14.8	0.2	21	1	AA63845	PCR primer for cDN
3047	14.8	0.2	20	1	ABR28754	Human CDC14 gene d	3120	14.8	0.2	21	1	AA63845	PCR primer for mec
3048	14.8	0.2	20	1	AB556505	PCR primer CX30-83	3121	14.8	0.2	21	1	AA63845	PCR primer for mec
3049	14.8	0.2	20	1	AB087739	Human ESRI exon 8.	3122	14.8	0.2	21	1	AA63845	Human genetic mark
3050	14.8	0.2	20	1	AA147461	Human MTHFR gene p	3123	14.8	0.2	21	1	AA63845	Primer for breast
3051	14.8	0.2	20	1	AA147461	Porcine CD 151 cod	3124	14.8	0.2	21	1	AA63845	Human polymorphic
3052	14.8	0.2	20	1	AB292414	Human oligonucleot	3125	14.8	0.2	21	1	AA63845	Human genetic mark
3053	14.8	0.2	20	1	AB292635	Human oligonucleot	3126	14.8	0.2	21	1	AA63845	Human genetic mark
3054	14.8	0.2	20	1	AB298845	Human oligonucleot	3127	14.8	0.2	21	1	AA63845	Class VII ribozyme
3055	14.8	0.2	20	1	AB290375	Human oligonucleot	3128	14.8	0.2	21	1	AA63845	Class I-XII ribozyme
3056	14.8	0.2	20	1	AB287286	Human oligonucleot	3129	14.8	0.2	21	1	AA63845	Class I-XII ribozyme
3057	14.8	0.2	20	1	AB287732	Human oligonucleot	3130	14.8	0.2	21	1	AA63845	Class I-XII ribozyme
3058	14.8	0.2	20	1	AB287605	Human oligonucleot	3131	14.8	0.2	21	1	AA63845	Class I-XII ribozyme
3059	14.8	0.2	20	1	AB293723	Human CCR3 oligon	3132	14.8	0.2	21	1	AA63845	Rice PCR primer SE
3060	14.8	0.2	20	1	AB293220	Human oligonucleot	3133	14.8	0.2	21	1	AA63845	Synthetic antisens
3061	14.8	0.2	20	1	AB286603	Human oligonucleot	3134	14.8	0.2	21	1	AA63845	Plant vector PCR p
3062	14.8	0.2	20	1	AB290434	Human oligonucleot	3135	14.8	0.2	21	1	AA63845	Human LDB-like pr
3063	14.8	0.2	20	1	AB290042	Human oligonucleot	3136	14.8	0.2	21	1	AA63845	Human proteolipid,
3064	14.8	0.2	20	1	AB285315	Human oligonucleot	3137	14.8	0.2	21	1	AA63845	Molecular beacon t
3065	14.8	0.2	20	1	AB293982	Human oligonucleot	3138	14.8	0.2	21	1	AA63845	Fluorescent-oligon
3066	14.8	0.2	20	1	AB298928	Human PDE4A oligon	3139	14.8	0.2	21	1	AA63845	Human lactoferrin
3067	14.8	0.2	20	1	AB288693	Human oligonucleot	3140	14.8	0.2	21	1	AA63845	Bacteriophage lamb
3068	14.8	0.2	20	1	AB291491	Human oligonucleot	3141	14.8	0.2	21	1	AA63845	NOV15 forward PCR
3069	14.8	0.2	20	1	AB293213	Human oligonucleot	3142	14.8	0.2	21	1	AA63845	Human genomic DNA
3070	14.8	0.2	20	1	AB292117	Human oligonucleot	3143	14.8	0.2	21	1	AA63845	Human genomic DNA
3071	14.8	0.2	20	1	AC622235	Mouse alipoprotein	3144	14.8	0.2	21	1	AA63845	Human GALT 8 speci
3072	14.8	0.2	20	1	AB277000	Bovine DGAT PCR pr	3145	14.8	0.2	21	1	AA63845	HBV ribozyme sube
3073	14.8	0.2	20	1	AB276933	Bovine DGAT BXC-DN	3146	14.8	0.2	21	1	AA63845	Caenorhabditis ele
3074	14.8	0.2	20	1	AB174193	Mouse short hetero	3147	14.8	0.2	21	1	AA63845	Human G-protein co
3075	14.8	0.2	20	1	AB270582	Insulin gene VNTR	3148	14.8	0.2	21	1	AA63845	Human G-protein co
3076	14.8	0.2	20	1	AC47290	Human apolipoprotei	3149	14.8	0.2	21	1	AA63845	Short interfering
3077	14.8	0.2	20	1	ABX04339	Mouse interleukin	3150	14.8	0.2	21	1	AA63845	Human src biomark
3078	14.8	0.2	20	1	ABX17732	Human urokinase pl	3151	14.8	0.2	21	1	AA63845	Human src biomark
3079	14.8	0.2	20	1	AA533839	EMPIA exon 8 spec	3152	14.8	0.2	21	1	AA63845	Stearoyl-CoA dease
3080	14.8	0.2	20	1	AA533846	PCR primer #3 used	3153	14.8	0.2	21	1	AA63845	Human NOVX reverse
3081	14.8	0.2	20	1	AC68760	Human VEGFR-1 chim	3154	14.8	0.2	22	1	AA63845	Human Huntington's
3082	14.8	0.2	20	1	ABX3775	Sequencing primer	3155	14.8	0.2	22	1	AA63845	Primer 6 for sequ
3083	14.8	0.2	20	1	AA161734	Human PCTAIRE prot	3156	14.8	0.2	22	1	AA63845	Primer for sequen
3084	14.8	0.2	20	1	ACD55682	Human calcium chan	3157	14.8	0.2	22	1	AA63845	PCR primer pi used
3085	14.8	0.2	20	1	AB144169	Chimeric antisense	3158	14.8	0.2	22	1	AA63845	PCR primer used to
3086	14.8	0.2	20	1	AA566488	Human ephrin-A2 cd	3159	14.8	0.2	22	1	AA63845	HLA class I gene s
3087	14.8	0.2	20	1	AA566486	Human ephrin-A2 cd	3160	14.8	0.2	22	1	AA63845	HLA class I gene s
3088	14.8	0.2	20	1	ACF36185	Delta constant re	3161	14.8	0.2	22	1	AA63845	Mahogany protein g
3089	14.8	0.2	20	1	AD37131	CK1s forward prime	3162	14.8	0.2	22	1	AA63845	Human PRO12 hybr
3090	14.8	0.2	20	1	ADD20586	Oreochromis niloti	3163	14.8	0.2	22	1	AA63845	Mouse wound healin
3091	14.8	0.2	20	1	AA622234	Human haematopoiet	3164	14.8	0.2	22	1	AA63845	Human CYP2C181 PCR
3092	14.8	0.2	20	1	ADD42189	Human infertility	3165	14.8	0.2	22	1	AA63845	Reverse transcript
3093	14.8	0.2	20	1	ADD81662	HIV PRT antisense	3166	14.8	0.2	22	1	AA63845	SNP specific upper
3094	14.8	0.2	20	1	AD39777	Porcine CD 151 rel	3167	14.8	0.2	22	1	AA63845	SNP specific upper
3095	14.8	0.2	20	1	AD39777	Reverse Aq4809 RT-	3168	14.8	0.2	22	1	AA63845	Human GSTT1+0 3187
3096	14.8	0.2	21	1	AA050784	HBV target sequenc	3169	14.8	0.2	22	1	AA63845	Human G-protein co
3097	14.8	0.2	21	1	AA055789	Type II procollage	3170	14.8	0.2	22	1	AA63845	Human TNF-receptor
3098	14.8	0.2	21	1	AA055255	Grapevine 5S rDNA	3171	14.8	0.2	22	1	AA63845	Rat Atp RT PCR pro
3099	14.8	0.2	21	1	AA116749	E.coli tRNA(Pro) a	3172	14.8	0.2	22	1	AA63845	Mouse HyPLI1 locu

3173	14.8	0.2	22	1	ABO88519	Human, GPCR, revers
3174	14.8	0.2	22	1	ABX09454	Arteriosclerosis-d
3175	14.8	0.2	22	1	ABX97168	Human CYP4501A2 pr
3176	14.8	0.2	22	1	ABX71248	Mouse HYP1LPI1 locu
3177	14.8	0.2	22	1	ABK15346	Cyclooxxygenase-2 (
3178	14.8	0.2	22	1	ACA54762	Human NF-kappaB as
3179	14.8	0.2	22	1	ADA05936	Human NOVX reverse
3180	14.8	0.2	22	1	ACD02547	PCR primer #2 for
3181	14.8	0.2	22	1	ADAI5387	Mouse HYP1LPI1 locu
3182	14.8	0.2	22	1	ADB95949	Mouse HYP1LPI1 PCR
3183	14.8	0.2	22	1	ADC84386	Human papillomavir
3184	14.8	0.2	22	1	ADC98229	Mouse type I hair
3185	14.8	0.2	22	1	ADBA47875	Human NOVX forward
3186	14.8	0.2	22	1	ADBA47875	Human NOVX forward
3187	14.8	0.2	26	1	AAAT70276	Sequence of sc1881
3188	14.8	0.2	26	1	AAAT70275	SS probe MRC059.
3189	14.8	0.2	26	1	AAAN92241	SS probe MRC060.
3190	14.8	0.2	26	1	AAAN92242	CDNA library produ
3191	14.8	0.2	26	1	AAAT7536	Human full length
3192	14.8	0.2	26	1	AAAD03682	Primer #4. Undlen
3193	14.8	0.2	26	1	AAAT23526	Human secreted sal
3194	14.8	0.2	26	1	AAAS20596	Human secreted sal
3195	14.8	0.2	26	1	ABSS52638	ZC7764 primer use
3196	14.8	0.2	26	1	AAAD45055	Human zalphali Lig
3197	14.8	0.2	26	1	AAAS20671	Primer #2 used to
3198	14.8	0.2	26	1	AAAD3853	Oligodeoxynucleic
3199	14.8	0.2	26	1	ABX24784	Human zslg63 PCR/s
3200	14.8	0.2	26	1	ABX93599	Oligo (dT) primer
3201	14.8	0.2	26	1	ACA62282	Anchored poly T RT
3202	14.8	0.2	27	1	AAAV1935	p1uescriptesK+ pha
3203	14.8	0.2	28	1	AAAA0358	Deoxy-T22-tagged s
3204	14.8	0.2	28	1	AAAF0856	RNA oligonucleotid
3205	14.8	0.2	28	1	AAAF0450	Puromycin linker D
3206	14.8	0.2	28	1	AAAF45359	AFC binding protei
3207	14.8	0.2	30	1	AAAF26222	Aminoacylation RNA
3208	14.8	0.2	30	1	ADCI6682	Porphyrin yezensis
3209	14.8	0.2	33	1	AAI44170	Human APEB1 gene,
3210	14.6	0.2	15	1	ABK32799	UDP-glucose:thiohy
3211	14.6	0.2	20	1	AAAT6167	Leishmania kinetop
3212	14.6	0.2	20	1	ABN83985	CP-1 (synthetic DN
3213	14.6	0.2	21	1	AAQ03091	Oligonucleotide pr
3214	14.6	0.2	21	1	AAAT10743	3' ribonucleoside
3215	14.6	0.2	21	1	AAAG1302	Reverse transcript
3216	14.6	0.2	21	1	AAQ75780	Reverse transcript
3217	14.6	0.2	21	1	AAQ75761	Human polymorphic
3218	14.6	0.2	21	1	AAZ26485	Oligonucleotide fo
3219	14.6	0.2	21	1	AAO13763	Oligo #10 hybridis
3220	14.6	0.2	21	1	AAO14885	HDA type analysis
3221	14.6	0.2	21	1	AAO42902	HDA type analysis
3222	14.6	0.2	21	1	AAO42902	Agrobacterium rhiz
3223	14.6	0.2	21	1	AAO35258	Agrobacterium rhiz
3224	14.6	0.2	21	1	AAO35262	Agrobacterium rhiz
3225	14.6	0.2	21	1	AAO35268	Chlamydia trachoma
3226	14.6	0.2	21	1	AAO70288	Human type II phos
3227	14.6	0.2	21	1	AAO61922	HIV replication in
3228	14.6	0.2	21	1	AAO61989	CMV antisense olig
3229	14.6	0.2	21	1	AAAT1995	Peptide nucleic ac
3230	14.6	0.2	21	1	AAAT01661	Human SH-PRP1 gene
3231	14.6	0.2	21	1	AAAT55317	HIV inhibitor #4.
3232	14.6	0.2	21	1	AAAT35001	Cytokeratin 19 mRN
3233	14.6	0.2	21	1	AAAT31784	Initiating oligo
3234	14.6	0.2	21	1	AAAT3889	Initiating oligo
3235	14.6	0.2	21	1	AAAT3889	Phosphorothioate o
3236	14.6	0.2	21	1	AAAT3890	Rat fibroblast gro
3237	14.6	0.2	21	1	AAAT7232	Telomerase reverse
3238	14.6	0.2	21	1	AAAT70731	PCR primer ABCR-EX
3239	14.6	0.2	21	1	AAV08273	PCR primer ABCR-EX
3240	14.6	0.2	21	1	AAV08280	Interleukin-15 gen
3241	14.6	0.2	21	1	AAV37790	Interleukin-15 gen
3242	14.6	0.2	21	1	AAV37793	Human osteosarcoma
3243	14.6	0.2	21	1	AAV10466	Human polymorphic
3244	14.6	0.2	21	1	AAZ26171	Human polymorphic
3245	14.6	0.2	21	1	AAZ26812	Human polymorphic
3246	14.6	0.2	21	1	AAZ26398	Human polymorphic
3247	14.6	0.2	21	1	AAZ26192	Human polymorphic
3248	14.6	0.2	21	1	AAZ26714	Human polymorphic
3249	14.6	0.2	21	1	AAZ26761	Human polymorphic
3250	14.6	0.2	21	1	AAAT17912	Anti-CMV oligonuc
3251	14.6	0.2	21	1	AAZ00585	Human glypican seq
3252	14.6	0.2	21	1	AAAT1751	Human v3 loop HIV
3253	14.6	0.2	21	1	AAAT32381	Abi variable light
3254	14.6	0.2	21	1	AAZ06694	Reverse PCR primer
3255	14.6	0.2	21	1	AAAT1984	Primer D3995 to ge
3256	14.6	0.2	21	1	AAAT4089	PCR primer for rCV
3257	14.6	0.2	21	1	AAAT54710	Human biallelic ma
3258	14.6	0.2	21	1	AAAT3847	Human biallelic ma
3259	14.6	0.2	21	1	AAAT09053	Human biallelic ma
3260	14.6	0.2	21	1	AAAT4157	Human biallelic ma
3261	14.6	0.2	21	1	AAAT88332	Human biallelic ma
3262	14.6	0.2	21	1	AAAT40708	Human biallelic ma
3263	14.6	0.2	21	1	AAAT3907	Human biallelic ma
3264	14.6	0.2	21	1	AAAT5773	Human biallelic ma
3265	14.6	0.2	21	1	AAAT72176	Human biallelic ma
3266	14.6	0.2	21	1	AAAT75738	Human biallelic ma
3267	14.6	0.2	21	1	AAAT76866	Human biallelic ma
3268	14.6	0.2	21	1	AAAT76031	Human biallelic ma
3269	14.6	0.2	21	1	AAAT97479	Human biallelic ma
3270	14.6	0.2	21	1	AAAT0279	Human fibronectin
3271	14.6	0.2	21	1	AAAT1664	Single nucleotide
3272	14.6	0.2	21	1	AAAT1649	Single nucleotide
3273	14.6	0.2	21	1	AAAT10973	Interleukin-6 (IL-
3274	14.6	0.2	21	1	AAAT94225	Interleukin-6 (IL-
3275	14.6	0.2	21	1	AAAT97685	Interleukin-6 (IL-
3276	14.6	0.2	21	1	AAAT97698	Interleukin-6 (IL-
3277	14.6	0.2	21	1	AAAT7698	Interleukin-6 (IL-
3278	14.6	0.2	21	1	AAAT5238	Meloidyone chltwo
3279	14.6	0.2	21	1	AAAT6069	beta-actin PCR pri
3280	14.6	0.2	21	1	AAAT6869	Human gene single
3281	14.6	0.2	21	1	AAAT97449	Human gene single
3282	14.6	0.2	21	1	AAAT97249	Human gene single
3283	14.6	0.2	21	1	AAAT96294	Human gene single
3284	14.6	0.2	21	1	AAAT6296	Human gene single
3285	14.6	0.2	21	1	AAAT6817	Human gene single
3286	14.6	0.2	21	1	AAAT6350	Human gene single
3287	14.6	0.2	21	1	AAAT97158	Human gene single
3288	14.6	0.2	21	1	AAAT95280	Human gene single
3289	14.6	0.2	21	1	AAAT95372	Human gene single
3290	14.6	0.2	21	1	AAAT62434	Cholinergic recept
3291	14.6	0.2	21	1	AAAT62422	SLC18A3 polymorphi
3292	14.6	0.2	21	1	AAAT62422	PCR primer for Hum
3293	14.6	0.2	21	1	AAAT91034	Human interleukin-
3294	14.6	0.2	21	1	AAAT76187	PI3G gene fragment
3295	14.6	0.2	21	1	AAAT23058	PDGF B hairpin/ham
3296	14.6	0.2	21	1	AAAT62077	Rainbow trout gale
3297	14.6	0.2	21	1	AAAT4644	Human beta-actin p
3298	14.6	0.2	21	1	AAAT62667	Human COL1A1 PCR p
3299	14.6	0.2	21	1	AAAT52024	Fanconi anemia FA
3300	14.6	0.2	21	1	AAAT13278	Human polymorphism
3301	14.6	0.2	21	1	AAAT60160	Human polymorphism
3302	14.6	0.2	21	1	AAAT60171	Clock gene Bmal2 (
3303	14.6	0.2	21	1	AAAT68528	In-situ analysis s
3304	14.6	0.2	21	1	AAAT70498	Human connective t
3305	14.6	0.2	21	1	AAAT67131	Antisense PCR prim
3306	14.6	0.2	21	1	AAAT22642	HCV-S1 overlapping
3307	14.6	0.2	21	1	AAAT33020	A thaliana AKIN1
3308	14.6	0.2	21	1	AAAT46645	Human interleukin
3309	14.6	0.2	21	1	AAAT52977	Human interleukin
3310	14.6	0.2	21	1	AAAT52958	Human interleukin
3311	14.6	0.2	21	1	AAAT52964	Human epoxide hydr
3312	14.6	0.2	21	1	AAAT57553	Human lactoferrin
3313	14.6	0.2	21	1	AAAT58273	Histamine N-methyl
3314	14.6	0.2	21	1	AAAT59762	Human acetyl choli
3315	14.6	0.2	21	1	AAAT598507	Human lactoferrin
3316	14.6	0.2	21	1	AAAT598319	Human UDP-glucuron
3317	14.6	0.2	21	1	AAAT597961	Endothelin-1 (EDN-
3318	14.6	0.2	21	1	AAAT594085	

3319	14.6	0.2	21	1	ABK94086	Endothelin-1 (EDN-	3392	14.6	0.2	22	1	AAK81837	PCR primer used to
3320	14.6	0.2	21	1	ABK94081	Endothelin-1 (EDN-	3393	14.6	0.2	22	1	AAK99208	Human apoptosis re
3321	14.6	0.2	21	1	ABK94242	Endothelin-1 (EDN-	3394	14.6	0.2	22	1	AAZ99687	Human Vth aggregat
3322	14.6	0.2	21	1	ABK94082	Endothelin-1 (EDN-	3395	14.6	0.2	22	1	AAZ49922	Human tumour suppr
3323	14.6	0.2	21	1	ABN86025	Mutagenic primer D	3396	14.6	0.2	22	1	AAZ44367	Human G protein-co
3324	14.6	0.2	21	1	AAI49183	Porcine CD 151 cod	3397	14.6	0.2	22	1	AAI11724	Human prothrombin
3325	14.6	0.2	21	1	ABZ95973	Human fibronectin	3398	14.6	0.2	22	1	AAK95380	Rat Gli1 coding se
3326	14.6	0.2	21	1	ABX94380	Human endothelial	3399	14.6	0.2	22	1	AAK37706	Human Rad51 antise
3327	14.6	0.2	21	1	ABX90552	Human p1GF A anti	3400	14.6	0.2	22	1	AAK74138	Reverse PCR primer
3328	14.6	0.2	21	1	ACC49728	Mouse CRH-R1 PCR p	3401	14.6	0.2	22	1	AAK501199	Human RAD51 antise
3329	14.6	0.2	21	1	ABT34056	Human pigmentation	3402	14.6	0.2	22	1	AAH14949	AD14949
3330	14.6	0.2	21	1	ABX10723	Human glycoprotein	3403	14.6	0.2	22	1	AAK92055	Rat PEX1 PCR prime
3331	14.6	0.2	21	1	ACF64056	IFNAR1 reverse PCR	3404	14.6	0.2	22	1	AAK58876	Human metastasis-a
3332	14.6	0.2	21	1	ACF64052	ESR1 reverse PCR p	3405	14.6	0.2	22	1	AAK58876	Human metastasis-a
3333	14.6	0.2	21	1	AAU53918	Interleukin 6 targ	3406	14.6	0.2	22	1	AAK58876	Human metastasis-a
3334	14.6	0.2	21	1	ACC42623	Human interleukin-	3407	14.6	0.2	22	1	AAK58876	Human metastasis-a
3335	14.6	0.2	21	1	ABT33411	NOVX PCR primer SE	3408	14.6	0.2	22	1	AAH79377	Human RNA uncoilin
3336	14.6	0.2	21	1	ABX56493	Human epidermal gr	3409	14.6	0.2	22	1	AAH74500	PCR primer used to
3337	14.6	0.2	21	1	ADAI3874	Short interfering	3410	14.6	0.2	22	1	AAH74340	PCR primer used to
3338	14.6	0.2	21	1	ADH78519	Probe sequence #22	3411	14.6	0.2	22	1	AAH78021	PCR primer for hum
3339	14.6	0.2	21	1	ADH78522	Probe sequence #25	3412	14.6	0.2	22	1	AAK84905	Primer Ag 36 (R) e
3340	14.6	0.2	21	1	ADCI6357	Short interfering	3413	14.6	0.2	22	1	AAK81868	Human PCNA random
3341	14.6	0.2	21	1	ADCI6357	Short interfering	3414	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3342	14.6	0.2	21	1	ADCI6357	Short interfering	3415	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3343	14.6	0.2	21	1	ADCI6357	Short interfering	3416	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3344	14.6	0.2	21	1	ADCI6357	Short interfering	3417	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3345	14.6	0.2	21	1	ADCI6357	Short interfering	3418	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3346	14.6	0.2	21	1	ADCI6357	Short interfering	3419	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3347	14.6	0.2	21	1	ADCI6357	Short interfering	3420	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3348	14.6	0.2	21	1	ADCI6357	Short interfering	3421	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3349	14.6	0.2	21	1	ADCI6357	Short interfering	3422	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3350	14.6	0.2	21	1	ADCI6357	Short interfering	3423	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3351	14.6	0.2	21	1	ADCI6357	Short interfering	3424	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3352	14.6	0.2	21	1	ADCI6357	Short interfering	3425	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3353	14.6	0.2	21	1	ADCI6357	Short interfering	3426	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3354	14.6	0.2	21	1	ADCI6357	Short interfering	3427	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3355	14.6	0.2	21	1	ADCI6357	Short interfering	3428	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3356	14.6	0.2	21	1	ADCI6357	Short interfering	3429	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3357	14.6	0.2	21	1	ADCI6357	Short interfering	3430	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3358	14.6	0.2	21	1	ADCI6357	Short interfering	3431	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3359	14.6	0.2	21	1	ADCI6357	Short interfering	3432	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3360	14.6	0.2	21	1	ADCI6357	Short interfering	3433	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3361	14.6	0.2	21	1	ADCI6357	Short interfering	3434	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3362	14.6	0.2	21	1	ADCI6357	Short interfering	3435	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3363	14.6	0.2	21	1	ADCI6357	Short interfering	3436	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3364	14.6	0.2	21	1	ADCI6357	Short interfering	3437	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3365	14.6	0.2	21	1	ADCI6357	Short interfering	3438	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3366	14.6	0.2	21	1	ADCI6357	Short interfering	3439	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3367	14.6	0.2	21	1	ADCI6357	Short interfering	3440	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3368	14.6	0.2	21	1	ADCI6357	Short interfering	3441	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3369	14.6	0.2	21	1	ADCI6357	Short interfering	3442	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3370	14.6	0.2	21	1	ADCI6357	Short interfering	3443	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3371	14.6	0.2	21	1	ADCI6357	Short interfering	3444	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3372	14.6	0.2	21	1	ADCI6357	Short interfering	3445	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3373	14.6	0.2	21	1	ADCI6357	Short interfering	3446	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3374	14.6	0.2	21	1	ADCI6357	Short interfering	3447	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3375	14.6	0.2	21	1	ADCI6357	Short interfering	3448	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3376	14.6	0.2	21	1	ADCI6357	Short interfering	3449	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3377	14.6	0.2	21	1	ADCI6357	Short interfering	3450	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3378	14.6	0.2	21	1	ADCI6357	Short interfering	3451	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3379	14.6	0.2	21	1	ADCI6357	Short interfering	3452	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3380	14.6	0.2	21	1	ADCI6357	Short interfering	3453	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3381	14.6	0.2	21	1	ADCI6357	Short interfering	3454	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3382	14.6	0.2	21	1	ADCI6357	Short interfering	3455	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3383	14.6	0.2	21	1	ADCI6357	Short interfering	3456	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3384	14.6	0.2	21	1	ADCI6357	Short interfering	3457	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3385	14.6	0.2	21	1	ADCI6357	Short interfering	3458	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3386	14.6	0.2	21	1	ADCI6357	Short interfering	3459	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3387	14.6	0.2	21	1	ADCI6357	Short interfering	3460	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3388	14.6	0.2	21	1	ADCI6357	Short interfering	3461	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3389	14.6	0.2	21	1	ADCI6357	Short interfering	3462	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3390	14.6	0.2	21	1	ADCI6357	Short interfering	3463	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr
3391	14.6	0.2	21	1	ADCI6357	Short interfering	3464	14.6	0.2	22	1	AAK76175	Human M-CSF PCR pr

OS Homo sapiens.
 XX MO9717445-A1.
 XX 15-MAY-1997.
 PD
 XX 08-NOV-1996; 96MO-FR001773.
 PF
 XX 10-NOV-1995; 95FR-00013576.
 PR
 XX (CNRS) CNRS CENT NAT RECH SCI.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 XX Tora L, Lutz Y, Trociet Y, Mandel J;
 PI WPI; 1997-281034/25.
 DR
 XX
 PT Antibody 1C2 used for treating or preventing neuro-degenerative diseases
 PT - associated with proteins containing long poly:glutamine repeats, e.g.
 PT Huntington's disease.
 PS
 XX Claim 21; Page 44; 69pp; French.
 XX
 CC The invention relates to a monoclonal antibody (MAb) 1C2 for the
 CC treatment of neurodegenerative diseases associated with the presence of
 CC polyglutamine repeat regions. This MAb is already known for its affinity
 CC to the TARA binding protein (TBP) transcription initiation factor,
 CC especially at the amino acid sequence LEEQQRQ00000 found at the N-
 CC terminus of TBP. MAb 1C2 has been shown to have a high affinity for
 CC polyglutamine repeats with a proportional affinity to the number of
 CC glutamine repeats. This affinity has been used to identify genes encoding
 CC proteins containing long polyglutamine repeats which are implicated in
 CC neurodegenerative diseases. A screen of an expression library, generated
 CC from a lymphoblastic cell line from a patient suffering from
 CC spinocerebellar ataxia (SCA), with MAb 1C2 isolated 6 new sequences
 CC (AA78906-78911) encoding polyglutamine repeats. This sequence is
 CC derived from clone AAD20 isolated from a patient suffering from SCA2. MAb
 CC 1C2, active fragment of it or nucleic acids encoding it are specifically
 CC used to treat Huntington's disease, SCA types 1-5 or 7, X-linked spin-
 CC bulbar muscular atrophy (Kennedy disease), dentatorubral-pallidolu-
 CC atrophy, dominant autosomal spinocerebellar ataxia, familial spastic
 CC paraplegia, bipolar affective disorder, manic depressive psychoses and
 CC schizophrenia
 XX
 XX Sequence 42 BP; 14 A; 14 C; 14 G; 0 T; 0 U; 0 Other;
 SQ
 XX
 Query Match 0.4%; Score 27.8; DB 1; Length 42;
 Best Local Similarity 93.5%; Pred. No. 35;
 Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7405 AGCAACATCAGCAGCAGCAGCAGCAGCA 7435
 Db 2 AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 32
 RESULT 6
 AAS13782
 ID AAS13782 standard; DNA; 42 BP.
 XX
 AC AAS13782;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Simple sequence repeat, SSR, #53.
 XX
 KM Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;
 KM cereal profiling; grass profiling; seed batch purity testing.
 XX
 OS Synthetic.
 XX
 XX NZ509193-A.
 PN
 XX 25-MAY-2001.
 PD

XX 03-JUN-2001; 2001NZ-00509193.
 PF
 XX 24-DEC-1999; 99AU-0004906.
 PR
 XX 04-MAY-2000; 2000AU-00007310.
 PR
 XX (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
 PA (UYSC-) UNIV SOUTHERN CROSS.
 PA (VIC-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
 PA (UYAD-) UNIV ADELAIDE.
 PA (ITWA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
 XX
 XX Forster JW, Jones ES;
 PI WPI; 2001-512563/56.
 DR
 XX
 PT New simple sequence repeats having 2 or more tandemly repeated nucleotide
 PT core elements isolated from ryegrass and fescue, useful for selecting of
 PT genes in grass or cereal breeding or profiling grass or cereal species
 PT varieties.
 PS
 XX Claim 13; Page 53; 72pp; English.
 XX
 CC The invention relates to a substantially purified or isolated nucleic
 CC acid (I) from ryegrass or fescue species including a simple sequence
 CC repeat (SSR), having 2 or more tandemly repeated nucleotide core elements
 CC 2-6 nucleotides in length. Also included are a nucleic acid primer
 CC suitable for amplifying an SSR, identifying (M) an SSR by preparing a
 CC library of ryegrass or fescue genomic DNA enriched for SSRs and
 CC identifying clones in the library containing SSRs, a library of ryegrass
 CC or fescue genomic DNA enriched for SSRs prepared by the M, selecting for
 CC a gene in grass or cereal breeding by identifying an SSR that is closely
 CC associated with the gene such that the SSR and the gene are
 CC preferentially co-inherited, and selecting for the SSR in the breeding, a
 CC method for DNA profiling grass or cereal species varieties by assessing
 CC variation between SSR varieties and testing the purity of grass or cereal
 CC seed batches by assessing variation within seed batch of an SSR. The SSRs
 CC may be used in the selection of genes in grass or cereal breeding, for
 CC profiling grass or cereal species varieties, for testing the purity of
 CC grass or cereal seed batches, and for DNA profiling to establish the
 CC distinct identity, uniformity and/or stability of a cultivar. The present
 CC sequence is a ryegrass or fescue SSR
 XX
 XX Sequence 42 BP; 14 A; 14 C; 14 G; 0 T; 0 U; 0 Other;
 SQ
 XX
 Query Match 0.4%; Score 27.8; DB 1; Length 42;
 Best Local Similarity 93.5%; Pred. No. 35;
 Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7405 AGCAACATCAGCAGCAGCAGCAGCAGCA 7435
 Db 1 AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 31
 RESULT 7
 AB246913
 ID AB246913 standard; DNA; 41 BP.
 XX
 AC AB246913;
 XX
 DT 26-JUN-2003 (first entry)
 XX
 DE Human ATP-binding cassette ABCA7 gene polymorphic site, #3697.
 XX
 KM Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19;
 KM polymorphic site; drug evaluation; drug screening; genotyping;
 KM genetic profiling; therapeutic customisation; adverse reaction;
 KM clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH variation replace(21,A)
 FT

```

FT      /*tag= a
XX      /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX      WO200252044-A2.
XX
XX      04-JUL-2002.
XX
XX      27-DEC-2001; 2001WO-JP011592.
XX
XX      27-DEC-2000; 2000JP-00399443.
XX      02-MAY-2001; 2001JP-00135256.
XX      27-AUG-2001; 2001JP-00256862.
XX
XX      (RIKE ) RIKEN KK.
XX
XX      Nakamura Y, Sekine A, Iida A, Saito S;
XX      WPI, 2002-583571/62.
XX
XX      Identifying individuals having a polymorphism, useful for determining the
XX      effectiveness or side effect of a drug or treatment protocol, comprises
XX      detecting at least one polymorphism in the drug metabolizing enzyme
XX      nucleic acid.
XX
XX      Claim 23; Page 129; 2785pp; English.
XX
XX      Sequences AB243217-AB250887 represent polymorphic sites within genes
XX      encoding enzymes associated with drug metabolism. The invention relates
XX      to methods and compositions for identifying individuals who have at least
XX      one polymorphism in such drug metabolizing enzyme-encoding genes. The
XX      polymorphisms may be identified in a nucleic acid sample using probes or
XX      primers specific for a sequence selected from AB243217-AB250887 using a
XX      variety of detection assays, including hybridisation assays, nucleic acid
XX      arrays and PCR-based methods. The invention also encompasses methods of
XX      evaluating and screening drugs using genetic polymorphism data. Genetic
XX      polymorphisms (SNPs), may be used in studying the relationship between
XX      DNA sequence variations and human diseases, conditions, and responses to
XX      drugs. SNPs are also useful as polymorphism markers for discovering genes
XX      that cause or exacerbate certain diseases. SNPs are particularly useful
XX      in the above respects as they are stable in populations, occur
XX      frequently, and have lower mutation rates than other genome variations
XX      such as repeating sequences. The detection and analysis of polymorphisms
XX      in genes encoding drug metabolising enzymes allows the customisation of
XX      drug therapies based upon the genetic profile of individual patients.
XX      This would not only take the guesswork out of selecting the drug with the
XX      greatest therapeutic effect for a particular patient, but would also
XX      reduce the likelihood of adverse reactions, thereby increasing safety.
XX      Methods of the invention are also useful in the drug discovery and
XX      approval processes. For example, individuals could be selected for
XX      clinical trials only if their genetic profiles indicate that they are
XX      capable of responding to a particular drug or drug class, and previously
XX      failed drug candidates could be revived if they were matched with more
XX      appropriate patient populations. The methods, data and compositions of
XX      the invention may therefore lead to an increase in the range of
XX      possible drug targets and decreases in the number of adverse drug
XX      reactions, failed drug trials, the time taken for a drug to be approved,
XX      the length of time patients are on medication and the number of different
XX      medications a patient needs to take before finding an effective therapy
XX
XX      SQ      Sequence 41 BP; 6 A; 4 C; 5 G; 26 T; 0 U; 0 Other;
XX
XX      Query Match      0.4%; Score 27.2; DB 1; Length 41;
XX      Best Local Similarity 80.0%; Pred. No. 43;
XX      Matches 32; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
XX
XX      QY      4467 TTTTGTGTTGAGCATGGGTTGGCT 4506
XX      |||||
XX      1 TTTTGTGTTTATTAAGATGAGTCTCACT 40
XX
XX      RESULT 8
XX      AB245507

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ID      AB245507 standard; DNA; 41 BP.
XX
XX      AC      AB245507;
XX
XX      DT      26-JUN-2003 (first entry)
XX
XX      DE      Human ATP-binding cassette ABCA7 gene polymorphic site, #2291.
XX
XX      KW      Human; drug metabolizing enzyme; gene; drug metabolism; chromosome 19;
XX      polymorphic site; drug evaluation; drug screening; genotyping;
XX      genetic profiling; therapeutic customisation; adverse reaction;
XX      clinical trial; drug approval; single nucleotide polymorphism; SNP; dr.
XX
XX      OS      Homo sapiens.
XX
XX      FH      Key      Location/Qualifiers
XX      FT      variation      replace(21,A)
XX      FT      /*tag= a
XX      FT      /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX      PN      WO200252044-A2.
XX
XX      PD      04-JUL-2002.
XX
XX      PF      27-DEC-2001; 2001WO-JP011592.
XX
XX      PR      27-DEC-2000; 2000JP-00399443.
XX      02-MAY-2001; 2001JP-00135256.
XX      27-AUG-2001; 2001JP-00256862.
XX
XX      PA      (RIKE ) RIKEN KK.
XX
XX      PI      Nakamura Y, Sekine A, Iida A, Saito S;
XX      WPI, 2002-583571/62.
XX
XX      PT      Identifying individuals having a polymorphism, useful for determining the
XX      effectiveness or side effect of a drug or treatment protocol, comprises
XX      detecting at least one polymorphism in the drug metabolizing enzyme
XX      nucleic acid.
XX
XX      PS      Claim 23; Page 102; 2785pp; English.
XX
XX      SQ      Sequences AB243217-AB250887 represent polymorphic sites within genes
XX      encoding enzymes associated with drug metabolism. The invention relates
XX      to methods and compositions for identifying individuals who have at least
XX      one polymorphism in such drug metabolizing enzyme-encoding genes. The
XX      polymorphisms may be identified in a nucleic acid sample using probes or
XX      primers specific for a sequence selected from AB243217-AB250887 using a
XX      variety of detection assays, including hybridisation assays, nucleic acid
XX      arrays and PCR-based methods. The invention also encompasses methods of
XX      evaluating and screening drugs using genetic polymorphism data. Genetic
XX      polymorphism data, particularly that relating to single nucleotide
XX      polymorphisms (SNPs), may be used in studying the relationship between
XX      DNA sequence variations and human diseases, conditions, and responses to
XX      drugs. SNPs are also useful as polymorphism markers for discovering genes
XX      that cause or exacerbate certain diseases. SNPs are particularly useful
XX      in the above respects as they are stable in populations, occur
XX      frequently, and have lower mutation rates than other genome variations
XX      such as repeating sequences. The detection and analysis of polymorphisms
XX      in genes encoding drug metabolising enzymes allows the customisation of
XX      drug therapies based upon the genetic profile of individual patients.
XX      This would not only take the guesswork out of selecting the drug with the
XX      greatest therapeutic effect for a particular patient, but would also
XX      reduce the likelihood of adverse reactions, thereby increasing safety.
XX      Methods of the invention are also useful in the drug discovery and
XX      approval processes. For example, individuals could be selected for
XX      clinical trials only if their genetic profiles indicate that they are
XX      capable of responding to a particular drug or drug class, and previously
XX      failed drug candidates could be revived if they were matched with more
XX      appropriate patient populations. The methods, data and compositions of
XX      the invention may therefore lead to an increase in the range of
XX      possible drug targets and decreases in the number of adverse drug
XX

```

CC reactions, failed drug trials, the time taken for a drug to be approved.
 CC the length of time patients are on medication and the number of different
 CC medications a patient needs to take before finding an effective therapy
 XX

SQ Sequence 41 BP; 6 A; 4 C; 5 G; 26 T; 0 U; 0 Other;

Query Match 0.4%; Score 27.2; DB 1; Length 41;
 Best Local Similarity 80.0%; Pred. No. 43;
 Matches 32; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 4467 TTTTGTCTGTCGAGCATGCGGTTGGCT 4506
 Db 1 TTTTGTCTGTCGAGCATGCGGTTGGCT 40

RESULT 9
 ID ABX79926 standard; cDNA; 33 BP.
 XX

AC ABX79926;
 DT 17-APR-2003 (first entry)
 XX

DE EST polymorphic DNA repeat polynucleotide #251.

XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 KM polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
 KM Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 KM Haw River syndrome; Huntington's disease; fragile-X syndrome;
 KM Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
 KM spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

XX Homo sapiens.

OS US6472154-B1.

PN 29-OCT-2002.

PD 31-DEC-1999; 99US-00475947.

PR 31-DEC-1999; 99US-00475947.

XX (TEXA) UNIV TEXAS SYSTEM.

PI Garner HR, Wren JD, Minna JD, Fondon JW;

XX WPI; 2003-208818/20.

PT Identifying a candidate polymorphic repeat within a coding sequence, for
 PT understanding or treating genetic disease, comprises detecting tandem
 PT repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability.

XX Example; Col 1089; 588bp; English.

PS The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to understand, treat or eliminate genetic
 CC diseases, predispositions or adverse drug-treatment reactions. Examples
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs
 XX
 XX
 SQ Sequence 33 BP; 11 A; 10 C; 11 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 26.2; DB 1; Length 33;
 Best Local Similarity 90.3%; Pred. No. 47;
 Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7405 AGCAACATCAGCAGCAGCAGCAGCAGCA 7435
 Db 2 AGCAGCAGCAGCAGCAGCAGCAGCAGTACGCA 32

RESULT 10
 ID AAT78910 standard; cDNA; 36 BP.
 XX

AC AAT78910;

DT 09-FEB-1998 (first entry)
 XX

DE Poly-glutamine repeat region coding sequence from clone DAN26.

XX Monoclonal antibody; neurodegenerative disease; polyglutamine; TBP;
 KM repeat region; affinity; TATA binding protein; Kennedy disease;
 KM transcription initiation factor; lymphoblastic cell line; schizophrenia;
 KM Huntington's disease; dominant autosomal spinocerebellar ataxia;
 KM X-linked spino-bulbar muscular atrophy; familial spastic paraplegia;
 KM dentatorubral-pallidolusial atrophy; bipolar affective disorder;
 KM manic depressive psychosis; ss.

XX Homo sapiens.

OS MO9717445-A1.

PN 15-MAY-1997.

PD 08-NOV-1996; 96WO-FR001773.

PR 10-NOV-1995; 95FR-00013576.

XX (CNRS) CNRS CENT NAT RECH SCI.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PI Tora L, Lutz Y, Trociet Y, Mandel J;

XX WPI; 1997-281034/25.

PT Antibody IC2 used for treating or preventing neuro-degenerative diseases
 PT - associated with proteins containing long poly-glutamine repeats, e.g.
 PT Huntington's disease.

XX Claim 21; Page 44; 69pp; French.

PS The invention relates to a monoclonal antibody (Mab) IC2 for the
 CC treatment of neurodegenerative diseases associated with the presence of
 CC polyglutamine repeat regions. This Mab is already known for its affinity
 CC to the TATA binding protein (TBP) transcription initiation factor,
 CC especially at the amino acid sequence LEEQQRQQRQ found at the N-
 CC terminus of TBP. Mab IC2 has been shown to have a high affinity for
 CC polyglutamine repeats with a proportional affinity to the number of
 CC glutamine repeats. This affinity has been used to identify genes encoding
 CC proteins containing long polyglutamine repeats which are implicated in
 CC neurodegenerative diseases. A screen of an expression library, generated
 CC from a lymphoblastic cell line from a patient suffering from
 CC spinocerebellar ataxia (SCA), with Mab IC2 isolated 6 new sequences
 CC (AAT78906-T78911) encoding polyglutamine repeats. This sequence is
 CC derived from clone DAN26 isolated from a patient suffering from dominant
 CC autosomal SCA type 7. Mab IC2, active fragment of it or nucleic acids
 CC encoding it are specifically used to treat Huntington's disease, SCA
 CC types 1-5 or 7, X-linked spino-bulbar muscular atrophy (Kennedy
 CC disease), dentatorubral-pallidolusial atrophy, dominant autosomal
 CC spinocerebellar ataxia, familial spastic paraplegia, bipolar affective
 CC disorder, manic depressive psychoses and schizophrenia
 XX
 XX
 SQ Sequence 36 BP; 13 A; 12 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 26.2; DB 1; Length 36;
 Best Local Similarity 90.3%; Pred. No. 54;
 Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7405 AGCAATCAGCAGCAGCAGCAGCAGCA 7435
 DB 2 AGCAGCAGCAGCAGCAGCAGCAGCAGCA 32

RESULT 11

AA244310
 ID AA244310 standard; DNA; 30 BP.

AC AA244310;

DT 04-APR-2000 (first entry)

DE Human SCA7 primer 1.

KW SCA7; human; spinocerebellar ataxia type 7; SCA1; SCA2; SCA3; SCA6;
 repeat expansion detection; RED analysis; detection; primer; ss.

OS Homo sapiens.

PN CA2245310-A.

PD 19-FEB-1999.

PF 19-AUG-1998; 98CA-02245310.

PR 19-AUG-1997; 97US-0056170P.

PA (MINU) UNIV MINNESOTA.

PI Koob MD, Rannum LP;

DR WPI; 2000-098181/09.

PT Identifying individuals at risk of developing spinocerebellar ataxia type
 7 by analyzing trinucleotide repeat regions of spinocerebellar ataxia
 type 7 gene.

PS Disclosure; Page 43; 66pp; English.

This invention describes a novel method for identifying individuals at
 risk for developing spinocerebellar ataxia type 7 (SCA7). The method
 comprises analyzing the CAG repeat region of a SCA7 gene to detect CAG
 repeats, where individuals at risk have at least 30 CAG repeats and those
 not at risk have less than 19 CAG repeats. The method is useful for
 identifying individuals at risk of developing SCA7 and also those at risk
 of developing SCA1, 2, 3 or 6. The use of genomic DNA in the repeat
 expansion detection (RED) analysis allows isolation of any potential
 trinucleotide repeat expansion regardless of the expression pattern.
 Utilization of different oligonucleotides in the RED assay allows any of
 the possible trinucleotide repeats to be detected, and the cyclized nature
 of the reaction makes it extremely sensitive. This sequence represents a
 primer used to amplify the human SCA7 gene which is described in the
 method of the invention

Sequence 30 BP; 10 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 25.8; DB 1; Length 30;
 Best Local Similarity 93.1%; Pred. No. 48;
 Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7407 CAACATCAGCAGCAGCAGCAGCAGCA 7435
 DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCA 29

RESULT 12

AA513781
 ID AA513781 standard; DNA; 30 BP.

XX AA513781;
 AC 08-MAY-2002 (first entry)
 DT Simple sequence repeat, SSR, #52.
 DE Simple sequence repeat, SSR, #52.
 KW Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;
 cereal profiling; grass profiling; seed batch purity testing.

OS Synthetic.

PN NZ509193-A.

PD 25-MAY-2001.

PF 03-JAN-2001; 2001NZ-00509193.

PR 24-DEC-1999; 99AU-00004906.

PR 04-MAY-2000; 2000AU-00007310.

PA (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.

PA (VIC-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.

PA (UTWA-) UNIV ADELAIDE.

PI Forster JW, Jones BS;

DR WPI; 2001-512563/56.

PT New simple sequence repeats having 2 or more tandemly repeated nucleotide
 core elements isolated from ryegrass and fescue, useful for selecting of
 genes in grass or cereal breeding or profiling grass or cereal species
 varieties.

PS Claim 13; Page 53; 72pp; English.

The invention relates to a substantially purified or isolated nucleic
 acid (i) from ryegrass or fescue species including a simple sequence
 repeat (SSR), having 2 or more tandemly repeated nucleotide core elements
 2-6 nucleotides in length. Also included are a nucleic acid primer
 suitable for amplifying an SSR, identifying (M) an SSR by preparing a
 library of ryegrass or fescue genomic DNA enriched for SSRs and
 identifying clones in the library containing SSRs, a library of ryegrass
 or fescue genomic DNA enriched for SSRs prepared by the M, selecting for
 a gene in grass or cereal breeding by identifying an SSR that is closely
 associated with the gene such that the SSR and the gene are
 preferentially co-inherited, and selecting for the SSR in the breeding, a
 method for DNA profiling grass or cereal species varieties by assessing
 variation between SSR varieties and testing the purity of grass or cereal
 seed batches by assessing variation within seed batch of an SSR. The SSRs
 may be used in the selection of genes in grass or cereal breeding, for
 profiling grass or cereal species varieties, and for testing the purity of
 grass or cereal seed batches, and for DNA profiling to establish the
 distinct identity, uniformity and/or stability of a cultivar. The present
 sequence is a ryegrass or fescue SSR

Sequence 30 BP; 10 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 25.8; DB 1; Length 30;
 Best Local Similarity 93.1%; Pred. No. 48;
 Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7407 CAACATCAGCAGCAGCAGCAGCAGCA 7435
 DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCA 29

RESULT 13

AA098457
 ID AA098457 standard; cDNA; 31 BP.

```

AC AA098457;
XX 23-APR-1996 (first entry)
XX Sense probe CAG-30.
DE
XX
XX Probe; trinucleotide repeat; myotonic dystrophy; DM, Mc-PK gene;
XX fluorescent label; fluorescein isothiocyanate; fragile X syndrome;
XX muscular dystrophy; Huntington's disease; ss.
XX
XX Synthetic.
XX
XX MO9525179-A1.
XX
XX 21-SEP-1995.
XX
XX
XX 08-MAR-1995; 95WO-US002861.
XX
XX 17-MAR-1994; 94US-00214823.
XX
XX (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
XX
XX Singer RH, Taneja KL;
XX
XX MPI; 1995-336982/43.
XX
XX Detecting tri-nucleotide repeat expansion by in situ hybridisation - with
XX detection sensitive enough to distinguish between probe bound to expanded
XX and normal repeat regions, esp. for myotonic dystrophy diagnosis.
XX
XX Disclosure; Page 38; 51pp: English.
XX
XX The sequences represented by AA098457 and AA098458 are synthetic probes
XX for the trinucleotide repeat CTG. These probes can be used in a method of
XX in situ hybridisation for the detection of a trinucleotide repeat
XX expansion. These probes were used specifically to identify myotonic
XX dystrophy (DM). DM is associated with an expanded CTG repeat in the 3'
XX untranslated region of the Mc-PK gene. These probes are labelled with a
XX fluorescent label (e.g. fluorescein isothiocyanate) and then used to
XX treat nucleated cells. The hybridisation of the probe to the expanded
XX trinucleotide repeat can then be detected by fluorescence microscopy. Due
XX to the large variation between expanded repeat size, and normal repeat
XX size in DM (5-27 repeats in non-expanded, 50-2000 repeats in expanded),
XX the expanded repeat will bind more probes. Only the expanded repeat will
XX bind enough of the probes to give a detectable fluorescent signal. By
XX detecting the number of transcripts in a cell of a diagnosed individual,
XX progress of treatment, and severity of the disease can be monitored. This
XX method can also be used to diagnose other diseases associated with
XX trinucleotide repeat expansions, such as fragile X syndrome, muscular
XX dystrophy and Huntington's disease. For some of these diseases a greater
XX detection specificity would be required due to the smaller difference in
XX repeat number between normal and infected individuals
XX
XX Sequence 31 BP; 10 A; 10 C; 10 G; 1 T; 0 U; 0 Other:
SQ
Query Match 0.3%; Score 25.8; DB 1; Length 31;
Best Local Similarity 93.1%; Pred. No. 50;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7407 CAACATCAGCAGCAGCAGCAGCAGCA 7435
DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCA 29
RESULT 14
AAZ24996
ID AAZ24996 standard; DNA; 31 BP.
XX
XX AAZ24996;
AC
XX
XX 24-DEC-1999 (first entry)
XX
XX Oligonucleotide CAG30 targeted to myotonic-protein kinase gene.

```

```

XX
XX Trinucleotide repeat; myotonic-protein kinase; myotonic dystrophy; probe;
XX in situ hybridisation; detection; expansion; fragile X syndrome; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX US5962332-A.
XX
XX 05-OCT-1999.
XX
XX
XX 11-DEC-1995; 95US-00570155.
XX
XX
XX 17-MAR-1994; 94US-00214823.
XX
XX 07-MAR-1995; 95US-00399499.
XX
XX
XX (UYMA-) UNIV MASSACHUSETTS.
XX
XX Taneja KL, Singer RH;
XX
XX MPI; 1999-579615/49.
XX
XX Detection of trinucleotide repeats.
XX
XX Disclosure; Col 25; 18pp: English.
XX
XX Oligonucleotides AAZ24983-224995 are targeted to the CTG trinucleotide
XX repeats found in the myotonic-protein kinase (Mc-PK) gene. Excessive
XX numbers of the trinucleotide repeats in the Mc-PK gene leads to the
XX disease myotonic dystrophy. The oligonucleotides are used to probe the 5'
XX -most 7 exons of 14 in the Mc-PK gene. This sequence is used as an
XX antisease control oligonucleotide for the hybridisation reaction. The
XX invention relates to a method for the detection of trinucleotide repeat
XX expansion, e.g. in the Mc-PK gene or FMR1 gene (leading to fragile X
XX syndrome) by in situ hybridization
XX
XX Sequence 31 BP; 10 A; 10 C; 10 G; 1 T; 0 U; 0 Other:
SQ
Query Match 0.3%; Score 25.8; DB 1; Length 31;
Best Local Similarity 93.1%; Pred. No. 50;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7407 CAACATCAGCAGCAGCAGCAGCAGCA 7435
DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCA 29
RESULT 15
ABK81863/c
ID ABK81863 standard; DNA; 25 BP.
XX
XX ABK81863;
AC
XX
XX 13-AUG-2002 (first entry)
XX
XX Lung specific gene probe #9.
XX
XX Lung specific gene; gene therapy; vaccine; lung cancer; cancer staging;
XX cancer monitoring; cancer diagnosis; imaging lung cancer; metastases;
XX probe; ss.
XX
XX Synthetic.
XX
XX WO200218576-A2.
XX
XX 07-MAR-2002.
XX
XX 27-AUG-2001; 2001WO-US026684.
XX
XX 28-AUG-2000; 2000US-0228378P.
XX
XX (DIAD-) DIADEXUS INC.
XX

```

PI Chen S, Macina RA, Sun Y, Recipon H;
 XX MPI; 2002-434904/46.
 DR
 PT New lung specific genes and their encoded proteins, useful in gene
 XX therapy or as a vaccine for treating lung cancer, as well as for
 PT measuring metastases of lung cancer, or staging, monitoring, diagnosing
 PT or imaging lung cancer.
 XX
 PS Example 10; Page 127; 206pp; English.
 XX
 CC The invention describes a new lung specific gene and it's variants. The
 CC lung specific gene proteins and genes are useful in gene therapy or as a
 CC vaccine for treating lung cancer. Lung specific genes are also useful for
 CC staging, monitoring, diagnosing or imaging lung cancer, as well as for
 CC measuring metastases of lung cancer. This sequence represents a probe
 CC used in microarray analysis to detect a lung specific genes thought to be
 CC involved in development of lung cancer
 SQ
 Sequence 25 BP; 5 A; 11 C; 2 G; 7 T; 0 U; 0 Other;
 Query Match 0.3%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5554 AGATGAGAGAGTGTGTGACGCA 5578
 DB 25 AGATGAGAGAGTGTGTGACGCA 1
 RESULT 16
 ADB81488/C
 ID ADB81488 standard; DNA; 25 BP.
 XX
 AC ADB81488;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Reverse PCR primer used to amplify human EIF2C1 DNA.
 XX
 KM PCR; ss; human; eukaryotic translation initiation factor 2C 1; EIF2C1;
 KM Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99; gene therapy;
 KM hyperproliferative disorder; familial hypercholesterolemia; cancer;
 KM polycystic kidney disease; cystic fibrosis; progeria syndrome;
 KM cytostatic; antileptemic; primer.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040321-A2.
 PD
 XX 15-MAY-2003.
 XX
 PF 04-NOV-2002; 2002WO-US035324.
 XX
 PR 08-NOV-2001; 2001US-00007078.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Ward DT, Watt AT;
 XX
 DR WPI; 2003-449448/42.
 XX
 PT New compound, having a sequence targeted to a nucleic acid encoding human
 PT collapsin response mediator protein 2, useful for preparing a composition
 PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
 PT cancer.
 XX
 PS Example 13; Page 74; 120pp; English.
 XX
 CC This invention relates to novel antisense oligonucleotides that modulate
 CC the expression of human eukaryotic translation initiation factor 2C 1
 CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
 CC Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an

CC intracellular membrane associated protein thought to be involved in
 CC cellular differentiation, such that altered expression of EIF2C1 can
 CC affect cell growth, morphology and tumorigenicity. Accordingly,
 CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
 CC or tissues can be used in gene therapy to treat various conditions
 CC including hyperproliferative disorders, familial hypercholesterolemia
 CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
 CC progeria syndrome. As such, the oligos of the present invention can be
 CC described as having cytostatic and antileptemic activities. This
 CC oligonucleotide sequence is the reverse PCR primer used to amplify human
 CC eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA of the
 CC invention.
 SQ
 Sequence 25 BP; 6 A; 7 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 0.3%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1801 GTGAACGTCGTGAGATACACTCT 1825
 DB 25 GTGAACGTCGTGAGATACACTCT 1
 RESULT 17
 ABL53423/C
 ID ABL53423 standard; DNA; 33 BP.
 XX
 AC ABL53423;
 XX
 DT 01-JUL-2002 (first entry)
 XX
 DE Pregnancy specific beta-1-glucoprotein 9.02 related primer 4.
 XX
 KM beta-1-glucoprotein; pregnancy; cytostatic; immunomodulatory; tumour;
 KM immunological disease; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 PN WO200206475-A1.
 PD
 XX 24-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-CN001097.
 XX
 PR 30-JUN-2000; 2000CN-00116902.
 XX
 PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-122636/16.
 XX
 PT Pregnancy specific beta 1-glucoprotein 9.02 polynucleotide and
 PT polypeptide, useful in diagnosis and treatment of tumor and immunological
 PT diseases.
 XX
 PS Example 4; Page 19; 35pp; Chinese.
 XX
 CC The invention relates to an isolated pregnancy specific beta-1-
 CC glucoprotein 9.02. The activity of the protein of the invention may be
 CC described as cytostatic and immunomodulatory. The polypeptide and encoded
 CC polynucleotide are applicable in diagnosis and treatment of tumour and
 CC immunological diseases. The screened compounds as well as their
 CC preparations are also useful for treating the diseases mentioned above.
 CC The current sequence represents a pregnancy specific beta-1-glucoprotein
 CC 9.02 related primer
 SQ
 Sequence 33 BP; 23 A; 5 C; 2 G; 3 T; 0 U; 0 Other;
 Query Match 0.3%; Score 25; DB 1; Length 33;
 Best Local Similarity 84.8%; Pred. No. 77;
 Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;


```

DE PCR probe used to isolate human E1F2C1 DNA.
KM PCR, see: human; eukaryotic translation initiation factor 2C 1; E1F2C1;
KM Co-e1F2C1; e1F2C1; Golgi ER protein 95kDa; GERp95; Q99; gene therapy;
KM hyperproliferative disorder; familial hypercholesterolaemia; cancer;
KM polycystic kidney disease; cystic fibrosis; progeroid syndrome;
KM cytosolic; antilipemic; probe.
XX
XX Homo sapiens.
OS
XX
XX
XX Key: Location/Qualifiers
FH modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= FAM, a fluorescent reporter dye"
FT modified_base 20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= TAMRA, a quencher dye"
XX
XX WO2003040321-A2.
XX
XX 15-MAY-2003.
XX
XX 04-NOV-2002; 2002MO-US035324.
XX
XX 08-NOV-2001; 2001US-00007078.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ward DT, Watt AT;
XX
XX WPI; 2003-449448/42.
XX
XX
XX New compound, having a sequence targeted to a nucleic acid encoding human
XX collapsin response mediator protein 2, useful for preparing a composition
XX for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX cancer.
XX
XX
XX Example 13; Page 74; 120pp; English.
XX
XX
XX This invention relates to novel antisense oligonucleotides that modulate
XX the expression of human eukaryotic translation initiation factor 2C 1
XX (E1F2C1). E1F2C1 is located on chromosome 1p34-35, and is also known as
XX (E1F2C1). E1F2C1, Golgi ER protein 95kDa, GERp95 and Q99. It is an
XX intracellular membrane associated protein thought to be involved in
XX cellular differentiation, such that altered expression of E1F2C1 can
XX affect cell growth, morphology and tumorigenicity. Accordingly,
XX antisense oligonucleotides that inhibit the expression of E1F2C1 in cells
XX or tissues can be used in gene therapy to treat various conditions
XX including hyperproliferative disorders, familial hypercholesterolaemia
XX and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX progeroid syndrome. As such, the oligos of the present invention can be
XX described as having cytostatic and antilipemic activities. This
XX oligonucleotide sequence is the PCR probe used to isolate human
XX eukaryotic translation initiation factor 2C 1 (E1F2C1) DNA of the
XX invention.
XX
XX
XX Sequence 24 BP; 4 A, 9 C; 6 G; 5 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.3%; Score 24; DB 1; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 71;
XX Matches 24; Conservatve 0; Mismatches 0; Indels 0; Gaps 0
OY 1774 CCAGGGAAGACCGCGGTGTATGCT 1797
DB 24 CCAGGGAAGACCGCGGTGTATGCT 1
XX
XX
XX RESULT 21
XX ID AA083645
XX AA083645 standard; DNA; 35 BP.
XX

```

AC	AAV83645;
XX	
DT	01-MAR-1999 (first entry)
DE	Oligonucleotide used in the construction of assay plasmids.
XX	
KW	Repetitive sequence; carcinogenic; human dietary component;
KM	DNA instability; cancer; diet; primer; ss.
XX	
OS	Synthetic.
XX	
PN	WO9845476-A1.
PD	15-OCT-1998.
XX	
PF	08-APR-1998; 98WO-GB0008659.
XX	
PR	08-APR-1997; 97GB-00007141.
XX	
PA	(FOOD-) FOOD RES INST.
XX	
PI	Schweizer M;
XX	
DR	WPI; 1999-024011/02.
XX	
PT	Assay for testing the carcinogenic properties of a test substance - by
XX	introduction of a reporter gene expression vector containing a repetitive
PT	DNA sequence that is unstable in cancer cells.
XX	
PS	Disclosure; Page 17; 103pp; English.
XX	
CC	The present sequence represents an oligonucleotide used in the
CC	construction of assay plasmids, which are used in the course of the
CC	invention. The specification describes an assay for testing the
CC	carcinogenic properties of a test substance. The assay comprises
CC	introducing into cells a reporter gene expression vector comprising a
CC	repetitive DNA sequence which exhibits instability in cancer cells;
CC	whereby instability of the repetitive DNA sequence affects expression of
CC	the reporter gene, exposing the resulting cells to the test substance and
CC	determining whether the test substance is carcinogenic or anti-
CC	carcinogenic by comparing the frequency of reporter gene expression in
CC	the resulting cells with the frequency of reporter gene expression in
CC	cells which have not been exposed to the test substance. The assay can be
CC	used to identify human dietary components that protect against DNA
CC	instability, and therefore some types of cancer, and can be used to
CC	contribute to the scientific basis for a healthy diet
XX	
SO	Sequence 35 BP; 2 A; 6 C; 5 G; 22 T; 0 U; 0 Other;
Query Match	0.3%; Score 23.6; DB 1; Length 35;
Best Local Similarity	86.7%; Pred.No.1.5e+02;
Matches 26; Conservative	0; Mismatches 4; Indels 0; Gaps 0
QY	4454 TGGCATGACTTTTTTTTTTTTTTTTTTTT 4483 3 TTGCCCGGCCTTTTTTTTTTTTTTTTTTTT 32
DB	
RESULT 22	
AA563444/C	
ID AA563444 standard; DNA; 35 BP.	
XX	
AC AA563444;	
XX	
DT 29-JAN-2002 (first entry)	
XX	
DE Oligonucleotide-nanoparticle probe #65.	
XX	
KW Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;	
KM nucleic acid detection; nanostructure; biochip; biofilter; drug delivery;	
XX ss.	
XX	
OS Synthetic.	

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XX PN WO200173123-A2.
XX PD 04-OCT-2001.
XX PF 28-MAR-2001, 2001WO-US010071.
XX PR 28-MAR-2000, 2000US-0192699P.
PR 26-APR-2000, 2000US-0200161P.
PR 26-JUN-2000, 2000US-00603830.
PR 26-JUN-2000, 2000US-0213906P.
PR 08-DEC-2000, 2000US-0254392P.
PR 11-DEC-2000, 2000US-0255235P.
PR 12-JAN-2001, 2001US-00760500.
PR 28-MAR-2001, 2001US-00820279.
XX PA (NANO-) NANOSPHERE INC.
XX PI Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;
PI Taton TA, Park S, Li Z;
XX DR WPI; 2001-656926/75.
XX PT Detecting and separating nucleic acid, useful e.g. for diagnosis
PT complementary to parts of the target.
XX PS Example 25; Fig 45; 404pp; English.
XX SC The invention relates to a method for detection of nucleic acid (I)
CC having at least 2 portions, comprising treatment with nanoparticles that
CC carry oligonucleotides complementary to at least 2 parts of (I), where
CC detectable change caused by hybridisation of the oligonucleotide to (I)
CC is observed. The method is used to detect (or to separate) specific (I),
CC e.g. for diagnosing a wide variety of diseases, sequencing, in forensic
CC analysis etc., and generally to detect analytes other than (I). The
CC oligonucleotide-derived nanoparticles are also useful for preparing
CC nanostructures useful, for example, as biochips, biofilters, mechanical
CC devices, separation membranes, chemical sensors, in computers, and for
CC drug delivery. Very stable nanoparticle-oligonucleotide conjugates can be
CC produced, allowing their direct use (as probes) in polymerase chain
CC reaction, i.e. they survive multiple heating/cooling cycles so do not
CC need to be added after amplification. (I) are detected by simple colour
CC change, without the need for special equipment, making possible rapid
CC field testing for e.g. pathogens. AAS63374-AAS63448 represent
CC oligonucleotide-nanoparticle probes, and related sequences, used in the
CC method of the invention
XX SQ Sequence 35 BP, 25 A; 3 C; 0 G; 7 T; 0 U; 0 Other;
XX SC
XX SC Query Match 0.3%; Score 23.6; DB 1; Length 35;
XX SC Best Local Similarity 86.7%; Pred. No. 1.5e+02;
XX SC Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4454 TGGCATGACATTTTCTTTTCTTTTCTTTT 4483
DB 30 TGATAAGGATTTTCTTTTCTTTTCTTTT 1

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RESULT 23
ABK65052/C
ID ABK65052 standard; DNA; 35 BP.
AC ABK65052;
XX
XX
DT 02-JUL-2002 (first entry)
XX
XX Nanoparticle-oligonucleotide #72.
XX
XX Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
KM 88.
XX
OS Synthetic.

```

XX PN WO200218643-A2.
XX PD 07-MAR-2002.
XX PF 10-AUG-2001, 2001WO-US025237.
XX PR 11-AUG-2000, 2000US-0224631P.
PR 08-DEC-2000, 2000US-0254392P.
PR 11-DEC-2000, 2000US-0255235P.
PR 12-JAN-2001, 2001US-00760500.
PR 28-MAR-2001, 2001US-00820279.
XX PA (NANO-) NANOSPHERE INC.
XX PI Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z, Park S;
XX DR WPI; 2002-258024/30.
XX PT Detecting nucleic acid, useful for diagnosis of genetic, viral or
PT bacterial disease, comprises hybridizing nanoparticles with attached
PT oligonucleotides to nucleic acid and detecting change brought about by
PT hybridization.
XX PS Example 25; Fig 45; 412pp; English.
XX SC The invention relates to a method of detecting a nucleic acid (NA) having
CC at least 2 portions comprising: (a) providing nanoparticles (NP) with
CC attached oligonucleotides (OGN), where OGN has a sequence complementary
CC to the sequence of NA; (b) contacting NA and NP under conditions
CC effective to allow hybridisation of OGN with NA, and (c) observing a
CC detectable change brought about by hybridisation of OGN with NA. The
CC method is useful for detecting a nucleic acid, separating a selected
CC nucleic acid from others and methods of nanofabrication. Detecting
CC analytes such as nucleic acids and proteins are useful for the diagnosis
CC of genetic, bacterial and viral diseases. The OGN-NP conjugates that use
CC cyclic disulphide linkers improve the sensitivity of diagnostic assays.
CC In particular assays using OGN-NP conjugates prepared using linkers
CC comprising a steroid residue attached to a cyclic disulphide have been
CC found to be approximately 10 times more sensitive than assays employing
CC conjugates prepared using alkanethiols or acyclic disulphides as the
CC linker. The OGN-NP conjugates are stable allowing them to be used
CC directly in PCR solutions. Therefore conjugates added as probes to a DNA
CC target to be PCR amplified can be carried through the 30 or 40 heating
CC cooling cycles of the PCR and are still able to detect the amplicons
CC without opening the tubes and causing contamination. ABK64981-ABK65055
CC represent nanoparticle-oligonucleotides of the invention
XX SQ Sequence 35 BP, 25 A; 3 C; 0 G; 7 T; 0 U; 0 Other;
XX SC
XX SC Query Match 0.3%; Score 23.6; DB 1; Length 35;
XX SC Best Local Similarity 86.7%; Pred. No. 1.5e+02;
XX SC Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4454 TGGCATGACATTTTCTTTTCTTTTCTTTT 4483
DB 30 TGATAAGGATTTTCTTTTCTTTTCTTTT 1

```

RESULT 24
ABS64695/C
ID ABS64695 standard; DNA; 35 BP.
AC ABS64695;
XX
XX
DT 15-NOV-2002 (first entry)
XX
XX Nucleic acid detection method associated polynucleotide #77.
DE Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
XX Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KM nanoparticle; viral RNA detection; bacterial DNA detection;
KM fungal DNA detection; nanoprobe conjugate; 88.
XX

XX	Synthetic.
OS	
FN	WO200246472-A2.
XX	
PD	13-JUN-2002.
XX	
PF	07-DEC-2001; 2001WO-US046418.
XX	
PR	08-DEC-2000; 2000US-0254392P.
PR	08-DEC-2000; 2000US-0254418P.
PR	11-DEC-2000; 2000US-0255235P.
PR	11-DEC-2000; 2000US-0255236P.
PR	12-JAN-2001; 2001US-00760500.
PR	28-MAR-2001; 2001US-00820279.
PR	09-APR-2001; 2001US-0282640P.
PR	10-AUG-2001; 2001US-00927777.
XX	
PA	(NANO-) NANOSPHERE INC.
XX	
PI	Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Eighanlian R,
PI	Taton TA, Garimella V, Li Z, Park S;
DR	WPI; 2002-608256/65.
XX	
PT	Detecting nucleic acid having two portions, by providing nanoparticles
PT	having oligonucleotides attached to it, contacting nucleic acid and
PT	nanoparticles to allow hybridization, and observing detectable change.
XX	
PS	Disclosure, Page 56; 442pp; English.
XX	
CC	The invention describes a method of detecting (M1) a nucleic acid having
CC	two portions, involving providing nanoparticles having oligonucleotides
CC	attached to it, which has a sequence complementary to sequence of two
CC	portions of nucleic acid, contacting nucleic acid and nanoparticles, to
CC	allow hybridization of oligonucleotides with two or more portions of
CC	nucleic acid, and observing a detectable change brought about by
CC	hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
CC	conjugates (II) and the aggregate probe are useful for detecting two or
CC	more nucleic acids (from a biological source) having at least two
CC	portions, such as viral RNA, bacterial or fungal DNA, a gene associated
CC	with a disease, synthetic, or structurally-modified natural or synthetic
CC	RNA or DNA, or a product of a polymerase chain reaction amplification.
CC	(II) is useful for preparing a nanoprobe conjugate for detecting an
CC	analyte, and for detecting a nucleic acid bound to an electrode surface.
CC	(I) and (II) are useful for fabrication, and for separating a selected
CC	nucleic acid having two portions from other nucleic acids. (I), (II) and
CC	the aggregate probe are useful for detecting an analyte (especially
CC	polyvalent analyte) in a sample. This sequence represents a
CC	polynucleotide used to demonstrate the method of the invention
XX	
SO	Sequence 35 BP; 25 A; 3 C; 0 G; 7 T; 0 U; 0 Other;
XX	
Query Match	0.3%; Score 23.6; DB 1; Length 35;
Best Local Similarity	86.7%; Pred. No. 1.5e+02;
Matches 26; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
XX	
QY	.4454 TGGCATGCACCTTTTTTTTTTTTTTTTTTTT 4483
DB	30 TGATAGGATTTTTTTTTTTTTTTTTTTTTTTT 1
XX	
RESULT 25	
ID	ABSG4690/C
AC	ABSG4690 standard; DNA; 35 BP.
XX	
DT	15-NOV-2002 (first entry)
XX	
DE	Nucleic acid detection method associated polynucleotide #72.
XX	
KW	Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;

KW		nanoparticle; viral RNA detection; bacterial DNA detection;
KV		fungal DNA detection; nanoprobe conjugate; ss.
XX	OS	Synthetic.
XX	PN	WO200246472-A2.
XX	PD	13-JUN-2002.
XX	PF	07-DEC-2001; 2001WO-US046418.
XX	PR	08-DEC-2000; 2000US-0254392P.
XX	PR	08-DEC-2000; 2000US-0254418P.
XX	PR	11-DEC-2000; 2000US-0255235P.
XX	PR	11-DEC-2000; 2000US-0255235P.
XX	PR	12-JAN-2001; 2001US-0076050U.
XX	PR	28-MAR-2001; 2001US-00820279.
XX	PR	09-APR-2001; 2001US-0282640P.
XX	PR	10-AUG-2001; 2001US-00927777.
XX	PA	(NANO-) NANOSPHERE INC.
XX	PI	Mitkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Eghanian R,
XX	PI	Tacon TA, Garimella V, Li Z, Park S;
XX	WP	WI: 2002-608256/65.
DR	XX	Detecting nucleic acid having two portions, by providing nanoparticles
PT	XX	having oligonucleotides attached to it, contacting nucleic acid and
PT	XX	nanoparticles to allow hybridization, and observing detectable change.
PS	XX	Example 25; Fig 45; 442pp; English.
CC	XX	The invention describes a method of detecting (M1) a nucleic acid having
CC	XX	two portions, involving providing nanoparticles having oligonucleotides
CC	XX	attached to it, which has a sequence complementary to sequence of two
CC	XX	portions of nucleic acid, contacting nucleic acid and nanoparticles, to
CC	XX	allow hybridisation of oligonucleotides with two or more portions of
CC	XX	nucleic acid, and observing a detectable change brought about by
CC	XX	hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
CC	XX	conjugates (II) and the aggregate probe are useful for detecting two or
CC	XX	more nucleic acids (from a biological source) having at least two
CC	XX	portions, such as viral RNA, bacterial or fungal DNA, a gene associated
CC	XX	with a disease, synthetic, or structurally-modified natural or synthetic
CC	XX	RNA or DNA, or a product of a polymerase chain reaction amplification.
CC	XX	(II) is useful for preparing a nanoprobe conjugate for detecting an
CC	XX	analyte, and for detecting a nucleic acid bound to an electrode surface.
CC	XX	(I) and (II) are useful for fabrication, and for separating a selected
CC	XX	nucleic acid having two portions from other nucleic acids. (I), (II) and
CC	XX	the aggregate probe are useful for detecting an analyte (especially
CC	XX	polyvalent analyte) in a sample. This sequence represents a
CC	XX	polynucleotide used to demonstrate the method of the invention
SO	XX	Sequence 35 BP; 25 A; 3 C; 0 G; 7 T; 0 U; 0 Other:
OY	DB	Query Match 0.3%; Score 23.6; DB 1; Length 35; Best Local Similarity 86.7%; Pred.No.1.5e+02; Matches 26; Conservative 0; Pmismatches 4; Indels 0; Gaps 0;
DB	XX	4454 TGGCATGACCTTTTTTTTTTTTTTTT 4483 30 TGATPAGGATTTCCTTTTTTTTTTTTTTTT 1
ID	AA	AAAL61667/c
XX	AA	AAAL61667 standard; DNA; 35 BP.
XX	AA	AAAL61667;
DT	22-SEP-2003	(first entry)
DE		Oligonucleotide #26 used in the nucleic acid detection method.

XX Nucleic acid detection; fabrication; ss.
 XX Unidentified.
 OS
 XX
 XX
 FT misc_feature 35 Location/Qualifiers
 FT /*tag= a
 FT /note= "Linked to steroid disulphide"
 XX
 XX WO2003035829-A2.
 PN
 PD 01-MAY-2003.
 XX
 XX 08-OCT-2002; 2002WO-US032088.
 PF
 XX 09-OCT-2001; 2001US-0327864P.
 PR 07-DEC-2001; 2001US-00008978.
 XX
 XX (NANO-) NANOSPHERE INC.
 PA
 XX
 XX Park S, Taton TA, Mirkin CA;
 PI
 DR WPI; 2003-430409/40.
 XX
 XX Detecting nucleic acid having two portions, by providing nanoparticles
 PT having oligonucleotides attached to it, contacting nucleic acid and
 PT nanoparticles to allow hybridization, and observing detectable change.
 XX
 XX Disclosure; Page 58; 467pp; English.
 PS
 XX The invention relates to a method of detecting a nucleic acid having two
 CC portions. The method involves providing nanoparticles having
 CC oligonucleotides attached to it which has a sequence complementary to
 CC sequence of two portions of nucleic acid, contacting nucleic acid and
 CC nanoparticles to allow hybridization of oligonucleotides with two or more
 CC portions of nucleic acid and observing a detectable change brought about
 CC by hybridization. The method and aggregate probes are useful for
 CC detecting two or more nucleic acids (from a biological source) having at
 CC least two portions such as viral RNA, bacterial or fungal DNA, a gene
 CC associated with a disease, synthetic or structurally modified natural or
 CC synthetic RNA or DNA, or a product of a polymerase chain reaction
 CC amplification. The invention is useful for preparing a nanoprobe
 CC conjugate for detecting an analyte and for detecting a nucleic acid bound
 CC to an electrode surface. It is also useful for fabrication and for
 CC separating a selected nucleic acid having two portions from other nucleic
 CC acids. The present sequence is an oligo used to illustrate the method of
 CC the invention
 XX
 XX Sequence 35 BP; 25 A; 3 C; 0 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 0.3%; Score 23.6; DB 1; Length 35;
 Best Local Similarity 86.7%; Pred. No. 1.5e+02;
 Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4454 TGGCATGAGCTTTT TTTT TTTT TTTT TTTT 4483
 DB 30 TGATAGGATTTT TTTT TTTT TTTT TTTT 1
 RESULT 27
 AAL61662/c
 ID AAL61662 standard; DNA; 35 BP.
 XX
 XX AAL61662;
 AC
 XX
 XX 22-SRP-2003 (first entry)
 DT
 XX
 XX Oligonucleotide #22 used in the nucleic acid detection method.
 DE
 XX
 XX Nucleic acid detection; fabrication; ss.
 KM
 XX
 XX Unidentified.
 OS

XX
 PN WO2003035829-A2.
 XX
 XX 01-MAY-2003.
 PD
 XX
 XX 08-OCT-2002; 2002WO-US032088.
 PF
 XX 09-OCT-2001; 2001US-0327864P.
 PR 07-DEC-2001; 2001US-00008978.
 XX
 XX (NANO-) NANOSPHERE INC.
 PA
 XX
 XX Park S, Taton TA, Mirkin CA;
 PI
 DR WPI; 2003-430409/40.
 XX
 XX Detecting nucleic acid having two portions, by providing nanoparticles
 PT having oligonucleotides attached to it, contacting nucleic acid and
 PT nanoparticles to allow hybridization, and observing detectable change.
 XX
 XX Example 25; Fig 45; 467pp; English.
 PS
 XX The invention relates to a method of detecting a nucleic acid having two
 CC portions. The method involves providing nanoparticles having
 CC oligonucleotides attached to it which has a sequence complementary to
 CC sequence of two portions of nucleic acid, contacting nucleic acid and
 CC nanoparticles to allow hybridization of oligonucleotides with two or more
 CC portions of nucleic acid and observing a detectable change brought about
 CC by hybridization. The method and aggregate probes are useful for
 CC detecting two or more nucleic acids (from a biological source) having at
 CC least two portions such as viral RNA, bacterial or fungal DNA, a gene
 CC associated with a disease, synthetic or structurally modified natural or
 CC synthetic RNA or DNA, or a product of a polymerase chain reaction
 CC amplification. The invention is useful for preparing a nanoprobe
 CC conjugate for detecting an analyte and for detecting a nucleic acid bound
 CC to an electrode surface. It is also useful for fabrication and for
 CC separating a selected nucleic acid having two portions from other nucleic
 CC acids. The present sequence is an oligo used to illustrate the method of
 CC the invention
 XX
 XX Sequence 35 BP; 25 A; 3 C; 0 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 0.3%; Score 23.6; DB 1; Length 35;
 Best Local Similarity 86.7%; Pred. No. 1.5e+02;
 Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4454 TGGCATGAGCTTTT TTTT TTTT TTTT TTTT 4483
 DB 30 TGATAGGATTTT TTTT TTTT TTTT TTTT 1
 RESULT 28
 AAD27123/c
 ID AAD27123 standard; RNA; 36 BP.
 XX
 XX AAD27123;
 AC
 XX
 XX 09-APR-2002 (first entry)
 DT
 XX
 XX RNA template CC(AU)26G for directing RNA synthesis by HCV RNA polymerase.
 DE
 XX
 XX Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
 KM lead compound; RNA polymerase; ss.
 XX
 XX Unidentified.
 OS
 XX US6322966-B1.
 PN
 XX
 XX 27-NOV-2001.
 PD
 XX
 XX 11-MAY-1999; 99US-00309670.
 PF
 XX
 XX 11-MAY-1999; 99US-00309670.
 PR

XX (ZHON/) ZHONG W.
PA (HONG/) HONG Z.
FA (LAOU/) LAO J Y N.
P1 Zhong W, Hong Z, Lau JYN;
XX
XX MPI, 2002-096587/13.
DR
PT Assay system for hepatitis C virus replicase activity comprises RNA
PT template with unstable, small stemloop capable of forming copy-back
PT structure, viral non-structural protein 5B, nucleoside triphosphates,
PT buffer.

Example 1; Fig 1C; 10pp; English.

The present invention relates to an assay system for hepatitis C virus (HCV) replicase activity. The assay system comprises an RNA template that has an unstable, small stemloop at the 3' end capable of forming a copy-back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP, and UTP nucleoside triphosphates (NTPs), where one of the NTP is radiolabelled and an assay buffer that supports replication activity of NS5B. The invention also relates to the identification of optimal properties of an RNA template for copy-back self-priming RNA synthesis of HCV. This activity can be used to screen for anti-HCV replicase compounds or to characterise the biological relevance of lead compounds. The optimal RNA templates can be used for developing a system to characterise HCV NS5B polymerase mechanistically and kinetically and for designing small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay system of the invention is useful for detecting HCV replicase activity. The nucleic acid synthesised by NS5B is detected by evaluating an autoradiograph of reaction products separated by gel electrophoresis. The present sequence is RNA template, CC(AU)2GG used to direct RNA synthesis by RNA polymerase proteins of HCV, BVDV and poliovirus. This sequence is used in the exemplification of the invention

SQ Sequence 36 BP; 28 A; 2 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 0.3%; Score 23.6; DB 1; Length 36;
Best Local Similarity 86.7%; Pred. No. 1.5e+02;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0.

CY 4458 ATGCAGCTTTTGTGCT 4487
DB 32 ATGCGTTTTTTTTTTTTTTT 3

RESULT 29
ABZ81767
ID ABZ81767 standard; DNA; 25 BP.
XX AC
XX ABZ81767;
DT 11-JUN-2003 (first entry)
DE
XX
DE Huntingdon's disease gene target region.
KW Huntingdon's disease; neurotropic; anticonvulsant; huntingtin; human;
KW gene therapy; ds.
OS Homo sapiens.
XX
XX
FH Key location/Qualifiers
FT misc_binding 1..25
FT /*tag= a
FT /bound_moiety= "Oligonucleotide"
FT /note= "hybridises to bases 1-25 of sequence given in
FT "ABZ81768"
FT misc_difference 13
FT /*tag= b
FT /note= "replaced by T following treatment"

WO2003013437-A2.

[illegible]

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PR 08-AUG-2001; 2001US-0310770P.
PR 08-AUG-2001; 2001US-0310889P.
PR 04-DEC-2001; 2001US-0337219P.
XX
XX (UYDE ) UNIV DELAWARE.
XX
XX Kniec EB, Parekh-Olmedo H;
XX
XX WPI; 2003-256478/25.
XX
XX
XX New single stranded oligonucleotides comprising a DNA domain having at
XX least one mismatch with respect to the genetic sequence of the
XX Huntington's disease gene to be altered, useful for treating or
XX preventing Huntington's disease.
XX
XX Example 1; Fig 6a; 133pp; English.
XX
XX The present sequence is that of a portion of a 52-mer RNA/DNA chimeric
XX oligonucleotide of the the glutamine (CAG) that is targeted to triplet
XX repeat region (see AB281767) of exon 1 of the human Huntington's disease
XX (HD) gene. This targeting results in a CAG (stop codon) nucleotide
XX exchange due to sliding of the repeat region, a phenomenon that can occur
XX with the methods of this invention. The oligonucleotide is an example of
XX claimed oligonucleotides of the invention for targeted alteration of the
XX HD gene. Such oligonucleotides can be used for the treatment or
XX prevention of HD
XX
XX Sequence 25 BP; 0 A; 8 C; 9 G; 0 T; 8 U; 0 Other;
XX
XX
XX Query Match 0.3%; Score 23.4; DB 1; Length 25;
XX Best Local Similarity 96.0%; Pred. No. 96;
XX Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX
XX 7410 CATCAGCAGCAGCAGCAGCAGCAGC 7434
XX |||||
XX 25 CAGCAGCAGCAGCAGCAGCAGCAGC 1
XX
XX
XX RESULT 31
XX AAQ95104
XX ID AAQ95104 standard; cDNA; 33 BP.
XX
XX AC AAQ95104;
XX
XX 06-MAR-1996 (first entry)
XX
XX Antisense 33mer phosphodiester-linked DNA helper.
XX
XX Antisense; phosphodiester linked; DNA helper; ss.
XX
XX Synthetic.
XX
XX Key misc_location/Qualifiers
XX FT 1.33
XX FT /tag= a
XX FT /note= "phosphodiester linked"
XX
XX WO9520679-A1.
XX
XX 03-AUG-1995.
XX
XX 26-JAN-1995; 95WO-US001048.
XX
XX 26-JAN-1994; 94US-00187694.
XX
XX (HYBR-) HYBRIDON INC.
XX
XX Cohen AS, Belenky A, Vilenchik M;
XX
XX WPI; 1995-275462/36.
XX
XX Detection of single-stranded oligo:nucleotide(s) - by annealing a
XX fluorescently labelled primer and a helper followed by a ligation

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PT reaction.
XX
XX Example; Page 33; 46pp; English.
XX
XX AAQ95104 is an antisense 33mer phosphodiester linked DNA helper. It was
XX used to demonstrate a new method for the detection of single stranded
XX oligonucleotides, including analogues and antisense oligos in biological
XX fluids
XX
XX Sequence 33 BP; 2 A; 1 C; 7 G; 23 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.3%; Score 23.4; DB 1; Length 33;
XX Best Local Similarity 81.8%; Pred. No. 1.5e+02;
XX Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX
XX 4450 TGGGTGCGATGACCTTTTGTGTTTGT 4482
XX |||||
XX 1 TGGGTGCGAGAGTTTGTGTTTGTGTTT 33
XX
XX
XX RESULT 32
XX ACC42844/c
XX ID ACC42844 standard; DNA; 33 BP.
XX
XX AC ACC42844;
XX
XX 01-SEP-2003 (first entry)
XX
XX DT
XX
XX Nuclear transition protein I-9.57 PCR primer #4.
XX
XX DE
XX
XX Nuclear transition protein I-9.57; tumour; cytostatic; haemopathy; PCR;
XX HIV infection; anti-HIV; immunological disease; inflammation; primer; ss.
XX
XX Unidentified.
XX
XX OS
XX
XX CN1380328-A.
XX
XX PN
XX
XX 20-NOV-2002.
XX
XX PD
XX
XX 10-APR-2001; 2001CN-00105924.
XX
XX PF
XX
XX 10-APR-2001; 2001CN-00105924.
XX
XX PR
XX
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
XX PA
XX
XX Mao Y, Xie Y;
XX
XX PI
XX
XX WPI; 2003-222560/22.
XX
XX DR
XX
XX Polypeptide-nuclear transformation protein -9.57 and polynucleotide for
XX coding this polypeptide.
XX
XX PS
XX
XX Example 5; Page 27; 29pp; Chinese.
XX
XX CC The present invention relates to nuclear transition protein I-9.57 and
XX its coding sequence. The protein can be used for treating several
XX diseases, such as malignant tumours, haemopathy, HIV infection,
XX immunological disease and various inflammations. The present sequence is
XX a PCR primer, which was used in an example from the invention. Note: The
XX present sequence is SRO ID 6 from the sequence listing. This sequence
XX differs from the SEQ ID 6 shown in the disclosure (see ACC42932)
XX
XX
XX Sequence 33 BP; 24 A; 4 C; 2 G; 3 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.3%; Score 23.4; DB 1; Length 33;
XX Best Local Similarity 81.8%; Pred. No. 1.5e+02;
XX Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX
XX 4464 TTTTGTGTTTGTGTTTGTGTTGTCATG 4496
XX |||||
XX 33 TTTTGTGTTTGTGTTTGTGTTGTCATG 1
XX

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```

RESULT 33
AAC63568
ID AAC63568 standard; DNA; 34 BP.
XX
AC AAC63568;
XX
DT 08-FEB-2001 (first entry)
XX
DE Minisequencing detection primer #6.
XX
XX PCR primer; restriction fragment identification;
XX polymorphic AFLP fragment; rice; plant breeding; ss.
XX
OS Oryza sativa.
XX
PN WO200061800-A2.
XX
PD 19-OCT-2000.
XX
PF 10-APR-2000; 2000WO-NL000234.
XX
PR 09-APR-1999; 99EP-00201112.
XX
PA (KEYG-) KEYGENE NV.
XX
PI Van Eljk MJT, Witsenboer H;
XX
DR WPI; 2000-679498/66.
XX
XX
PT Determining the presence of restriction fragments in restriction fragment
PT sample mixture comprises specific extension/elongation of an
PT oligonucleotide sequence that is complementary to a fragment to be
PT detected.
XX
PS Example 8; Page 34; 51pp; English.
XX
XX
CC The present invention relates to a method for determining the presence or
CC absence of a target restriction fragment in a mixture of restriction
CC fragments, using an oligonucleotide sequence that is complementary to
CC part of the target restriction fragment. The present sequence is a PCR
CC primer. This primer was used to sequence a polymorphic AFLP fragment from
CC a sample of rice DNA. The AFLP fragment was used to exemplify the method
CC of the present invention. The method of the present invention is useful
CC for analysing nucleic acid sequences, e.g. for determining the presence
CC or absence of AFLP markers especially for routine and/or throughput
CC screening, for instance, in plant breeding
XX
SQ Sequence 34 BP; 3 A; 4 C; 8 G; 19 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 23.4; DB 1; Length 34;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
QY 4469 TTTTGTCTGTGACATGGGGTT 4501
DB 1 TTTTGTCTGTGACATGGGGTT 33
XX
RESULT 34
AB281770
ID AB281770 standard; DNA; 35 BP.
XX
AC AB281770;
XX
XX 11-JUN-2003 (first entry)
XX
DE Huntington's disease gene target region for oligonucleotide HD3T/25.
XX
XX Huntington's disease; noctropic; anticonvulsant; huntingtin; human;
XX gene therapy; ds.
XX
OS Homo sapiens.
XX

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```

FH Key Location/Qualifiers
FT misc_binding 5..15
FT /tag= a
FT /bound moiety= "Oligonucleotide HD3T/25"
FT /note= "Hybridises to bases 15-25 of sequence given in
FT AB281771"
FT misc_difference 16
FT /tag= b
FT /note= "mismatch with oligonucleotide HD3T/25"
FT misc_binding 17..29
FT /tag= a
FT /bound moiety= "Oligonucleotide HD3T/25"
FT /note= "Hybridises to bases 1-13 of sequence given in
FT AB281771"
XX
PN WO2003013437-A2.
XX
XX 20-FEB-2003.
XX
PF 07-AUG-2002; 2002WO-US025352.
XX
PR 07-AUG-2001; 2001US-0310757P.
PR 08-AUG-2001; 2001US-0310770P.
PR 08-AUG-2001; 2001US-0310889P.
PR 04-DEC-2001; 2001US-0337219P.
XX
XX (UYDE ) UNIV DELAWARE.
XX
XX Kmiec EB, Parekh-Olmado H;
XX
DR WPI; 2003-256478/25.
XX
XX
PT New single stranded oligonucleotides comprising a DNA domain having at
PT least one mismatch with respect to the genetic sequence of the
PT Huntington's disease gene to be altered, useful for treating or
PT preventing Huntington's disease.
XX
PS Example 4; Fig 13a; 133pp; English.
XX
XX
CC The present sequence is that of a portion of the glutamine triplet repeat
CC region of exon 1 of the human Huntington's disease (HD) gene (see also
CC AB281760). This region of exon 1 is targeted by a modified single-
CC stranded oligonucleotide of the invention, HD3T/25 (see AB281771), which
CC has a single mismatch with respect to the present target sequence, and
CC which converts a CAG (glutamine) codon in HD exon 1 to CUG (leucine).
CC HD3T/25 is an example of claimed oligonucleotides for targeted alteration
CC of the HD gene that comprise a chemically modified single-stranded
CC oligonucleotide having at least one mismatch with respect to the HD gene.
CC Such oligonucleotides can be used for the treatment or prevention of HD,
CC and also have the effect of inhibiting the formation of huntingtin
CC aggregates, a characteristic of HD
XX
SQ Sequence 35 BP; 10 A; 12 C; 9 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 23.4; DB 1; Length 35;
Best Local Similarity 81.8%; Pred. No. 1.6e+02;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
QY 7403 CAAGCAATCATGACGACGACGACGACGCA 7435
DB 2 CAAGTCCTTCAGACGACGACGACGACGCA 34
XX
RESULT 35
AAA40362
ID AAA40362 standard; DNA; 28 BP.
XX
AC AAA40362;
XX
XX 10-NOV-2000 (first entry)
XX
DE PbluescriptSK+ phagemid primer SEQ ID NO: 12.
XX

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KM Primer; cloning; ligation; ss.
XX
XX Synthetic.
XX
XX WO200036088-A1.
XX
XX 22-JUN-2000.
XX
XX 17-DEC-1999; 99WO-US030277.
XX
XX 17-DEC-1998; 98US-00213834.
XX
XX (ROMA/) ROMANTCHIKOV Y.
XX
XX Romanchikov Y;
XX
XX WPI; 2000-442381/38.
XX
XX Inserting a nucleic acid into a circular vector comprising joining their
XX ends, melting, and reannealing ends at two different concentrations,
XX useful for cloning small amounts of nucleic acids and forming genomic
XX libraries.
XX
XX Example 4; Page 68; 71pp; English.
XX
XX This invention describes a novel method (M1) for inserting a nucleic acid
XX (N1) into a circular vector (V1) comprising joining ends of N1 and V1
XX under a first nucleic acid concentration, melting hybridized cohesive
XX circularization ends, and reannealing the ends at a second concentration.
XX The methods are useful for the cloning small amounts of nucleic acids and
XX forming genomic libraries of complex populations of DNA or cDNA. The
XX methods allow the cloning of minute amounts of nucleic acids efficiently
XX and avoids the size selection problems of prior art systems. Larger
XX nucleic acid fragments are just as easily cloned, allowing highly
XX representative libraries to be made. Vector to vector ligation is avoided
XX using the methods. AAA40351-A40366 represents primers used to illustrate
XX the method of the invention
XX
XX Sequence 28 BP; 0 A; 2 C; 2 G; 24 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 23.2; DB 1; Length 28;
XX Best Local Similarity 89.3%; Pred. No. 1.2e+02;
XX Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 4460 GGACTTTTTTTTTTTTTTTTTGCTC 4487
XX 1 GGCCTTTTTTTTTTTTTTTTTTTT 28
XX
XX RESULT 36
XX AAQ83940/c
XX ID AAQ83940 standard; DNA; 30 BP.
XX
XX AC AAQ83940;
XX
XX 25-MAR-2003 (revised)
XX 04-OCT-1995 (first entry)
XX
XX Oligonucleotide clamp o, for producing comb-type branched polymer.
XX
XX HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss.
XX
XX Synthetic.
XX
XX OS
XX
XX Key location/Qualifiers
XX FH modified_base 1
XX PT /*tag= a
XX PT /note= "Modified with SP(O-)(=O)-"
XX
XX MO9501365-A1.
XX
XX 12-JAN-1995.
XX

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PF 05-JUL-1994; 94WO-US007557.
XX
XX 02-JUL-1993; 93US-00087386.
XX
XX (LYNX-) LYNX THERAPEUTICS INC.
XX
XX PI Gryaznov SM;
XX
XX WPI; 1995-060944/08.
XX
XX Synthesis of branched polymers and novel branched polymeric structures -
XX used as molecular probes esp. for detecting poly-nucleotide(s).
XX
XX Example 8; Page 33; 52pp; English.
XX
XX The sequences given in AAQ83938, AAQ83952 and AAQ83940 are used in the
XX construction of an oligonucleotide clamp. The clamp is a comb-type
XX branched polymer which has 3' termini and was used to bind a target
XX sequence comprising a segment of the HIV pol and nef genes in single
XX stranded or double stranded forms. An oligonucleotide clamp is a compound
XX capable of forming a covalently closed macromolecule or a stable circular
XX complex after specifically binding to the target polynucleotide.
XX Oligonucleotide clamps generally comprise one or more oligonucleotide
XX moieties capable of specific binding to the target molecule and one or
XX more pairs of binding moieties covalently linked to the oligonucleotide
XX moieties. Upon annealing of the oligonucleotides moieties to the target
XX polynucleotide, the binding moieties of a pair are brought into
XX juxtaposition so that they form a stable covalent or non-covalent linkage
XX or complex. The interaction of the binding moieties effectively clamps
XX the specifically annealed oligonucleotide moieties to the target
XX polynucleotide. (updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 30 BP; 27 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 23.2; DB 1; Length 30;
XX Best Local Similarity 89.3%; Pred. No. 1.4e+02;
XX Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 4464 TTTTTTTTTTTTTTTTTTTGCTTGAG 4491
XX 30 TTTTTTTTTTTTTTTTTTTTGTG 3
XX
XX RESULT 37
XX AAF60462/c
XX ID AAF60462 standard; DNA; 30 BP.
XX
XX AC AAF60462;
XX
XX 27-APR-2001 (first entry)
XX
XX Oligonucleotide clamp #22.
XX
XX Oligonucleotide clamp; ds.
XX
XX Unidentified.
XX
XX OS
XX
XX US6180777-B1.
XX
XX 30-JAN-2001.
XX
XX 03-JAN-1997; 97US-00787321.
XX
XX 12-JAN-1996; 96US-0009918P.
XX
XX (PARB ) BAYER CORP.
XX
XX Horn T;
XX
XX WPI; 2001-201911/20.
XX
XX Synthesizing branched nucleic acids useful as diagnostic and molecular
XX probes, involves combining first units having halokylamino groups and
XX

```

PT second units having thiol or phosphorothioate groups.
 XX
 PS Example 8; Col 19; 20pp; English.
 XX
 CC The present invention relates to a method for synthesizing a branched or
 CC multiply connected macromolecular structure, comprising oligonucleotide
 CC clamps (OC). The macromolecular structure is capable of specifically
 CC binding to a target molecule, and can therefore be used as probes. At
 CC least one OC comprises a target binding sequence that binds specifically
 CC and stably with the target molecule, and at least two OCs comprise signal
 CC generation moieties capable of generating a detectable signal in the
 CC presence of the target molecule. In addition the OCs are connected to one
 CC another by thiolalkylamino, or thiophosphorylalkylamino bridges. The
 CC present sequence is an OC used in the present invention
 XX
 SQ Sequence 30 BP; 27 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 0.3%; Score 23.2; DB 1; Length 30;
 Best Local Similarity 89.3%; Pred. No. 1.4e+02;
 Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4464 TTTTGTCTGCTGAG 4491
 Db 30 TTTTGTCTGCTGAG 3
 RESULT 38
 ADA26489/c
 ID ADA26489 standard; DNA; 32 BP.
 XX
 AC ADA26489;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE DNA nanolithography method example oligonucleotide G1.
 KW ss; direct-write nanolithography; nanoscopic tip; nanoscale pattern;
 KM patterning; scanning probe microscopic tip; nanoparticle; nanoarray.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 32 /*tag= a
 FT /mod_base= OTHER
 FT /note= "contains a thiol group (CH2)3SH at the 5' end"
 FT
 XX
 FN WO2003048314-A2.
 XX
 PD 12-JUN-2003.
 XX
 PF 02-DEC-2002; 2002WO-US038252.
 XX
 PR 30-NOV-2001; 2001US-0337598P.
 XX
 PR 07-MAR-2002; 2002US-0362924P.
 XX
 PA (UNW-) UNIV NORTHWESTERN TECHNOLOGY TRANSFER PR.
 XX
 PI Mirkin CA, Demers ML, Ginger DS;
 XX
 DR WPI; 2003-671287/63.
 XX
 PT Depositing nucleic acid on substrate by direct-write nanolithography, by
 PT positioning nanoscopic tip relative to substrate, to transfer nucleic
 PT acid to substrate and generate stable nucleic acid nanoscale pattern.
 XX
 PS Disclosure; Page 38; 76pp; English.
 XX
 CC The invention relates to a method of depositing nucleic acid onto a
 CC substrate by direct-write nanolithography, by positioning at least one
 CC nanoscopic tip relative to a substrate so that the tip and substrate
 CC approach each other, and the nucleic acid is transferred from the tip to
 CC the substrate to generate a stable nucleic acid nanoscale pattern on the

CC substrate which is hybridizable with complementary nucleic acid. The
 CC method is useful for generating nanoscale patterns of nucleic acid on a
 CC substrate, in which before transfer the tip is modified to allow the
 CC nucleic acid to wet the tip and the nucleic acid is modified to chemisorb
 CC or covalently bond to the substrate upon transfer. The method is also
 CC useful for direct patterning of modified nucleic acid onto a substrate,
 CC by linking a scanning probe microscopic tip with a modified nucleic acid
 CC and positioning the inked tip close enough to the substrate to effect
 CC transfer of the nucleic acid to the substrate to form a nanoscale
 CC pattern. Another use for the method is for assembling nanoparticles (e.g.
 CC gold nanoparticles) to form nanoscale patterns, by depositing from a
 CC nanoscopic tip a first nucleic acid onto a substrate to form a deposit
 CC with lateral nanoscale features of 1000 nm or less by direct write
 CC nanolithography, hybridizing the nucleic acid deposit with the
 CC nanoparticle, where the nanoparticle is functionalized with a second
 CC nucleic acid which is either complementary to the first or complementary
 CC to the nucleic acid of a linking strand which links the second nucleic
 CC acid to the first. Deposition of nucleic acid on the substrate is
 CC repeated to form a nanoarray of the nucleic acid and the hybridization is
 CC carried out with the nanoarray. The method is suitable for writing
 CC preconcieved nanoscale features directly, without use of expensive and
 CC potentially destructive methods such as electron beam and
 CC photolithographic methods. The structures can be built up, if desired,
 CC without degrading existing structures. Complicated stamps and resists are
 CC not needed. Improvements in the consistency and stability of the
 CC nanolithography can be observed. This sequence represents an example of a
 CC nucleic acid that can be used in the method of the invention.
 XX
 SQ Sequence 32 BP; 23 A; 4 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 0.3%; Score 23.2; DB 1; Length 32;
 Best Local Similarity 89.3%; Pred. No. 1.5e+02;
 Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4464 TTTTGTCTGCTGAG 4491
 Db 31 TTTTGTCTGCTGAG 4
 RESULT 39
 AAX88521
 ID AAX88521 standard; DNA; 33 BP.
 XX
 AC AAX88521;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE Conus stercusmuscarum contryphan PCR primer DHOG 496.
 XX
 KW Contryphan; leu-tryphan; anticonvulsant; neuroprotective; venom;
 KM cone snail; neurodegenerative disorder; epilepsy; neurotoxic injury;
 KM hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident;
 KM brain trauma; spinal chord trauma; myocardial infarct; physical trauma;
 KM drowning; suffocation; perinatal asphyxia; hypoglycaemia; migraine;
 KM senile dementia; Alzheimer's disease; amyotrophic lateral sclerosis;
 KM Parkinson's disease; Huntington's disease; Down's syndrome; PCR primer;
 KM Korsakoff's disease; schizophrenia; neuronal damage; seizure; ss.
 XX
 OS Synthetic.
 OS Conus stercusmuscarum.
 XX
 PN WO9933865-A1.
 XX
 PD 08-JUL-1999.
 XX
 PF 16-DEC-1998; 98WO-US026789.
 XX
 PR 24-DEC-1997; 97US-0068737P.
 XX
 PR 16-APR-1998; 98US-00061026.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 PI Jacobsen R, Jimenez E, Cruz LJ, Olivera BM, Gray WR, Grilley M,

PI Watkins M, Hillyard DR;
 XX
 DR WPI; 1999-419087/35.
 XX
 PT New pure contryphan peptides.
 XX
 PS Example 3; Page 20; 48pp; English.
 XX
 CC The present sequence represents a PCR primer for a contryphan
 CC peptide sequence. Contryphan peptides are found in the venom of cone
 CC snails. The contryphan peptides are useful as anticonvulsant agents, as
 CC neuroprotective agents, for managing pain, and for treating
 CC neurodegenerative disorders, especially those resulting from an
 CC overstimulation of excitatory amino acid receptors. The contryphans are
 CC useful for the treatment and alleviation of epilepsy and as a general
 CC anticonvulsant agent. The contryphans are also useful to reduce
 CC neurotoxic injury associated with conditions of hypoxia, anoxia, or
 CC ischemia which typically follows stroke, cerebrovascular accident, brain
 CC or spinal chord trauma, myocardial infarct, physical trauma, drownings,
 CC suffocation, perinatal asphyxia, or hypoglycaemic events. The contryphans
 CC are further useful for the treatment of Alzheimer's disease, senile
 CC dementia, amyotrophic lateral sclerosis, Parkinson's disease,
 CC Huntington's disease, Down's syndrome, Korsakoff's disease,
 CC schizophrenia, AIDS dementia, multi-infarct dementia, and neuronal damage
 CC associated with uncontrolled seizures. The contryphans are further useful
 CC in controlling pain and are effective in the treatment of migraine. They
 CC can be used prophylactically or to relieve the symptoms associated with a
 CC migraine episode
 CC
 XX
 SO Sequence 33 BP; 0 A; 1 C; 2 G; 30 T; 0 U; 0 Other;
 Query Match 0.3%; Score 23.2; DB 1; Length 33;
 Best Local Similarity 89.3%; Pred. No. 1.6e+02;
 Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4461 GACCTTTTCTTTTCTT 4488
 DB 1 GCGCTTTTCTTTTCTT 28
 RESULT 40
 AAV83644/c
 ID AAV83644 standard; DNA; 35 BP.
 AC AAV83644;
 XX
 DT 01-MAR-1999 (first entry)
 XX
 DE Oligonucleotide used in the construction of assay plasmids.
 XX
 KW Repetitive sequence; carcinogenic; human dietary component;
 KW DNA instability; cancer; diet; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9845476-A1.
 XX
 PD 15-OCT-1998.
 XX
 PF 08-APR-1998; 98WO-GB000869.
 XX
 PR 08-APR-1997; 97GB-00007141.
 XX
 PA (FOOD-) FOOD RES INST.
 XX
 PI Schweizer M;
 XX
 DR WPI; 1999-024011/02.
 XX
 XX Assay for testing the carcinogenic properties of a test substance - by
 PT introduction of a reporter gene expression vector containing a repetitive
 PT DNA sequence that is unstable in cancer cells.
 XX

PS disclosure; Page 17; 103pp; English.
 XX
 CC The present sequence represents an oligonucleotide used in the
 CC construction of assay plasmids, which are used in the course of the
 CC invention. The specification describes an assay for testing the
 CC carcinogenic properties of a test substance. The assay comprises
 CC introducing into cells a reporter gene expression vector comprising a
 CC repetitive DNA sequence which exhibits instability in cancer cells,
 CC whereby instability of the repetitive DNA sequence affects expression of
 CC the reporter gene, exposing the resulting cells to the test substance and
 CC determining whether the test substance is carcinogenic or anti-
 CC carcinogenic by comparing the frequency of reporter gene expression in
 CC the resulting cells with the frequency of reporter gene expression in
 CC cells which have not been exposed to the test substance. The assay can be
 CC used to identify human dietary components that protect against DNA
 CC instability, and therefore some types of cancer, and can be used to
 CC contribute to the scientific basis for a healthy diet
 CC
 XX
 SO Sequence 35 BP; 22 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 0.3%; Score 23.2; DB 1; Length 35;
 Best Local Similarity 89.3%; Pred. No. 1.7e+02;
 Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4456 GCATGACCTTTTCTTTTCTT 4483
 DB 35 GCCCGGCGCTTTTCTTTTCTT 8
 RESULT 41
 ABL56419/c
 ID ABL56419 standard; DNA; 33 BP.
 AC ABL56419;
 XX
 DT 22-JUL-2002 (first entry)
 XX
 DE Oligonucleotide 1 hybridising to plasmid pXL3010.
 XX
 KW transgene; mitochondrial disease; myopathy; ischaemia; stenosis;
 KW lysosomal storage disease; hormonal disorder; haemophilia; inflammation;
 KW rheumatoid polyarthritis; beta-thalassemia; cancer; neurodegeneration;
 KW cardiovascular disease; hypertension; hyperlipidaemia; obesity; vaccine;
 KW ss.
 XX
 OS Synthetic.
 XX
 PN WO200213758-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 10-AUG-2001; 2001WO-FR002606.
 XX
 PR 18-AUG-2000; 2000FR-00010730.
 XX
 PR 11-OCT-2000; 2000US-0239246P.
 XX
 PA (AVERT) AVENTIS PHARMA SA.
 XX
 PI Scherman D, Bectan M, Bigey P;
 XX
 DR WPI; 2002-269145/31.
 XX
 XX Regulating expression of transgenes in plants and animals, useful e.g.
 PT for gene therapy, comprises cotransfection with a transgene and a
 PT sequence that expresses an inhibitory transcript.
 XX
 PS Example 1; Page 52; 123pp; French.
 XX
 CC The specification describes a method for regulating expression of a
 CC selected transgene in vivo. The method comprises introducing, into a non-
 CC human animal tissue or target cell a nucleic acid comprising the
 CC transgene and encoding a transcript (T1); and a nucleic acid that encodes
 CC a transcript (T2) that inhibits T1 specifically. Both nucleic acids are

CC co-expressed so that activity of T1 is inhibited constitutively by T2.
 CC The nucleic acids are controlled by a transcriptional promoter and the
 CC activity of T2 and/or T1 can be regulated by an external agent. The
 CC method is used to regulate a transgene, in animals and plants.
 CC particularly for control of therapeutic transgenes in treatment of
 CC genetic anomalies and defects, e.g. mitochondrial diseases, myopathy,
 CC ischaemia, stenosis, lysosomal storage diseases, hormonal disorders,
 CC haemophilia, inflammation (rheumatoid polyarthritis), beta-thalassemia,
 CC cancer (by inducing apoptosis or expression of toxins),
 CC neurodegeneration, cardiovascular diseases (hypertension),
 CC hyperlipidemia (obesity), and in preparation of vaccines. Transgenic
 CC animals containing T1 and T2 are useful as experimental models of
 CC diseases and transgenic plants are useful for studying the effects of
 CC specific genes on development etc. Oligonucleotides ABL56419-20 were used
 CC to construct vectors for use in the course of the invention
 XX
 SQ Sequence 33 BP; 2 A; 11 C; 12 G; 8 T; 0 U; 0 Other;
 Query Match 0.3%; Score 23; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7413 CAGCAGCAGCAGCAGCAGCA 7435
 DB 29 CAGCAGCAGCAGCAGCAGCA 7
 RESULT 42
 ID AAX07466 standard; cDNA; 26 BP.
 XX
 AC AAX07466;
 XX
 DT 08-JUN-1999 (first entry)
 XX
 DE Human BS124 specific EST clone oligonucleotide.
 XX
 DE BS124; breast; cancer; detection; diagnosis; prevention; treatment; EST;
 KW ss.
 KM
 XX
 OS Synthetic.
 XX
 PN WO9859049-A1.
 XX
 PD 30-DEC-1998.
 XX
 PR 19-JUN-1998; 98WO-US012862.
 XX
 PR 20-JUN-1997; 97US-00879354.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hodges SC, Kjaas MR, Kratochvil JD, Russell JC;
 PI Scheffel CP, Stroupe SD, Yu H;
 XX
 DR WPI; 1999-105623/09.
 XX
 PT New isolated BS124 polynucleotides and polypeptides - used for detecting,
 PT diagnosing, preventing or treating diseases or conditions of the breast,
 PT such as breast cancer.
 XX
 PS Disclosure; Page 97; 125pp; English.
 XX
 CC The sequence is that of an oligonucleotide used in the isolation of a
 CC BS124-specific EST clone. It is useful for detecting, diagnosing,
 CC staging, preventing or treating, or determining predisposition to
 CC diseases or conditions of the breast, such as breast cancer
 XX
 SQ Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 U; 0 Other;
 Query Match 0.3%; Score 22.8; DB 1; Length 26;
 Best Local Similarity 92.3%; Pred. No. 1.3e+02;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4464 TTTTGTGCTTG 4489
 DB 1 TTTTGTGCTTG 26
 RESULT 43
 ID AAX78723 standard; DNA; 26 BP.
 XX
 AC AAX78723;
 XX
 DT 03-SEP-1999 (first entry)
 XX
 DE Human pancreatic PA153 EST-specific clone primer 12.
 XX
 KW Pancreatic disease; PA153; human; cytostatic; detection; antigen;
 KW anti-PA153; antagonist; therapy; treatment; tumour; metastasis;
 KW gene therapy; EST; expressed sequence tag; primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9931274-A2.
 XX
 PD 24-JUN-1999.
 XX
 PR 11-DEC-1998; 98WO-US026441.
 XX
 PR 15-DEC-1997; 97US-00990568.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hodges SC, Kjaas MR, Kratochvil JD, Roberts-Rapp U;
 PI Russell JC, Stroupe SD;
 XX
 DR WPI; 1999-405041/34.
 XX
 PT PA153 cDNA transcribed from pancreatic tissue.
 XX
 PS Example 2; Page 121; 123pp; English.
 XX
 CC This invention describes novel contiguous and partially overlapping cDNA
 CC sequences and their encoded polypeptides, designated PA153, transcribed
 CC from human pancreatic tissue and which have cytostatic activity. The
 CC PA153 polynucleotides, proteins and antibodies are all useful in methods
 CC of detection. Detection of PA153 polynucleotide, antigens or anti-PA153
 CC antibodies (antagonists) can also be used in vivo for therapeutic use,
 CC e.g. treatment of pancreatic disease, tumours or metastases. Antisense
 CC PA153 polynucleotides can be used in gene therapy of pancreatic diseases.
 CC AAX78712-K78725 represent primers used in the method of the invention
 XX
 SQ Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 U; 0 Other;
 Query Match 0.3%; Score 22.8; DB 1; Length 26;
 Best Local Similarity 92.3%; Pred. No. 1.3e+02;
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4464 TTTTGTGCTTG 4489
 DB 1 TTTTGTGCTTG 26
 RESULT 44
 ID AAV71936 standard; DNA; 27 BP.
 XX
 AC AAV71936;
 XX
 DT 18-FEB-1999 (first entry)

```

XX DE Anchored poly T RT-PCR primer.
XX KW Normalised; cDNA library; mRNA cloning; reverse transcription;
XX KM Immobilise; screening; hybridisation; nucleic acid amplification;
XX KM expression pattern; drug development; PCR primer; RT-PCR; ss.
XX OS Synthetic.
XX PN WO9851789-A2.
XX PD 19-NOV-1998.
XX PF 13-MAY-1998; 98NO-DK000186.
XX PR 13-MAY-1997; 97DK-00000547.
XX PR 19-MAY-1997; 97US-00871030.
XX PR 27-MAR-1998; 98DK-00000432.
XX PA (DISP-) DISPLAY SYSTEMS BIOTECH APS.
XX PI Warthoe PR;
XX DR WPI; 1999-009772/01.
XX PT Preparation of normalised, subdivided cDNA libraries from mRNA - by
XX PT reverse transcription and amplification, used to screen for new genes and
XX PT interacting proteins, potential drugs, and for diagnosis.
XX PS Example 1; Page 29; 71pp; English.
XX CC The invention relates to preparation of a normalised, subdivided library
XX CC of amplified cDNA from the coding regions of mRNA in a sample. The method
XX CC involves reverse transcription, with at least one cDNA primer of formula
XX CC 5'-Con1-dn2-Wn3-Nn4 to form first stand cDNA where Con1 = any sequence
XX CC of 1-100 nucleotides; dn = deoxythymidyl; n2 is at least 1; n3 and n4
XX CC are both 0, or n3 is 1 and n4 is at least 1; followed by second strand
XX CC cDNA synthesis using the first strand as template and a second cDNA
XX CC primer of a similar formula, in the presence of DNA polymerase I (or its
XX CC Klenow fragment) and amplification of double-stranded cDNA with a set of
XX CC amplification primers. Comparison of cDNA in the prepared library with a
XX CC database (a computer-generated list of molecular weights of restricted
XX CC DNA fragments of known sequence) is used to determine presence of an
XX CC expressed protein in a cell, also to detect changes in such expression
XX CC (particularly for diagnosis of disease). Surfaces (chip) having amplified
XX CC cDNA stably immobilised on it, obtained by a similar method, are used to
XX CC screen for genes of a particular family, by hybridisation with nucleic
XX CC acid from the family (to identify new genes) and to detect differences in
XX CC expression patterns between cells. The polypeptides expressed by the
XX CC libraries can be used for drug development. Sequences AAV71935 to
XX CC AAV71946 represent primers used to exemplify the method of the invention
XX SQ Sequence 27 BP; 0 A; 1 C; 1 G; 25 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 22.8; DB 1; Length 27;
XX Best Local Similarity 92.3%; Pred. No. 1.4e+02;
XX Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
XX Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

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XX KM Promoter PR-1; salicylic acid, 2,6-dichloroisonicotinic acid;
XX KM benzo(1,2,3)thiadiazole-7-carboxylic acid 5-methyl ester;
XX KM transgenic plant; PCR; primer; ss.
XX OS Synthetic.
XX OS Arabidopsis thaliana.
XX PN WO9803536-A1.
XX PD 29-JAN-1998.
XX PF 18-JUL-1997; 97WO-US012626.
XX PR 23-JUL-1996; 96US-0027228P.
XX PA (NOVS ) NOVARTIS CORP.
XX PI Lebel EG, Ryals JA, Thorne L, Uknes SJ, Ward ER;
XX DR WPI; 1998-120690/11.
XX PT New chemically inducible promoter from Arabidopsis - used to regulate
XX PT gene expression in response to e.g. salicylic acid.
XX PS Example 9; Page 32; 60pp; English.
XX CC Primer P41+ corresponds to nucleotides -735 to -706 relative to the
XX CC transcription start site in the upstream region (see AAV15448) of the
XX CC Arabidopsis PR-1 gene (see AAV15448). It was used in non-coding strand
XX CC analysis of the PR-1 promoter region. In vivo footprinting analysis was
XX CC performed of the PR-1 promoter region. Inducible in vivo footprints are
XX CC located at positions -629 and -628 and at position -604 on the coding
XX CC strand and at position -641 on the non-coding strand. The use of PR-1
XX CC promoter fragments to regulate gene expression in plants in the presence
XX CC of chemical inducers is disclosed
XX SQ Sequence 29 BP; 0 A; 2 C; 0 G; 27 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 22.8; DB 1; Length 29;
XX Best Local Similarity 92.3%; Pred. No. 1.5e+02;
XX Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 4463 CTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
XX Db 1 CTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

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XX RESULT 46
XX ID AAV15487 standard; DNA; 29 BP.
XX AC AAV15487;
XX XX 20-JUL-1998 (first entry)
XX DT PR-1 promoter primer P41+ for in vivo footprinting.
XX DE
XX PF

```

```

XX Key Location/Qualifiers
XX FT modified_base 29 /*tag= a
XX FT /mod_base= OTHER
XX FT /note="labelled with Fluorescein"
XX PN EP1207210-A1.
XX PD 22-MAY-2002.
XX PF 13-NOV-2001; 2001EP-00126930.

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XX 15-NOV-2000; 2000EP-00124897.
XX
XX (HOF ) ROCHE DIAGNOSTICS GMBH.
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Dietmaier W;
XX
XX MPI; 2002-437469/47.
XX
XX Analyzing repeat sequences in DNA using a probe which hybridizes to
XX adjacent repetitive and non-repetitive regions and determining hybrid
XX melting point is useful to detect microsatellite instability such as in
XX hereditary cancer.
XX
XX Claim 16; Page 7; 19pp; English.
XX
XX The present invention relates to a method for analysing a target nucleic
XX acid consisting of repetitive and non-repetitive sequences. The method
XX comprises hybridising a polynucleotide probe comprising a segment
XX complementary to a non-repetitive region and a segment complementary to
XX an adjacent repetitive region, where the second segment consists of a
XX defined number of repeats, and determining the melting point temperature
XX of the hybrid. The method is used to analyse microsatellites, especially
XX microsatellite instability, particularly as a means for detecting
XX hereditary tumours. Alternatively, the method is used to identify an
XX individual in a population. The present sequence is a probe for
XX Mononucleotide repeat locus BAT25, and was used to illustrate the
XX invention
XX
XX Sequence 29 BP; 26 A; 2 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match      0.3%; Score 22.8; DB 1; Length 29;
XX Best Local Similarity 92.3%; Pred. No. 1.5e+02;
XX Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 4464 TTTTGTGCTG 4489
XX |||||
XX 26 TTTTGTGCTG 1
XX
XX RESULT 47
XX ADA14837
XX ADA14837 standard; DNA; 30 BP.
XX
XX ADA14837;
XX
XX 06-NOV-2003 (first entry)
XX
XX Hairpin oligonucleotide, #2, used in an example of the invention.
XX
XX Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;
XX quenchable fluorescing agent; microarray; semiconductor; nanocrystal;
XX rhodamine B-labelled dye; detection; gold support; ss.
XX
XX Synthetic.
XX
XX Key      Location/Qualifiers
XX PH      1
XX FT      modified_base 1
XX FT      /tag= a
XX FT      /mod_base= OTHER
XX FT      /note= "OTHER= thiol group"
XX FT      misc_binding 6..25
XX FT      /tag= b
XX FT      /bound_moiety= "Target sequence #2"
XX FT      /note= "Forms a double-stranded region with the target
XX FT      sequence shown in examples 3, 4 and 5"
XX FT      modified_base 30
XX FT      /tag= c
XX FT      /mod_base= OTHER
XX FT      /note= "OTHER= amino group"
XX
XX US2003013109-A1.
```

```
XX 16-JAN-2003.
XX
XX 21-JUN-2002; 2002US-00176055.
XX
XX 21-JUN-2001; 2001US-0299460P.
XX
XX (BALL/) BALLINGER C T.
XX (LOCA/) LOCASCIO M.
XX (LAND/) LANDRY D P.
XX
XX Ballinger CT, Locascio M, Landry DP,
XX
XX MPI; 2003-596312/56.
XX
XX Hairpin sensor useful for detecting a target nucleotide sequence in a
XX sample, comprises a hairpin loop assembly including a complementary probe
XX and a quenchable fluorescing agent.
XX
XX Example 3; Page 11; 16pp; English.
XX
XX The invention discloses a hairpin sensor comprising a hairpin loop
XX assembly including a complementary probe positioned between a first
XX inverse repeat arm and a second inverse repeat arm, and a quenchable
XX fluorescing agent joined, directly or indirectly, to the end of the
XX second inverse repeat arm of the hairpin loop assembly opposite the
XX complementary probe. Also claimed is a microarray comprising the hairpin
XX sensor, where the end of the first inverse repeat arm opposite the
XX complementary probe is bound, directly or indirectly, to a support, a kit
XX for detecting a target nucleotide sequence in a sample comprising the
XX hairpin sensor, and a support, and a hairpin sensor system, in which the
XX particle is conductive or semi-conductive, including at least one of the
XX above hairpin sensor assemblies. The hairpin sensor further comprises a
XX functional group joined to the end of the first inverse repeat arm
XX opposite the complementary probe, or first spacer opposite the first
XX inverse repeat arm, the functional group selected from amino, carboxyl,
XX thiol and hydroxyl. Further, the sensor comprises a ligand positioned
XX between the second inverse repeat arm and the quenchable fluorescing
XX agent, where the ligand is selected from mercapto, hydroxyl, amino,
XX nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The
XX second spacer is positioned between the second inverse repeat arm and the
XX quenchable fluorescing agent which comprises a semiconductor nanocrystal
XX or rhodamine B-labelled dye. Within the microarray the support is capable
XX of accepting a charge. At least one hairpin sensor comprises two or more
XX hairpin sensors. The two or more hairpin sensors include complementary
XX probes that are the same or different and respective quenchable
XX fluorescing agents that are the same or different. The two or more
XX hairpin sensors are arranged in a spatially-defined pattern. The sensor
XX and system are useful for detecting a target nucleotide sequence in a
XX sample. Further, the method involves identifying the target nucleotide
XX sequence by the location of the complementary probe to which the target
XX nucleotide sequence binds. The two or more hairpin sensors include
XX complementary probes or quenchable fluorescing agents, that are
XX different. The sequence presented is the hairpin oligonucleotide, #2,
XX used in an example of the invention.
XX
XX Sequence 30 BP; 1 A; 4 C; 4 G; 21 T; 0 U; 0 Other;
XX
XX Query Match      0.3%; Score 22.8; DB 1; Length 30;
XX Best Local Similarity 92.3%; Pred. No. 1.6e+02;
XX Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 4461 GACTTTTGTG 4486
XX |||||
XX 3 GAGTTTGTGCTC 28
XX
XX RESULT 48
XX ADE71592/C
XX ID ADE71592 standard; DNA; 32 BP.
XX
XX ADE71592;
XX
```

DT	29-JAN-2004	(first entry)
XX		
DE	Magneto-gold nanoparticle probe #2.	
KM	Magneto-gold nanoparticle; probe; ss; core nanoparticle;	
KW	non-allowing gold shell; shell nanoparticle; gold salt.	
XX		
OS	Synthetic.	
PN	US2003129608-A1.	
PD	10-JUL-2003.	
XX		
PF	22-MAY-2002; 2002US-00153483.	
PR	25-MAY-2001; 2001US-0293861P.	
PR	28-DEC-2001; 2001US-00034451.	
PR	28-DEC-2001; 2001WO-US050825.	
XX		
PA	(MIRK/) MIRKIN C. A.	
PA	(CAOY/) CAO Y.	
PA	(JINR/) JIN R.	
PI	Mirkin CA, Cao Y, Jin R;	
XX		
DR	WPI; 2004-031299/03.	
XX		
PT	Core/shell nanoparticle for detecting target molecules, e.g. nucleic	
PT	acids, comprises inner metal-containing nanoparticle core, outer non-	
PT	allowing gold shell, and oligonucleotides attached to gold shell.	
XX		
PS	Example 5; Page 8; 21pp; English.	
XX		
CC	The invention relates to a core/shell nanoparticle comprising an inner	
CC	metal-containing nanoparticle core and an outer non-allowing gold shell	
CC	surrounding the nanoparticle core. Oligonucleotides may be attached to	
CC	the gold shell. The invention also relates to preparation of core/shell	
CC	nanoparticles by treating inner metal-containing nanoparticle cores	
CC	simultaneously with a solution containing gold salt and a solution	
CC	containing a reducing agent to produce a non-allowing gold shell	
CC	surrounding the nanoparticle cores, and isolating the core/shell	
CC	nanoparticles. Detection of target analytes, e.g. a nucleic acid, bound	
CC	to a surface comprises contacting the surface with a solution comprising	
CC	a core/shell nanoparticle receptor conjugate under conditions effective	
CC	to allow binding of nanoparticle conjugates with the bound nucleic acid,	
CC	subjecting the nanoparticle conjugate to an external magnetic field to	
CC	accelerate movement of the nanoparticle conjugate to the surface, to	
CC	promote binding interaction between the nanoparticle conjugate and target	
CC	analyte, removing any nanoparticle conjugates that have not bound with	
CC	the target analyte and observing a detectable change brought about by a	
CC	binding interaction of the target analyte with the nanoparticle	
CC	conjugates. The invention is used for detecting target molecules such as	
CC	nucleic acids, peptides and proteins. The optical properties of	
CC	core/shell nanoparticles form a new calorimetric channel for nanoparticle	
CC	-based DNA detection. This sequence represents a magneto-gold	
CC	nanoparticle probe used in the scope of the invention.	
XX		
XX		
SQ	Sequence 32 BP; 24 A; 4 C; 0 G; 4 T; 0 U; 0 Other;	
XX		
Query Match	0.3%; Score 22.8; DB 1; Length 32;	
Best Local Similarity	92.3%; Pred. No. 1.8e+02;	
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY	4458 ATGCACCTTTTCTTTTCTTTTCTTTT 4483	
DB		
	26 AGGAGGTTTTTTTTTTTTTTTTTTT 1	
RESULT 49		
AAL44170		
ID	AAL44170 standard; DNA; 33 BP.	
AC	AAL44170;	

XX	03-OCT-2002	(first entry)
DT		
XX	Porphyra yezoensis cytochrome C - related PCR primer, SEQ ID NO 4.	
DE		
XX	Cytochrome C; ss; maturation protein; nitrogen oxide trapping;	
KM	polluted atmosphere purification; PCR; primer.	
XX		
OS	Porphyra yezoensis.	
XX		
PN	MO200259339-A1.	
XX		
PD	01-AUG-2002.	
XX		
PF	23-JAN-2002; 2002WO-JP000467.	
XX		
PR	23-JAN-2001; 2001JP-00014510.	
XX		
PA	(UTNI-) UNIV NIPPON.	
PI	Oku T, Nishio T, Sato T;	
XX		
DR	WPI; 2002-557951/59.	
XX		
PT	Production of cytochrome c by culturing prokaryote transformed with	
PT	vector containing e.g. DNA of signal peptide and of eukaryotic cytochrome	
PT	c maturation protein for use in reagents and drugs for trapping nitrogen	
XX	oxide.	
PS	Example 1; Page 7-8; 27pp; Japanese.	
XX		
CC	The invention comprises a method for the production of cytochrome C. The	
CC	method involves culturing a prokaryote that has been transformed with a	
CC	vector encoding a signal peptide and a cytochrome C maturation protein.	
CC	The method of the invention is useful for producing cytochrome C.	
CC	Cytochrome C produced by the method of the invention is used in reagents	
CC	and drugs for trapping nitrogen oxide (e.g. in purifying liquid	
CC	atmosphere by trapping nitrogen oxide). The present DNA sequence	
CC	represents a Porphyra yezoensis cytochrome C - related PCR primer	
XX		
SEQ	Sequence 33 BP; 1 A; 3 C; 3 G; 26 T; 0 U; 0 Other;	
	Query Match	0.3%; Score 22.8; DB 1; Length 33;
	Best Local Similarity	92.3%; Pred. No. 1.9e+02;
	Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	4463 CTTTCTTTTCTTTTCTTTTCTTTGCTT 4488	
DB	8 CTTTCTTTTCTTTTCTTTTCTTTTCTTT 33	
RESULT 50		
AAT93827		
ID	AAT93827 standard; DNA; 34 BP.	
AC	AAT93827;	
XX		
DT	25-MAR-2003 (revised)	
DT	24-FEB-1998 (first entry)	
DE	Antitumoural phosphodiester oligonucleotide 17 with cytotoxic activity.	
XX		
KM	Phosphodiester; selective binding; cell viability; growth;	
KM	tumoural cell line; cytotoxic activity; tumour cell; lymphoma;	
KM	lymphoblastic tumour; ss.	
XX		
OS	Synthetic.	
XX		
PH	Key	Location/Qualifiers
FT	modified_base	1..34
FT		/*tag= a
FT		/note= "phosphodiester oligonucleotide"
XX		

PT acid, comprises inner metal-containing nanoparticle core, outer non-
PT alloying gold shell, and oligonucleotides attached to gold shell.
PS Example 2; Fig 2; 21pp; English.
XX
CC The invention relates to a core/shell nanoparticle comprising an inner
CC metal-containing nanoparticle core and an outer non-alloying gold shell
CC surrounding the nanoparticle core. Oligonucleotides may be attached to
CC the gold shell. The invention also relates to preparation of core/shell
CC nanoparticles by treating inner metal-containing nanoparticle cores
CC simultaneously with a solution containing gold salt and a solution
CC containing a reducing agent to produce a non-alloying gold shell
CC surrounding the nanoparticle cores, and isolating the core/shell
CC nanoparticles. Detection of target analytes, e.g. a nucleic acid, bound
CC to a surface comprises contacting the surface with a solution comprising
CC a core/shell nanoparticle receptor conjugate under conditions effective
CC to allow binding of nanoparticle conjugates with the bound nucleic acid,
CC subjecting the nanoparticle conjugate to an external magnetic field to
CC accelerate movement of the nanoparticle conjugate to the surface, to
CC promote binding interaction between the nanoparticle conjugate and target
CC analyte, removing any nanoparticle conjugates that have not bound with
CC the target analyte and observing a detectable change brought about by a
CC binding interaction of the target analyte with the nanoparticle
CC conjugates. The invention is used for detecting target molecules such as
CC nucleic acids, peptides and proteins. The optical properties of
CC core/shell nanoparticles form a new calorimetric channel for nanoparticle
CC based DNA detection. This sequence represents a magnetic-gold
CC nanoparticle probe used in the scope of the invention.
XX
SQ Sequence 35 BP; 26 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 0.3%; Score 22.8; DB 1; Length 35;
Best Local Similarity 92.3%; Pred. No. 2e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4458 ATGACCTTTTTTTTTTTTTTTTTTTT 4483
Db 26 AGGAGCTTTTTTTTTTTTTTTTTTTT 1

RESULT 53
AA94315/c
ID AAA94315 standard; DNA; 29 BP.
XX
AC AAA94315;
XX
DT 11-JAN-2001 (first entry)
XX
DE RNA-protein fusion oligonucleotide 30-P.
XX
KW RNA-protein fusion; protein library; protein isolation; gene cloning; ss.
XX
OS Synthetic.
XX
FT Key Location/Qualifiers
FT modified_base 29 /*tag= a
FT /mod_base= OTHER
FT /note= "attached to puromycin, a peptide acceptor"
XX
PN WO200047775-A1.
XX
PD 17-AUG-2000.
XX
PF 01-FEB-2000; 2000WO-US002589.
XX
PR 09-FEB-1999; 99US-00247190.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Szwedak JM, Roberts RW, Liu R;
XX
DR WPI; 2000-533022/48.

XX
PT Producing protein or DNA libraries which are useful for improving
PT existing proteins, by in vitro translating protein coding sequences to
PT produce RNA-protein fusions and incubating these protein fusions under
PT high salt conditions.
XX
PS Disclosure; Page 43; 121pp; English.
XX
CC The present sequence is one of a number of oligonucleotides which were
CC used for the generation of RNA-protein fusions, including fusions having
CC a myc epitope tag. The RNA-protein fusions comprise a protein covalently
CC linked to the 3' end of its own mRNA. This is accomplished by synthesis
CC and in vitro or in situ translation of an mRNA molecule with a peptide
CC acceptor attached to its 3' end. The RNA-protein fusions are incubated
CC under high salt conditions to produce a protein library. This method is
CC useful for improving or altering existing proteins, as well as for
CC isolating new proteins and nucleic acid or small molecule targets. It may
CC also be used to improve human or humanised single-chain antibodies for
CC the treatment of a number of diseases. The method is useful for the
CC isolation of proteins with specific binding properties, for screening
CC cDNA libraries and cloning new genes on the basis of protein-protein
CC interactions. Unlike prior art, the new method does not rely on
CC maintaining the integrity of an mRNA:ribosome:nascent chain ternary
CC complex, which is very fragile and is therefore of limited use. The
CC method does not rely on topological links between the protein and the
CC nucleic acid so that the information of the protein is retained and can
CC be recovered in readable, nucleic acid form
XX
SQ Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.3%; Score 22.6; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.7e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4460 GGACTTTTTTTTTTTTTTTTGCTT 4488
Db 29 GCTTTTTTTTTTTTTTTTTTTTTTTT 1

RESULT 54
AAS0066/c
ID AAS0066 standard; DNA; 29 BP.
XX
AC AAS0066;
XX
DT 12-SEP-2001 (first entry)
XX
DE Synthetic branched encoding molecule sequence.
XX
KW Addressing element; microarray; protein display;
XX
KW branched encoding molecule; ss.
XX
OS Synthetic.
XX
FT Key Location/Qualifiers
FT modified_base 9..10 /*tag= a
FT /mod_base= OTHER
FT /note= "XXA, where X is a branching monomer, linked to
FT nucleotide 16 of sequence in AAS0065 via a (Hexaethylene
FT oxide)n linkage"
FT modified_base 30 /*tag= b
FT /mod_base= OTHER
FT /note= "Other= Covalently linked to puromycin"
XX
PN WO200116352-A1.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US023414.
XX
PR 27-AUG-1999; 99US-0151261P.
XX

```

XX (PHYL-) PHYLLOS INC.
XX
XX Kuimells RG;
XX
XX WPI; 2001-183261/18.
XX
XX Encoding and sorting in vitro translated proteins, useful for the
XX identification of desired binding partners, comprises attaching a nucleic
XX acid linker to the protein and binding an encoding molecule to the
XX linker.
XX
XX Example 3; Fig 9B; 48pp; English.
XX
XX The sequence represents part of a branched encoding molecule used in
XX methods to hybridise a capture probe to the addressing element of a DNA
XX linker attached to an in vitro translated protein, in order to immobilise
XX the protein to a solid support. The new methods are useful for tagging or
XX encoding in vitro translated proteins with unique and minimal encoding
XX molecules and sorting these molecules onto solid supports. They are also
XX useful for the identification of a desired binding partner. The method
XX allows the use of pre-made sets of universal encoding molecules, such as
XX nucleic acid(s) (analogues). These can be used in conjunction with
XX corresponding universal microarrays or sets of microparticles to create
XX new protein display systems which are flexible, modular, scalable and
XX cost effective. The method allows the use of nucleic acid analogue which
XX are not susceptible to enzymatic incorporation or polymerisation and are
XX superior to conventional DNA/RNA. The proteins can also be labelled with
XX fluorescent groups which can be used to monitor the protein in real time.
XX The absence of RNA is advantageous as they can adopt secondary structures
XX which are difficult to predict and can interfere with hybridisation steps
XX and protein folding/function
XX
XX Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 22.6; DB 1; Length 29;
XX Best Local Similarity 86.2%; Pred. No. 1.7e+02;
XX Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 4460 GGACCTTTTGTGCTT 4488
XX |||
XX 29 GGTGTTTTTTTTTTTTTTTTTTT 1
XX
XX RESULT 55
XX AAH20990/c
XX ID AAH20990 standard; DNA; 29 BP.
XX
XX AAH20990;
XX
XX 31-AUG-2001 (first entry)
XX
XX C-myc epitope puromycin linker primer #1.
XX
XX C-myc; epitope; detection; amplification; biomedical diagnosis;
XX environmental monitoring; primer; ss.
XX
XX Unidentified.
XX
XX WO200142494-A2.
XX
XX 14-JUN-2001.
XX
XX 20-OCT-2000; 2000MO-EP010336.
XX
XX 10-DEC-1999; 99DE-01059857.
XX
XX (AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX Birstaller P, Konz D;
XX
XX WPI; 2001-381706/40.
XX

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```

PT System for detecting immobilized analyte, useful e.g. for biomedical
PT diagnosis, has as detection agent specific polypeptide coupled to nucleic
PT acid for signal amplification.
XX
XX Example; Page 6; 12pp; German.
XX
XX This invention describes a novel test system (A) which comprises at least
XX one immobilized analyte (I) on an insoluble carrier and a polypeptide
XX detection agent (II), specific for (I) and conjugated, via a linker, to
XX an amplifier (III). (A) is used for direct, in vitro detection of (I)
XX with amplification of the signal by polymerase chain reaction (PCR), or a
XX related technique, applied to (III). The method is useful in biomedical
XX diagnosis and environmental monitoring and can be used to detect a wide
XX range of (I), e.g. diagnostic or pharmaceutical agents, secondary
XX metabolites, herbicides or pesticides. (A) allow simultaneous, parallel
XX detection of many different analyses (high throughput capacity).
XX relatively simply (only a few incubation and washing steps are required)
XX and with high sensitivity and selectivity. This sequence represents
XX primer used in the amplification of the c-myc DNA fragment which encodes
XX an epitope used to illustrate the method of the invention
XX
XX Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 22.6; DB 1; Length 29;
XX Best Local Similarity 86.2%; Pred. No. 1.7e+02;
XX Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 4460 GGACCTTTTGTGCTT 4488
XX |||
XX 29 GGTGTTTTTTTTTTTTTTTTTTT 1
XX
XX RESULT 56
XX AAK98637/c
XX ID AAK98637 standard; DNA; 29 BP.
XX
XX AAK98637;
XX
XX 19-APR-2002 (first entry)
XX
XX S cerevisiae alpha factor receptor STE2 vector linker..
XX
XX Biological material detection; electrophoresis; bioprobe isolation;
XX alpha factor receptor; STE2; linker; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 29
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "modified by puromycin"
XX
XX WO200204656-A2.
XX
XX 17-JAN-2002.
XX
XX 26-JUN-2001; 2001WO-EP007259.
XX
XX 07-JUL-2000; 2000DE-01033194.
XX
XX (XZIL-) XZILION GMBH & CO KG.
XX
XX Figner P, Polakowski T;
XX
XX WPI; 2002-154934/20.
XX
XX Detecting and purifying biological material by (di)electrophoresis,
XX useful e.g. for separating tissues and viruses, comprises using a probe
XX that alters (di)electrophoretic properties.
XX
XX Example 1; Page 12; 20pp; German.
XX

```


CC Libraries can be used for drug development. Sequences AAV1935 to
 CC AAV1946 represent primers used to exemplify the method of the invention
 CC
 SQ Sequence 27 BP; 2 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.3%; Score 22.2; DB 1; Length 27;
 Best Local Similarity 88.9%; Pred. No. 1.8e+02;
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTTGTGCTGA 4490
 Db 1 TTTTGTGCTGA 27

RESULT 59
 AAH28290
 ID AAH28290 standard; RNA; 32 BP.

XX AAH28290;
 XX
 DT 05-SEP-2001 (first entry)
 XX

DE 3' untranslated region sequence from GADD45 gene.

KW mRNA protein complex; tumour development; cell aging; death;
 KW ribonucleic profile; RNA-binding protein; ss.

OS Unidentified.

PN WO200148480-A1.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US035583.

PR 28-DEC-1999; 99US-0173338P.

PA (KEENE/) KEENE J D.

PI Keene JD, Tenenbaum SA, Carson C;

DR WPI; 2001-425706/45.

PT Partitioning endogenous mRNA-protein complexes in vivo, by contacting
 PT sample comprising the complex with ligand that binds to a component of
 PT the complex and separating complex by binding ligand with a binding
 PT molecule.

PS Example 6; Page 30; 49pp; English.

CC The specification describes a method for partitioning endogenous cellular
 CC mRNA-protein (mRNP) complexes. The method comprises contacting a
 CC biological sample comprising mRNP complex with ligand that specifically
 CC binds a component of mRNP complex, separating mRNP complex by binding the
 CC ligand with a molecule specific for ligand, which is attached to the
 CC solid support and then collecting the mRNP complex by removing the
 CC complex from the support. The method is useful for in vivo partitioning
 CC of cellular mRNA-protein complexes in a biological sample. The method is
 CC useful for determining the ribonucleic profile of a cell which has numerous
 CC uses including monitoring of tumour development, state of growth or state
 CC of development, perturbations of a biological system such as disease,
 CC drug or toxin treatment and the state of cell aging or death,
 CC distinguishing ribonucleic profiles among organisms, to discriminate
 CC between transcriptional and post-transcriptional contributions to gene
 CC expression and to track the movement of RNAs through RNP complexes,
 CC including the interactions of combinations of proteins with RNAs in RNP
 CC complexes. AAH28291-AAH28316 represent sequences derived from the 3'
 CC untranslated region (UTR) of mRNA of various genes. The sequences contain
 CC target sequences for RNA-binding proteins

XX Sequence 32 BP; 2 A; 2 C; 2 G; 0 T; 26 U; 0 Other;

Query Match 0.3%; Score 22.2; DB 1; Length 32;

Best Local Similarity 11.1%; Pred. No. 2.3e+02;
 Matches 3; Conservative 21; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTTGTGCTGA 4490
 Db 5 UUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 31

RESULT 60
 ABN83375/C
 ID ABN83375 standard; DNA; 32 BP.

XX ABN83375;
 XX

DT 15-AUG-2002 (first entry)
 XX

DE Mononucleotide repeat locus BAT26 probe #2.

KW Mononucleotide repeat locus; human; BAT26; probe; microsatellite; tumour;
 KW ss.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH modified_base 1

FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "labelled with LightCycler fluorescent dye LC-Red-
 640"

PN BP1207210-A1.

PD 22-MAY-2002.

PF 13-NOV-2001; 2001EP-00126930.

PR 15-NOV-2000; 2000EP-00124897.

PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Dietmaier W;

DR WPI; 2002-437469/47.

PT Analyzing repeat sequences in DNA using a probe which hybridizes to
 PT adjacent repetitive and non-repetitive regions and determining hybrid
 PT melting point is useful to detect microsatellite instability such as in
 PT hereditary cancer.

PS Claim 16; Page 7; 19pp; English.

CC The present invention relates to a method for analysing a target nucleic
 CC acid consisting of repetitive and non-repetitive sequences. The method
 CC comprises hybridising a polynucleotide probe comprising a segment
 CC complementary to a non-repetitive region and a segment complementary to
 CC an adjacent repetitive region, where the second segment consists of a
 CC defined number of repeats, and determining the melting point temperature
 CC of the hybrid. The method is used to analyse microsatellites, especially
 CC microsatellite instability, particularly as a means for detecting
 CC hereditary tumours. Alternatively, the method is used to identify an
 CC individual in a population. The present sequence is a probe for
 CC Mononucleotide repeat locus BAT26, and was used to illustrate the
 CC invention

XX Sequence 32 BP; 27 A; 1 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.3%; Score 22.2; DB 1; Length 32;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTTGTGCTGA 4490
 TTTTGTGCTGA 4490

Db 32 TTTTTTTTTTTTTTTTTTTTNA 6

RESULT 61

ABK51385/c
ID ABK51385 standard; DNA: 33 BP.

XX
AC ABK51385;

XX
DT 30-JUL-2002 (first entry)

XX
DE Human cytokine signal inhibitor 12.76, PCR primer 4.

XX
KW Human, cytokine signal inhibitor 12.76; cancer; HIV; PCR; primer; ss;

XX
KM human immunodeficiency virus infection.

XX
OS Homo sapiens.

XX
PN CN1331180-A.

XX
PD 16-JAN-2002.

XX
PF 28-JUN-2000; 2000CN-00116854.

XX
PR 28-JUN-2000; 2000CN-00116854.

XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX
PI Mao Y, Xie Y;

XX
DR WPI; 2002-305492/35.

XX
PT Polypeptide-human cytokine signal inhibitor 12.76 and polynucleotide for

XX
PT coding it.

XX
XX Example 4; Page 20 (Disclosure); 36pp; Chinese.

XX
PS The present invention relates to a new polypeptide, human cytokine signal
CC inhibitor 12.76, and the polynucleotide encoding it. The invention also
CC describes the process for preparing the polypeptide by DNA recombination,
CC and the application of the polypeptide in treating diseases such as
CC cancer and human immunodeficiency virus (HIV) infection. The antagonist
CC of the polypeptide and its medical action, and the application of the
CC polynucleotide are also disclosed. The present nucleic acid sequence
CC represents PCR primer 4 that was used in the methods of the invention to
CC isolate the coding sequence of the human cytokine signal inhibitor 12.76
CC of the invention

XX
SQ Sequence 33 BP; 22 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

XX
Query Match 0.3%; Score 22.2; DB 1; Length 33;

XX
Best Local Similarity 88.9%; Pred. No. 2.4e+02;

XX
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4466 TTTTGTGCTGAGA 4492

Db 33 TTTTGTGCTGAGA 7

RESULT 62

ABK81861
ID ABK81861 standard; DNA: 22 BP.

XX
AC ABK81861;

XX
DT 13-AUG-2002 (first entry)

XX
DE Lung specific gene PCR primer #19.

XX
KW Lung specific gene; gene therapy; vaccine; lung cancer; cancer staging;

XX
KM cancer monitoring; cancer diagnosis; imaging lung cancer; metastases;

XX
KM PCR; primer; ss.

OS Synthetic.

XX
PN W0200218576-A2.

XX
PD 07-MAR-2002.

XX
PF 27-AUG-2001; 2001WO-US026684.

XX
PR 28-AUG-2000; 2000US-0228378P.

XX
PA (DIAD-) DIADEXUS INC.

XX
PI Chen S, Macina RA, Sun Y, Recipon H;

XX
DR WPI; 2002-434904/46.

XX
PT New lung specific genes and their encoded proteins, useful in gene
PT therapy or as a vaccine for treating lung cancer, as well as for
PT measuring metastases of lung cancer, or staging, monitoring, diagnosing
PT or imaging lung cancer.

XX
PS Example 10; Page 127; 206pp; English.

XX
CC The invention describes a new lung specific gene and its variants. The
CC lung specific gene proteins and genes are useful in gene therapy or as a
CC vaccine for treating lung cancer. Lung specific genes are also useful for
CC staging, monitoring, diagnosing or imaging lung cancer, as well as for
CC measuring metastases of lung cancer. This sequence represents a PCR
CC primer used in microarray analysis to isolate a lung specific gene
CC thought to be involved in development of lung cancer

XX
SQ Sequence 22 BP; 4 A; 6 C; 4 G; 8 T; 0 U; 0 Other;

XX
Query Match 0.3%; Score 22; DB 1; Length 22;

XX
Best Local Similarity 100.0%; Pred. No. 1.4e+02;

XX
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5514 CCGACCTTGAGATTATTCCTGT 5535

Db 1 CCGACCTTGAGATTATTCCTGT 22

RESULT 63

AAS20595
ID AAS20595 standard; DNA: 26 BP.

XX
AC AAS20595;

XX
DT 23-APR-2002 (first entry)

XX
DE Human zsig63 cDNA sequencing primer ZC7231.

XX
KW Human; zsig63; chromosome 4q12-4q13; salivary protein; antimicrobial; ss;
KW microbial infection; tooth decay; periodontal disease; thrush; emphysema;
KW gastrointestinal disease; urinary tract infection; vaginal infection;
KW skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;
KW acquired immunodeficiency syndrome; AIDS; lung infection; sarcoïdosis;
KW chronic bronchitis; gene therapy; protein therapy; primer; ZC7231.

XX
OS Homo sapiens.

XX
PN US6331413-B1.

XX
PD 18-DEC-2001.

XX
PF 17-MAR-2000; 2000US-00527345.

XX
PR 17-MAR-1999; 99US-0124820P.

XX
PA (ZYMO) ZYMOGENETICS INC.

XX
PI Adler DA, Shepard PO;

```

DR WPI; 2002-096707/13.
XX Polynucleotides encoding salivary proteins useful as anti-microbial
PT agents.
XX
XX Example 1; Col 53; 29pp; English.
XX
CC The invention relates to a polynucleotide derived from the 4q12-4q13
CC region of human chromosome 4 and encoding a zsig63 polypeptide, a
CC secreted salivary protein with anti-microbial activity. Due to their
CC microbical activity, the sequences can be used in the study of microbial
CC infections, e.g. for recombinant production of anti-microbial proteins.
CC The sequences can be used in the treatment of tooth decay, periodontal
CC disease, thrush, gastrointestinal disease, urinary tract infections,
CC vaginal infections, skin infections, epithelial wounds, chronic tissue
CC damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung
CC infections, sarcoidosis, emphysema and chronic bronchitis. This sequence
CC represents a sequencing primer for cDNA encoding human zsig63
CC
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;
XX
Query Match      0.3%; Score 22; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1.8e+02;
Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 4464 TTTTGTGCTTG 4489
    |||||
DB 1 TTTTGTGCTTG 26
XX
RESULT 64
ABS52637
ID ABS52637 standard; DNA; 26 BP.
XX
AC ABS52637;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human secreted salivary protein zsig63 PCR primer ZC7231.
XX
KM Human; secreted salivary protein; zsig63; immunogen; zsig63-cytokine;
KM antibody-cytokine; in vivo killing; pathological microbe; bacteria;
KM fungal; viral; infection; salivary gland; anti-microbial; dental caries;
KM tooth decay; periodontal disease; thrush; gastrointestinal disease;
KM urinary tract infection; vaginal infection; skin infection; microflora;
KM epithelial wound; pathogenic colonisation; invasion; pro-inflammation;
KM chronic tissue damage; vascular system; diabetes; anti-inflammatory;
KM incompetent immune system; AIDS; acquired immunodeficiency syndrome;
KM chemotherapy; radiation treatment; lung infection; cystic fibrosis;
KM digestion; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002081701-A1.
XX
PD 27-JUN-2002.
XX
PF 03-AUG-2001; 2001US-00922480.
XX
PR 17-MAR-1999; 99US-0124820P.
XX
PR 17-MAR-2000; 2000US-00527345.
XX
PA (ADLER/) ADLER D A.
XX
PI (SHEP/) SHEPPARD P O.
XX
PI Adler DA, Sheppard PO;
XX
DR WPI; 2002-635468/68.
XX
PT Novel secreted salivary protein, zsig63 and polynucleotide encoding it
PT useful for treating microbial infections, inflammatory conditions, dental
PT caries and lung infections associated with cystic fibrosis.
XX

```

```

PS Example 1; Page 29; 33pp; English.
XX
XX The present invention relates to a new secreted salivary protein, zsig63.
CC The invention is useful for detecting in a test sample, the presence of
CC an antagonist or agonist of zsig63 protein activity. The invention is
CC also useful as an immunogen for producing an antibody to zsig63
CC polypeptide. zsig63-cytokine fusion proteins or antibody-cytokine fusion
CC proteins are useful for enhancing in vivo killing of target tissues.
CC Pharmaceutical composition comprising purified zsig63 polypeptide are
CC useful in the treatment of conditions associated with pathological
CC microbes, including bacterial, fungal and viral infections. High
CC expression of zsig63 in salivary gland suggests that anti-microbial
CC polypeptides are useful for treatment of dental caries (tooth decay),
CC periodontal disease, thrush and gastrointestinal disease. Other
CC applications can be used in urinary tract infections, vaginal infections,
CC prevention of infection in skin and other epithelial wounds. The
CC polypeptides can be used to establish normal microflora and protect
CC against pathogenic colonisation and invasion. The invention is useful
CC when pro-inflammatory activity is desired. Applications for such pro-
CC inflammatory activity include the treatment of chronic tissue damage,
CC particularly in areas having a limited or damaged vascular system e.g.,
CC damage in extremities associated with diabetes. Antagonists to zsig63
CC polypeptides may be useful as anti-inflammatory agents. The invention is
CC useful for the treatment of patients having incompetent immune system,
CC such as AIDS (acquired immunodeficiency syndrome) patients or individuals
CC that have undergone chemotherapy, radiation treatment. The invention is
CC also useful for the treatment of lung infections associated with cystic
CC fibrosis and its agonists or antagonists are useful for aiding digestion.
CC The present nucleic acid sequence represents a PCR primer that was used
CC in the methods of the invention for identification of zsig63
CC
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;
XX
Query Match      0.3%; Score 22; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1.8e+02;
Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 4464 TTTTGTGCTTG 4489
    |||||
DB 1 TTTTGTGCTTG 26
XX
RESULT 65
AAD45054
ID AAD45054 standard; DNA; 26 BP.
XX
AC AAD45054;
XX
DT 27-DEC-2002 (first entry)
XX
DE ZC7231 primer used in the identification of human zsig63 DNA.
XX
KM Human; secreted salivary protein; zsig63 protein; host defense protein;
KM immune modulating factor; antipathogenic; cell-cell signalling molecule;
KM growth factor; cytokine; growth factor hormone activity; dental caries;
KM infection; tooth decay; periodontal disease; gastrointestinal disease;
KM thrush; urinary tract infection; vaginal infection; diabetes; obesity;
KM anti-inflammatory; chronic tissue damage; lung dysfunction; restenosis;
KM gene therapy; salivary gland dysfunction; prostate gland dysfunction;
KM forensic DNA profiling; chondrosarcoma; atherosclerosis; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002090677-A1.
XX
PD 11-JUL-2002.
XX
PF 03-AUG-2001; 2001US-00923236.
XX
PR 17-MAR-1999; 99US-0124820P.
XX
PR 17-MAR-2000; 2000US-00527345.
XX
PA (ADLER/) ADLER D A.
XX

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PA      (SHEP//) SHEPPARD P O .
PI      Adler DA, Shepard PO;
XX      WPI, 2002-642378/69.
DR      Novel secreted salivary polypeptide, zsig63, useful as antimicrobial
XX      agent for treating microbial infection, dental caries, periodontal
XX      disease, thrush gastrointestinal disease, and for aiding digestion.
PS      Example 1; Page 29; 33pp; English.
XX
CC      The invention relates to human secreted salivary polypeptide designated
CC      as zsig63 and nucleic acid molecules encoding such polypeptides. zsig63
CC      can be used in detecting agonists and antagonists of its activity, and is
CC      also useful as a host defense polypeptide, immune modulating factor,
CC      antipathogenic polypeptide, cell-cell signaling molecule, growth factor,
CC      cytokine, or as secreted extracellular matrix associated proteins with
CC      growth factor hormone activity. It is useful for treating conditions
CC      associated with pathological microbes, including bacterial, fungal and
CC      viral infections, for treating dental caries (tooth decay), periodontal
CC      disease, thrush and gastrointestinal disease, for treating urinary tract
CC      infection, vaginal infection and for preventing infection in skin and
CC      other epithelial wounds. zsig63 is useful for establishing normal
CC      microflora and protect against pathogenic colonisation and invasion, for
CC      treating chronic tissue damage e.g. damage in extremities associated with
CC      diabetes and useful as anti-inflammatory agents. It is useful as a marker
CC      of lung dysfunction, salivary gland dysfunction, or dysfunction of
CC      prostate gland. It is also therapeutically useful for aiding digestion.
CC      Polynucleotides of the invention are used in gene therapy for increasing
CC      or inhibiting zsig63 activity, for detecting abnormalities on human
CC      chromosome 4 associated with disease or other human traits and as
CC      diagnostics in forensic DNA profiling. Sequences of the invention are
CC      useful for stimulating proliferation or differentiation of cardiac
CC      myocytes, for proliferation or differentiation of adipocytes and for
CC      inhibiting chondrocytes, atherosclerosis, restenosis and obesity. The
CC      present sequence is a primer used in the identification of human zsig63
CC      DNA
SO      Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

Qy      Query Match          0.3%; Score 22; DB 1; Length 26;
        Best Local Similarity 88.5%; Pred. No. 1.8e+02;
        Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Dy      4464 TTTTCTTTTTTTTTTTTGCTGTG 4489
        ||| | | | | | | | | | | | | | | | :
        1 TTTTTTTTTTTTTTTTTTTTTT 26

RESULT 66
AADS5692 standard; DNA; 26 BP.
AADS5692;
AC      AAD55692;
AT      27-OCT-2003 (revised)
DT      07-AUG-2003 (first entry)
DE      Bovine viral diarrhea virus gene 5' end amplifying PCR primer.
DM      Bovine Viral Diarrhea Virus: BVDV, infection; vaccine; prophylaxis;
KW      gene therapy; PCR; primer; ss.
OS      Peativirus type 1.
PD      WO2003023041-A2.
PN      20-MAR-2003.
PF      05-SEP-2002; 2002WO-EP0009925.
PR      06-SEP-2001; 2001DE-01043813.
```

```

PA      '(BOEH ) BOEHRINGER INGELHEIM VETMEDICA GMBH.
XX
PI      Elbers K, Meyer C, Von Freyburg M, Meyers G;
XX
DR      WPI; 2003-333043/31.
XX
PT      New DNA molecule useful for manufacturing a vaccine for the prophylaxis
PR      and treatment of Bovine Viral Diarrhea Virus (BVDV) infections, comprises
PP      a sequence complementary to a BVDV RNA.
XX
PS      Example 1; Page 20; 73pp; English.
XX
CC      The invention relates to a DNA molecule containing a sequence
CC      complementary to a Bovine Viral Diarrhea Virus (BVDV) RNA. The RNA when
CC      introduced into susceptible host cells, induces the generation of
CC      infectious BVDV particles. The attenuated BVDV clone or strain is useful
CC      in the manufacture of a vaccine for the prophylaxis and treatment of BVDV
CC      infections. The invention is useful in gene therapy. The present sequence
CC      is a PCR primer used to amplify BVDV gene. (Updated on 27-OCT-2003 to
XX      standardise OS field)
SQ      Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;
OY      Query Match          0.3%; Score 22; DB 1; Length 26;
DB      Best Local Similarity   88.5%; Pred.No. 1.8e+02;
        Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
        4464 TTTTNTTTTTTTTTTTTTTTTTTCGTCGTG 4489
           ||||| | ||||| | ||||| | ||||| :
           1 TTTTNTTTTTTTTTTTTTTTTTTTTTTV 26

RESULT 67
ID      ABX93598
ABX93598     ABX93598 standard; DNA; 26 BP.
AC
AX      ABX93598;
XX
DT      28-MAY-2003 (first entry)
XX
DE      Human zslg63 PCR/sequencing primer ZC7231.
XX
KW      ss; PCR; zslg63; adhesin; salivary gland; dental carries;
KW      periodontal disease; thrush; gastrointestinal disease; epithelial wound;
KW      urinary tract infection; vaginal infection; skin infection; diabetes; AIDS;
KW      pro-inflammatory; chronic tissue damage; vascular system; digestive;
KW      lung infection; cystic fibrosis; lung dysfunction; emphysema;
KW      salivary gland carcinoma; Pneumocystis carinii infection;
KW      chronic bronchitis; prostate dysfunction; prostate adenocarcinoma;
KW      cell culture media; gene therapy; human chromosome 4q12-q13;
KW      dentinogenesis imperfecta; dentin dysplasia type II.
XX
OS      Synthetic.
XX
PN      US2002173027-A1.
XX
PD      21-NOV-2002.
XX
PF      03-AUG-2001; 2001US-00922469.
XX
PR      17-MAR-1999; 99US-0124820P.
PR      17-MAR-2000; 2000US-00527345.
XX
PA      (ADLER/) ADLER D A.
PA      (SHEP/) SHEPPARD P O.
XX
PI      Adler DA, Sheppard PO;
XX
WPI; 2003-328428/31.
XX
PT      Novel isolated zslg63 polypeptide, member of the adhesin family, useful
PP      for treating dental carries, periodontal disease, thrush.
```

PT gastrointestinal disease, urinary tract infections, vaginal infections,
PT skin infections.

PS Example 1, Page 29; 32pp; English.

XX The invention relates to an isolated zsig63 polypeptide comprising at
CC least 90% identity to an amino acid sequence which comprises domain 1 of
CC zsig63, domain 2, domain 3, mature zsig63 and full length zsig63. Also
CC included are the polynucleotide encoding zsig63, a zsig63 expression
CC vector, a cultured cell comprising the vector and expressing the protein,
CC a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37, 38-
CC 126, 127-219 or 16-219 of zsig63 and an additional protein), using a
CC zsig63 reporter gene construct to identify zsig63 agonists, and producing
CC an anti-zsig63 antibody using zsig63 immunogenic peptides, zsig63 is
CC useful for detecting in a test sample, the presence of antagonist of
CC zsig63 protein activity. Zsig63 has antimicrobial activity and since
CC exhibit high expression in salivary gland, can be used for treating
CC dental caries, periodontal disease, thrush, and gastrointestinal
CC disease, urinary tract infections, vaginal infections, skin infections
CC and other epithelial wounds. The polypeptides can be used to establish
CC normal microflora and protect against pathogenic colonization and
CC invasion. Zsig63 can also be used for providing pro-inflammatory activity
CC for treating chronic, tissue damage particularly in areas having limited
CC or damaged vascular system, e.g. in diabetes, and for treating
CC immunocompromised AIDS patients or in individuals that have undergone
CC chemotherapy, radiation treatment, for treating lung infections e.g. in
CC cystic fibrosis. Detection of zsig63 polypeptide at relatively high
CC levels in the trachea may indicate that such polypeptides may serve as a
CC marker of lung dysfunction. Zsig63 is also useful in diagnosing
CC conditions associated with salivary gland or lung dysfunction including
CC salivary gland carcinoma, Pneumocystis carinii infection, emphysema,
CC chronic bronchitis, prostate dysfunctions such as prostate
CC adenocarcinoma, aiding digestion, and as components of defined cell
CC culture media and may be used to replace serum that is commonly used in
CC culture. The DNA is useful in gene therapy applications to increase or
CC inhibit zsig63 activity, and for detecting abnormalities on human
CC chromosome 4 (e.g. 4q12-q13), associated with dentinogenesis imperfecta,
CC and dentin dysplasia type II). Zsig63 is an adhesin family member. The
CC present sequence is a primer used to isolate and sequence nucleic acids
CC encoding human zsig63

XX SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

Query Match 0.3%; Score 22; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1.8e+02;
Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTGCTTG 4489

DB 1 TTTTGTGCTTG 26

RESULT 68

ACF36382 ACF36382 standard; DNA; 26 BP.

AC ACF36382;

DT 04-DEC-2003 (first entry)

DE Nucleotide sequence of a second back primer.

XX Nucleic acid manipulation: mRNA profiling; polymerase chain reaction;
KM electrophoresis; PCR; primer; ss.

XX Synthetic.

XX WO2003064691-A2.

XX 07-AUG-2003.

PF 28-JAN-2003; 2003WO-IB000843.

XX

PR 29-JAN-2002; 2002US-0352215P.

XX (GLOB-) GLOBAL GENOMICS AB.

PI Linmarsson S, Ernfor P, Bauren G, Metsis A, Pihlak A;

PI Montellus A;

DR WPI; 2003-618365/58.

PT Producing a population of double-stranded product DNA molecules, useful
PT for mRNA profiling, comprises amplification by nested polymerase chain
PT reaction.

PS Claim 6; Page 85; 105pp; English.

CC The invention relates to producing a population of double-stranded
CC product DNA molecules comprising amplification by a nested PCR method.
CC The method is useful in profiling mRNA transcribed in a system under
CC investigation. The oligonucleotides are used as size standards in
CC electrophoresis, and as internal controls allowing for calculation of
CC relative amounts of material present. The present sequence represents a
CC specific example of a PCR primer used in the method of the invention

XX SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

Query Match 0.3%; Score 22; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1.8e+02;
Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTGCTTG 4489

DB 1 TTTTGTGCTTG 26

RESULT 69

AAZ43904 AAZ43904 standard; DNA; 27 BP.

AC AAZ43904;

DT 10-MAR-2000 (first entry)

DE M. tuberculosis ipo-beta primer 17.

XX RNA polymerase: ipo-beta; detection; diagnostic; trap probe; primer; ss.

OS Mycobacterium tuberculosis.

PN EP962536-A1.

PD 08-DEC-1999.

PF 29-MAY-1999; 99EP-00110458.

PR 04-JUN-1998; 98DE-01024900.

PA (HOFF) ROCHE DIAGNOSTICS GMBH.

PI Weindel K, Brand J;

DR WPI; 2000-055287/05.

PT Selective detection of nucleic acids by amplification with labeled
PT primers and detection with a trap probe.

PS Example 1c; Page 19; 27pp; German.

CC This invention describes a novel method for the selective detection of
CC nucleic acids which comprises amplification of the nucleic acid with the
CC help of labeled primers and detection with a trap probe. The methods and
CC reagents are used for the detection of a marker primer and at least 2
CC immobilized (or immobilizable) trap probes with the corresponding nucleic
CC acid sequence of interest for mutation analysis. The method can be used

to detect a specific sequence in a sample of one or more nucleic acids by using several sets of primers and trap probes (i.e. in an array). The methods are useful in molecular biology and diagnostic applications, especially for simultaneous detection of multi-pathogens, typing of organisms, analyzing genetic diversity and sequencing of genes or genomes. This sequence represents a primer used in the method of the invention

Sequence 27 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 1 Other;

Query Match 0.3%; Score 22; DB 1; Length 27;
Best Local Similarity 91.7%; Pred No. 1.9e+02;
Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0

Oy 4464 TTTTCTTTTTTTTTTTTTTGCT 4487
|||||
Db 4 TTTTCTTTTTTTTTTTTTTTTTT 27
|||||

RESULT 70
ABQ76254
ID ABQ76254 standard; DNA; 27 BP.
XX
AC ABQ76254;
XX
DT 08-NOV-2002 (first entry)
XX
DE Murine SCCE 5'-RACE oligonucleotide SEQ ID 42.
XX
KW SCCE; murine; stratum corneum chymotryptic enzyme; kallikrein 7;
KM serine protease; transgenic mammal; skin; skin disease; skin cancer;
KV hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
KX pruritus; atopic dermatitis; eczema; acne; itch; KIM7; ss.
XX
OS Mus musculus.
XX
PN WO200262135-A2.
XX
PD 15-AUG-2002.
XX
PE 08-FEB-2002; 2002MO-IB001300.
XX
PR 09-FEB-2001; 2001CA-0232655.
PR 09-FEB-2001; 2001DK-00000218.
PA (EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
P1 Egellrud T, Hansson L;
P1 WPI; 2002-643380/69.
DR Transgenic mammal or its embryo useful as model for human disease, has
PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
PT enzyme operably linked to promoter that drives its expression in skin.
PS Example 6; Page 36; 74pp; English.

This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologous sequence or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of inflammatory skin diseases selected from diseases consisting of epidermal

	CC	hyperkeratosis; acanthosis, epidermal inflammation, dermal inflammation,
	CC	pustules, atopic dermatitis, eczema, acne and inherited skin diseases
	CC	with epidermal hyperkeratosis. The mammal of the invention is also useful
	CC	as a model for further studies of itch mechanisms and the testing of
	CC	potential compounds and compositions for relieve of various skin diseases
	CC	where itch is a component. This sequence represents a 5' RACE cDNA
	CC	synthesis primer used in a method of detecting homologues to human
	CC	stratum corneum chymotryptic enzyme, SCCEB, gene. SCCB is a serine
	CC	protease synonymous with human kallikrein 7 (KLK7) and is used in the
	CC	development of the transgenic mammals described in the invention
	XX	
SQ	Sequence 27 BP;	0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;
	Query Match	0.3%; Score 22; DB 1; Length 27;
	Best Local Similarity	88.5%; Pred. No. 1.9e+02;
	Matches 23;	Conservative 1; Mismatches 2; Indels 0; Caps 0
Oy	4464	TGCTTCGTGGCCTTG 4489 TTTTTTT
Dd	1	TTTTTTTTTTTTTTTTTTTTV 26
<hr/>		
RESULT 71		
ID	ABX12469	standard; DNA; 27 BP.
XX	AC	
XX	ABX12469;	
DT	10-MAY-2003	(first entry)
XX	Coxsackie B virus 4 (CBV-4) strain VD2921, PCR primer dIT26V.	
DE	XX	
KW	Coxsackie virus stratin VD2921; diabetogenic coxsackie B virus-4; CBV-4; strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3D; diabetes; diabetogenic enterovirus; beta cell loss; blindness; renal failure; leg amputation; PCR; primer; se. OS Coxsackievirus. PN WO2002103060-A2. PD 27-DEC-2002. PF 19-JUN-2002; 2002WO-IB003278. PR 20-JUN-2001; 2001SE-00002198. PA (INNO-) INNOVENTUS PROJECT AB. PI Tuveno HT, Frisk GE, Yan H; DR WFI; 2003-278229/27. PT Polymerase chain reaction and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 strain VD2921. PS Example 5; Page 44; 79pp; English. XX The invention describes a polymerase chain reaction (PCR) and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4) strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B, P3C and P3D nucleic acids). The methods and primers are used for the detection of CBV-4 strain VD2921 which is associated with diabetes (diabetogenic enterovirus). Early detection of the diabetes e.g. cells, can improve prognosis by allowing treatment e.g. with antiviral drugs, to prevent further loss of beta cells and severe long term consequences of diabetes including blindness, renal failure and leg amputations. This sequence represents a primer used to determine the genomic structure of diabetogenic coxsackie B virus 4 (CBV-4) strain VD2921 SQ Sequence 27 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 1 Other;	

Query Match 0.3%; Score 22; DB 1; Length 27;
 Best Local Similarity 88.5%; Pred. No. 1.9e+02;
 Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTGCTG 4489
 |||||
 DB 2 TTTTGTGCTG 27

RESULT 72

AA517761 standard; DNA; 31 BP.

AC AA517761;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Oligo d(T) PCR primer.
 XX
 XX Oligo d(T); ss; differential subtraction; PCR primer;
 KM double exponential elimination; tumour.
 XX
 OS Synthetic.
 XX
 XX US6316192-B1.
 XX
 PN 13-NOV-2001.
 XX
 PD 11-MAR-1999; 99US-00268505.
 XX
 PF 11-MAR-1999; 99US-00268505.
 XX
 PR 11-MAR-1999; 99US-00268505.
 XX
 PA (LUOJ/) LUO J.
 XX
 PI Luo J;
 XX
 DR WPI; 2002-074371/10.
 XX
 PT Selective elimination of non-targeted DNA sequences for rapid isolation
 PT and enrichment of the differences of DNA fragments between two pools of
 PT DNA, comprises converting testers to drivers.
 XX
 PS Claim 6; Col 5; 23pp; English.
 XX

The invention comprises rapid isolation and enrichment of the differences of DNA fragments between two pools of DNA, comprises converting to undesirable testers (DNA being subtracted) to drivers (DNA used to subtract) and re-utilising converted drivers in repeats of subtraction to achieve double exponential elimination of undesirable tester sequences. The method comprises (a) attaching a nucleic acid fragment to 1 or more polymerase chain reaction (PCR) adapters to form an adapter-attached nucleic acid fragment, followed by amplifying the adapter-attached nucleic acid fragment through PCR with primers containing nucleic acid sequences complementary to nucleic acid sequences of the adapter to form an adapter-attached nucleic acid tester, (b) mixing the adapter-attached nucleic acid tester with a nucleic acid driver that contains no attached adapter or contains an attached adapter whose sequence differs from the adapter, to form a nucleic acid mixture, (c) denaturing and re-annealing the tester/driver nucleic acid mixture, (d) adding to the nucleic acid mixture an effective amount of reagents necessary for removing the adapter sequence from the tester/driver hetero-duplex and (e) repeating step (c) to (d) at least once (no amplification takes place and no additional driver is added). The method is used for rapid isolation and enrichment of the differences of DNA fragments between two pools of DNA e.g. in the search for tumour specific sequences. The method has 2 improvements over the methods disclosed by Yang et al. (1996), Hysteyn et al. (1993), Straus et al. (1990) by (i) bypassing the need of a polymerase chain reaction (PCR) amplification or physical separation of desirable testers from undesirable ones in each repeat of subtraction, it eliminates the necessity of tester dilution in each repeat of subtraction, and (ii) by utilising the converted driver from each repeat of subtraction, it eliminates the need for re-introducing additional

CC driver into hybridisation in each repeat of subtraction. The present
 CC sequence is an Oligo d(T) PCR primer used in the method of the invention
 XX
 SQ Sequence 31 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 1 Other;

Query Match 0.3%; Score 22; DB 1; Length 31;
 Best Local Similarity 88.5%; Pred. No. 2.3e+02;
 Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTGCTG 4489
 |||||
 DB 6 TTTTGTGCTG 31

RESULT 73

AA509500 standard; DNA; 32 BP.

AC AA509500;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE SMART PCR primer #2.
 XX
 XX Heat-labile uracil-DNA glycosylase; UNG; UDG; PCR primer; SMART;
 KM PCR control; LCR control; ligase chain reaction; carry-over prevention;
 KM ss.
 XX
 OS Synthetic.
 XX
 XX WO200151623-A1.
 XX
 PN 19-JUL-2001.
 XX
 PD 10-JAN-2001; 2001WO-N0000008.
 XX
 PF 12-JAN-2000; 2000NO-00000163.
 XX
 PR 27-OCT-2000; 2000NO-00005428.
 XX
 PA (BIOT-) BIOTEC ASA.
 XX
 PI Lanes O, Willaen NP, Guddal PH, Gjellervik DR;
 XX
 DR WPI; 2001-451854/48.
 XX
 PT New cod liver uracil-DNA glycosylase enzyme, useful in monitoring or
 PT controlling a reaction system multiplying DNA sequences or in carry-over
 PT prevention procedures.
 XX
 PS Example 2; Page 20; 59pp; English.
 XX

The sequence represents a SMART PCR primer used to synthesise first strand cDNA from Atlantic cod in order to isolate cDNAs encoding heat-labile uracil-DNA glycosylase, (UNG/UDG). The enzyme is useful in CC monitoring and/or controlling a reaction system multiplying DNA CC sequences, e.g. PCR (polymerase chain reaction) or LCR (ligase chain reaction). The enzyme is also useful in carry-over prevention procedures
 XX
 SQ Sequence 32 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 2 Other;

Query Match 0.3%; Score 22; DB 1; Length 32;
 Best Local Similarity 85.2%; Pred. No. 2.4e+02;
 Matches 23; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTTGTGCTG 4490
 |||||
 DB 6 TTTTGTGCTG 32

RESULT 74

ABA01204 standard; DNA; 32 BP.

XX

[illegible]

BR	29-MAR-2000; 2000CN-00115295.
XX	(BLOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX	
XX	Mao Y, Xie Y;
PI	
DR	WPI; 2002-010782/01.
XX	
PS	New polypeptide applicable in diagnosis and treatment of malignant tumor,
PT	hemopathy, HIV infection, immunological diseases and inflammation,
PT	comprises the human ribosomal S4 protein 12.
XX	
PS	Example 4; Page 14; 33pp; Chinese.
CC	The invention relates to human ribosomal S4 protein 12 with cytosolic,
CC	virucidal, immunomodulatory, antiinflammatory and haemostatic activity.
CC	The protein and encoding polynucleotide are used in diagnosis and
CC	treatment of malignant tumour, haemopathy, human immunodeficiency virus
CC	(HIV) infection, immunological diseases and various inflammations. The
CC	polynucleotide is useful in gene therapy. The present sequence is that of
CC	a PCR primer, useful to the invention
SQ	
Sequence	33 BP; 5 A; 4 C; 4 G; 20 T; 0 U; 0 Other;
Query Match	0.3%; Score 22; DB 1; Length 33;
Best Local Similarity	83.3%; Pred. No. 2.ee+02;
Matches	25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY	4452 GGTCGATGGACCTTTTTTTTTTTTTTTT 4481
Dd	4 GCTTGCAITGCAGATTTTTTTTTTTTTTT 33
RESULT 76	
ID	AAQ95960 standard; DNA; 25 BP.
AC	AAQ95960;
DT	06-FEB-1996 (first entry)
DE	Oligonucleotide biotin-T25 for novel nucleic acid immobilisation method.
KW	Immobilisation; solid support; salt; cationic detergent; capture probe;
KV	hybridisation; primer; template-dependent extension; target organism;
XX	sequencing; genetic polymorphism; ss.
OS	Synthetic.
FH	Key Location/Qualifiers
FT	misc_feature 1
FT	/tag= a
FT	/note= "biotinylated"
XX	'009515970-AI.
PD	15-JUN-1995.
PE	06-DEC-1994; 94MO-US014096.
PR	06-DEC-1993; 93US-00162397.
PR	16-NOV-1994; 94US-00341148.
PA	(MOL-) MOLECULAR TOOL INC.
PL	Nikiforov T, Knapp MR;
DR	WPI; 1995-224282/29.
XX	
XX	Immobilising synthetic nucleic acid on solid support - by incubation in
XX	presence of salt or cationic detergent, for use in hybridisation assays,
XX	sequencing and analysis of polymorphism.


```

XX (UYJO ) UNIV JOHNS HOPKINS.
PA (MORP-) MORPHOTEX INC.
PA (NICO/) NICOLAIDES N C.
PA (SAS/) SAS P M.
PA (GRAS/) GRASSO L.
PA (VOGE/) VOGELSTEIN B.
XX (KINZ/) KINZLER K W.
XX
XX Nicolaides NC, Saks PM, Grasso L, Vogelstein B, Kinzler KW;
XX WPI; 2002-083004/11.
XX
XX Generating mutation in gene using cells which contain defective mismatch
XX repair gene, useful to generate genetically altered mutations with new
XX output traits.
XX
XX Example 5; Fig 7, 59pp; English.
XX
XX The patent discloses a method for generating hypermutable organisms.
XX dominant negative alleles of human mismatch repair genes can be used to
XX generate hypermutable cells and organisms. They increase the rate of
XX spontaneous mutations by reducing the effectiveness of DNA repair and
XX thereby render the cells or animals hypermutable. The method is used to
XX produce genetically altered organisms to produce new output traits. The
XX present sequence is a bacterial poly purine nucleotide phosphorylase
XX (polyPMP) DNA fragment containing an in-frame polyA tract. This sequence
XX is used in the exemplification of the invention
XX
XX Sequence 25 BP; 21 A; 1 C; 2 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 21.8; DB 1; Length 25;
XX Best Local Similarity 92.0%; Pred. No. 1.8e+02;
XX Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 25 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

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RESULT 82
ABK86170
ID ABK86170 standard; DNA; 25 BP.
XX
AC ABK86170;
XX
DT 24-SEP-2002 (first entry)
XX
DE Oligo dT primer #3 used in method to study gene expression.
XX
KW Oligo dT primer; gene expression analysis; primer; ss.
XX
OS Synthetic.
XX
PN WO200236828-A2.
XX
PD 10-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-US045401.
XX
PR 01-NOV-2000; 2000US-0244933P.
XX
PA (GENO-) GENOMIC SOLUTIONS INC.
XX
PI Kane MD, Dombkowski AA, Nagel AC;
XX
DR WPI; 2002-508123/54.
XX
PT Identifying and characterizing gene expression in samples, for
XX identifying mRNAs expressed at different levels, comprises employing an
XX primer having an oligo-dT primer of a specific sequence and a
XX detectable marker at its 5' end.

```

PS Example 2; Page 21; 45pp; English.
XX
XX The invention relates to systems for identification and characterization
XX of gene expression in one or more samples, comprising an identifier having
XX a specific oligo-dT primer sequence, where the identifier comprises a
XX detectable marker at its 5' end. The system is useful for identifying any
XX or all genes expressed in a given in vivo or in vitro RNA sample, as well
XX as the relative differences in mRNA between 2 or more samples, where
XX desired, for supporting discovery of new genes, and for identifying mRNAs
XX that are expressed at different levels between 2 or more samples. The new
XX system or method addresses limitations of prior methods by comprising
XX compositions and systems that incorporate new strategies where molecular
XX or biochemical assay compositions and systems are linked to DNA or RNA
XX sequence databases for optimal resource efficiency in assaying gene
XX expression. The system has the following advantages over existing
XX methods: (a) prior sequence information or clone library construction is
XX not needed to enable the assay; (b) provides immediate sequence
XX information in addition to information concerning changes or differences
XX in mRNA level; (c) generates cDNA fragments from all mRNAs present in the
XX in one assay; (d) generates common molecular biology
XX techniques; and (d) does not require prior knowledge of the sequence of
XX the genome of the organism under investigation and can be employed in
XX organisms lacking significant genomic sequence information. The present
XX sequence represents an oligo dT primer used in the method of the
XX invention
XX
XX Sequence 25 BP; 0 A; 0 C; 2 G; 23 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 21.8; DB 1; Length 25;
XX Best Local Similarity 92.0%; Pred. No. 1.8e+02;
XX Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

```

RESULT 83
ADC54009
ID ADC54009 standard; DNA; 25 BP.
XX
AC ADC54009;
XX
DT 18-DEC-2003 (first entry)
XX
DE Oligonucleotide of the invention SEQ ID NO:4.
XX
KW ss; probe carrier; discharge.
XX
OS Synthetic.
XX
PN JP2003035711-A.
XX
PD 07-FEB-2003.
XX
PF 28-MAR-2002; 2002JP-00093023.
XX
PR 28-MAR-2001; 2001JP-00094400.
XX
PA (CANO) CANON KK.
XX
DR WPI; 2003-535999/51.
XX
PT Probe carrier manufacturing method for inkjet system, involves scanning
XX liquid discharge head in direction orthogonal to scanning direction, at
XX angle satisfying predetermined relation.
XX
PS Example 2; SEQ ID NO 4; 17pp; Japanese.
XX
XX The invention relates to a novel probe carrier and the method for
XX manufacturing the carrier. The invention enables stable discharge of
XX solution, and removes liquid droplets adhering to discharge nozzle. The

CC Present sequence is used in the exemplification of the invention.
 XX Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

SEQ Query Match 0.3%; Score 21.8; DB 1; Length 25;
 Best Local Similarity 92.0%; Pred. No. 1.8e+02;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTGCTT 4488
 DB 1 TTTTGTGCTT 25

RESULT 84
 ADC54008/C
 ID ADC54008 standard; DNA; 25 BP.

AC ADC54008;
 XX 18-DEC-2003 (first entry)
 XX DE Oligonucleotide of the invention SEQ ID NO:3.
 XX KM ss; probe carrier; discharge.

XX OS Synthetic.

XX PN JP2003035711-A.

XX PD 07-FEB-2003.

XX PF 28-MAR-2002; 2002JP-00093023.

XX PR 28-MAR-2001; 2001JP-00094400.

XX PA (CANO) CANON KK.

XX DR WPI; 2003-535999/51.

XX PT Probe carrier manufacturing method for inkjet system, involves scanning
 PT liquid discharge head in direction orthogonal to scanning direction, at
 PT angle satisfying predetermined relation.

XX PS Example 2; SEQ ID NO 3; 17pp; Japanese.

XX CC The invention relates to a novel probe carrier and the method for
 CC manufacturing the carrier. The invention enables stable discharge of
 CC solution, and removes liquid droplets adhering to discharge nozzle. The
 CC present sequence is used in the exemplification of the invention.

XX SQ Sequence 25 BP; 25 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 21.8; DB 1; Length 25;
 Best Local Similarity 92.0%; Pred. No. 1.8e+02;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTGCTT 4488
 DB 25 TTTTGTGCTT 1

RESULT 85
 AAN70276
 ID AAN70276 standard; DNA; 26 BP.

XX AC AAN70276;
 XX XX

DT 03-OCT-2002 (revised)

DT 26-MAY-1991 (first entry)

DE Sequence of scissile link probe MRC060 (HL).

XX KM Hybridisation; probe; ss.

XX OS Synthetic.

XX PN EP227976-A.

XX PD 08-JUL-1987.

XX PF 04-DEC-1986; 86EP-00116906.

XX PR 05-DEC-1985; 85US-00805279.

XX PA (MEIO-) MEIOGENICS INC.

PI Duck P, Bender R, Crosby W, Robertson JG;

DR WPI; 1987-186567/27.

XX PT Synthetic nucleic acid probes - comprising two nucleic acid sequences
 XX linked by a scissile linkage.

XX PS Example; p29; 46pp; English.

XX CC The patent claims a new molecule of formula (NA1)----S----(NA2)n. NA1 and
 CC NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
 CC linkage; n= 1 or 1,000, which is used for the detection of specific DNA
 CC or RNA sequences in a test soln. The scissile link probes may be PL
 CC (permanent linkage to Solid Support) or HL (Hydrolyzable linkage to Solid
 CC Support). The differential lability of DNA and RNA may be exploited in a
 CC heterogeneous system when the scissile linkage is an RNA molecule. In the
 CC examples, counter probe molecules 9 through 16 were used to determine
 CC suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
 CC OS field.)

XX SQ Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;

Query Match 0.3%; Score 21.8; DB 1; Length 26;
 Best Local Similarity 76.0%; Pred. No. 2e+02;
 Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTGCTT 4488
 DB 1 TTTTGTGCTT 25

RESULT 86
 AAN70275

ID AAN70275 standard; DNA; 26 BP.

XX AC AAN70275;
 XX XX

DT 03-OCT-2002 (revised)

DT 26-MAY-1991 (first entry)

DE Sequence of scissile link probe MRC059 (HL).

XX KM Hybridisation; probe; ss.

XX OS Synthetic.

XX PN EP227976-A.

XX PD 08-JUL-1987.

XX PF 04-DEC-1986; 86EP-00116906.

XX PR 05-DEC-1985; 85US-00805279.

XX PA (MEIO-) MEIOGENICS INC.

PI Duck P, Bender R, Crosby W, Robertson JG;

DR WPI; 1987-186567/27.

```

PT Synthetic nucleic acid probes - comprising two nucleic acid sequences
XX linked by a scissile linkage.
PS Example; p29; 46pp; English.
CC The patent claims a new molecule of formula (NA1---S---NA2)n. NA1 and
CC NA2 are noncomplementary nucleic acid sequences; --S-- = a scissile
CC linkage; n= 1 or 1,000, which is used for the detection of specific DNA
CC or RNA sequences in a test soln. The scissile link probes may be PL
CC (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC Support). The differential liability of DNA and RNA may be exploited in a
CC heterogeneous system when the scissile linkage is an RNA molecule. In the
CC examples, counter probe molecules 9 through 16 were used to determine
CC suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC OS field.)
XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;
XX
Query Match 0.3%; Score 21.8; DB 1; Length 26;
Best Local Similarity 76.0%; Pred.No.2e+02;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
CY 4464 TTTT TTTT TTTT TTTT TTTT TGCTT 4488
Db 1 TTTT TTTT TUUUU TTTT TTTT TT 25
RESULT 87
AAN92241
ID AAN92241 standard; DNA; 26 BP.
AC
XX AAN92241;
AC
XX 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 25-APR-1990 (first entry)
DE SS probe MRCO59.
DE
XX
XX Probe MRCO59; solid support; ribonuclease.
KW
XX
XX Synthetic.
OS
XX Key Location/Qualifiers
FH misc_feature 1..10
FT /tag= a
FT /note= "deoxyribonucleotides."
FT misc_feature 11..14
FT /tag= b
FT /note= "ribonucleotides."
FT misc_feature 15..26
FT /tag= c
FT /note= "deoxyribonucleotides."
XX
XX W08910415-A.
XX
XX 02-NOV-1989.
XX
XX 29-APR-1988; 88US-00187814.
XX
XX 29-APR-1988; 88US-00187814.
XX
XX (MELO-) MEIOGENICS INC.
XX
XX Duck P, Bender R,
PI
XX
XX MPI; 1989-339977/46.
XX
XX Detecting target nucleic acid molecules - using excess complementary
XX nucleic acid probes and nicking to complete a cycling sequence.
XX
XX Disclosure; Page 24; 34pp; English.
XX

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```

CC CC Probe MRCO59 is bound by a hydrolysable linkage to a solid support at its
CC 3' end. It is used by reacting excess probe with a target nucleic acid;
CC nicking hybridised probe at least once within a predetermined sequence to
CC form 2 or more probe fragments hybridised to the target sequence, which
CC results in the probe fragments becoming hybridised to another probe; and
CC identifying probe fragments, so detecting the target sequence. The probe
CC can react with target sequence to complete a cycling sequence. Using this
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC be obt. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC RNase H or ExoIII. (Updated on 31-Oct-2002 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
CC
XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;

Oy . 4464 TTTT TTTT TTTT TTTT TTTT GCT 4488
    ||||| ||||| ||||| ||||| |||||
    1 TTTT TTTT TTTT TTTT TTTT TTTT 25

Db

RESULT 88
AAN92242
ID AAN92242 standard; DNA; 26 BP.
XX
AC AAN92242;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 25-APR-1990 (first entry)
XX
DE SS probe MRCO60.
XX
KW Probe MRCO60; solid support; ribonuclease.
XX
OS Synthetic.
OS
OS Key Location/Qualifiers
FH 1..12
FT misc_feature /tag= a
FT /note= "deoxyribonucleotides."
FT misc_feature /tag= b
FT /note= "ribonucleotides."
FT misc_feature /tag= c
FT /note= "deoxyribonucleotides."
XX
XX WO8910415-A.
XX
XX 02-NOV-1989.
XX
XX 29-APR-1988; 88US-00187814.
XX
XX 29-APR-1988; 88US-00187814.
XX
XX (MEIO-) MEIOGENICS INC.
XX
XX Duck P, Bender R;
XX
XX WPI; 1989-339977/46.
XX
XX
XX Detecting target nucleic acid molecules - using excess complementary
XX nucleic acid probes and nicking to complete a cycling sequence.
XX
XX Disclosure; Page 24; 34pp; English.
XX
XX Probe MRCO60 is bound by a hydrolysable linkage to a solid support at its
XX 3' end. It is used by reacting excess probe with a target nucleic acid;
XX nicking hybridised probe at least once within a predetermined sequence to
XX form 2 or more probe fragments hybridised to the target sequence, which
XX

```


CC results in the probe fragments becoming hybridised to another probe; and
CC identifying probe fragments, so detecting the target sequence. The probe
CC can react with target sequence to complete a cycling sequence. Using this
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC be obt'd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
CC
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;
Query Match 0.3%; Score 21.8; DB 1; Length 26;
Best Local Similarity 76.0%; Pred. No. 2e+02;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT GCTT 4488
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 25
RESULT 89
AAAF7536
ID AAF7536 standard; DNA; 26 BP.
XX
AC AAF7536;
XX
DT 23-MAY-2001 (first entry)
XX
DE CDNA library production method related oligonucleotide SEQ ID NO: 5.
XX
KM CDNA library production; SCLA; gene chip technology;
XX differential screening; pathological diagnosis; genetic identification;
KM single-cell CDNA library amplification; ds.
XX
OS Synthetic.
XX
PN US6197554-B1.
XX
PD 06-MAR-2001.
XX
PF 20-NOV-1998; 98US-00197951.
XX
PR 20-NOV-1998; 98US-00197951.
XX
PA (LINS/) LIN S.
PA (CHUO/) CHUONG C.
PA (YING/) YING S.
XX
PI Lin S, Chuong C, Ying S;
XX
DR WPI; 2001-243448/25.
XX
PT Generating a complete full-length CDNA library from single cells for use
PT in gene chip technology, involves reverse transcribing intracellular
PT mRNA, adding polynucleotide tail and amplifying formed cDNAs.
XX
PS Disclosure; Col 11-12; 11pp; English.
XX
XX The present invention describes a method of producing full-length CDNA
CC libraries from single cells, designated single-cell CDNA library
CC amplification (SCLA). The method is useful in gene chip technology,
CC differential screening, pathological diagnosis, physiological prognosis
CC and genetic identification. No further information about this sequence is
CC given in the specification
XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;
Query Match 0.3%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT GCTT 4488
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 25

RESULT 90
AAD03682
ID AAD03682 standard; DNA; 26 BP.
XX
AC AAD03682;
XX
DT 19-JUN-2001 (first entry)
XX
DE Human full length zcytor13 CDNA isolating polyA PCR primer, ZC7764b.
XX
KM Human: phosphodiesterase; PDE; zcytor13; antiasthmatic; antiarthritic;
KM antipsoriatic; cyrostatic; antiatherosclerotic; antifertility;
KM cardiant; antiinflammatory; dermatological; wound healing; antiviral;
KM antibacterial; therapy; inflammatory bowel disease; diverticulitis;
KM spermatogenesis; sperm capacitation; immunononreceptive; vaccine;
KM cancer; reperfusion ischemia; psoriasis; melanoma; myocarditis; PID;
KM pelvic inflammatory disease; eczema; scleroderma; vasoconstriction;
KM heart arrhythmia; congestive heart disease; muscle spasm; fatigue;
KM chromosomal abnormality; gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200125444-A2.
XX
PD 12-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US027734.
XX
PR 07-OCT-1999; 99US-00414025.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Novak JE, Gao Z;
XX
DR WPI; 2001-266312/27.
XX
PT Novel human phosphodiesterase polypeptide, zcytor13 and polynucleotide
PT encoding it, for detecting human chromosomal abnormalities, identifying
PT modulators and treating inflammatory and cardiovascular diseases.
XX
PS Example 1C; Page 118; 122pp; English.
XX
XX The patent discloses novel human phosphodiesterase (PDE), zcytor13 CDNA
CC and its corresponding protein. Zcytor13 protein is used to promote wound
CC healing in tissues, to exhibit anti-bacterial and anti-viral effects and
CC to identify modulators (e.g. agonists or antagonists). Zcytor13, its
CC agonists or antagonists are useful in the treatment of inflammatory heart
CC or cardiovascular conditions, muscle inflammation, inflammation during
CC and after surgery, arthritis, asthma, inflammatory bowel disease or
CC diverticulitis, for modulating spermatogenesis, sperm capacitation, as
CC immunononreceptive or anti-fertility vaccine and for treating male
CC infertility. Zcytor13 protein and its antibodies are used to diagnose
CC cancer, reperfusion ischemia, asthma, psoriasis and melanoma. Zcytor13
CC proteins are used to enhance fertilisation. Zcytor13 antagonists are used
CC to treat myocarditis, atherosclerosis, pelvic inflammatory disease (PID),
CC psoriasis, eczema, scleroderma and other inflammatory diseases. Zcytor13
CC sequences and/or its antibodies are useful for treatment of disorders
CC associated with vasoconstriction, heart arrhythmia, congestive heart
CC disease, muscle spasms and fatigue. They are used for detecting human
CC chromosomal abnormalities. Zcytor13 cDNAs are used in gene therapy.
CC Zcytor13-cytokine fusion proteins or antibody-cytokine fusion proteins
CC are useful for enhancing in vivo killing of target tissue. The present
CC sequence is a polyA PCR primer, ZC7764b which is used to isolate full
CC length zcytor13 CDNA by screening human placental CDNA library
XX
SQ Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
Query Match 0.3%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTGTGCTT 4488
 |||||
 KW
 DB 1 TTTTGTGCTT 25

RESULT 91
 AAF23526
 ID AAF23526 standard; DNA; 26 BP.
 XX
 AC AAF23526;
 XX
 DT 22-MAR-2001 (first entry)
 XX
 DE Primer #4.
 XX
 KW Primer; mRNA; amplification; ss.
 XX
 OS Unidentified.
 XX
 PN WO200075356-A1.
 XX
 PD 14-DEC-2000.
 XX
 PF 04-JUN-1999; 99WO-US012461.
 XX
 PR 04-JUN-1999; 99WO-US012461.
 XX
 PA (LINS/) LIN S.
 PA (YING/) YING S.
 PA (CHUO/) CHUONG C.
 PA (WIDE/) WIDELITZ R B.
 PI Lin S, Ying S, Chuong C, Widelitz RB;
 DR WPI; 2001-061734/07.
 XX
 PT Generating amplified messenger RNA sequences from single cells, involves
 PT cycling steps of reverse transcription, denaturation, double-stranded DNA
 PT sequences and in vitro transcription.
 PS
 PS Disclosure; Page 17; 31pp; English.
 XX
 CC The present invention relates to generating amplified messenger RNAs with
 CC polymerase reaction activity, comprising cycling steps of reverse
 CC transcription, denaturation, double-stranded cDNA synthesis and in vitro
 CC transcription. The invention is used for generating amplified mRNAs from
 CC limited mRNAs from single cells
 CC
 CC Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;
 SQ
 Query Match 0.3%; Score 21.8; DB 1; Length 26;
 Best Local Similarity 92.0%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
 Matches 23; Conservative 0; Mismatches 2;
 Qy 4464 TTTTGTGCTT 4488
 |||||
 DB 1 TTTTGTGCTT 25

RESULT 92
 AAS20596
 ID AAS20596 standard; DNA; 26 BP.
 XX
 AC AAS20596;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Human zsig63 cDNA sequencing primer ZC7764a.
 XX
 KW Human; zsig63; chromosome 4q12-q13; salivary protein; antimicrobial; ss;
 KW microbial infection; tooth decay; periodontal disease; thrush; emphysema;
 KW gastrointestinal disease; urinary tract infection; vaginal infection;
 KW skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;

KW acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis;
 KW chronic bronchitis; gene therapy; protein therapy; primer; ZC7764a.
 XX
 OS Homo sapiens.
 XX
 PN US6331413-B1.
 XX
 PD 18-DEC-2001.
 XX
 PF 17-MAR-2000; 2000US-00527345.
 XX
 PR 17-MAR-1999; 99US-0124820P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Adler DA, Sheppard FO;
 DR WPI; 2002-096707/13.
 XX
 PT Polynucleotides encoding salivary proteins useful as anti-microbial
 PT agents.
 PS
 PS Example 1; Col 53; 29pp; English.
 XX
 CC The invention relates to a polynucleotide derived from the 4q12-4q13
 CC region of human chromosome 4 and encoding a zsig63 polypeptide, a
 CC secreted salivary protein with anti-microbial activity. Due to their
 CC microbial activity, the sequences can be used in the study of microbial
 CC infections, e.g. for recombinant production of anti-microbial proteins.
 CC The sequences can be used in the treatment of tooth decay, periodontal
 CC disease, thrush, gastrointestinal disease, urinary tract infections,
 CC vaginal infections, skin infections, epithelial wounds, chronic tissue
 CC damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung
 CC infections, sarcoidosis, emphysema and chronic bronchitis. This sequence
 CC represents a sequencing primer for cDNA encoding human zsig63
 CC
 CC Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
 SQ
 Query Match 0.3%; Score 21.8; DB 1; Length 26;
 Best Local Similarity 92.0%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
 Matches 23; Conservative 0; Mismatches 2;
 Qy 4464 TTTTGTGCTT 4488
 |||||
 DB 1 TTTTGTGCTT 25

RESULT 93
 ABS52638
 ID ABS52638 standard; DNA; 26 BP.
 XX
 AC ABS52638;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Human secreted salivary protein zsig63 PCR primer ZC7764a.
 XX
 KW Human; secreted salivary protein; zsig63; immunogen; zsig63-cytokine;
 KW antibody-cytokine; in vivo killing; pathological microbe; bacteria;
 KW fungal; viral; infection; salivary gland; anti-microbial; dental caries;
 KW tooth decay; periodontal disease; thrush; gastrointestinal disease;
 KW urinary tract infection; vaginal infection; skin infection; microflora;
 KW epithelial wound; pathogenic colonisation; invasion; pro-inflammatory;
 KW chronic tissue damage; vascular system; diabetes; anti-inflammatory;
 KW incompetent immune system; AIDS; acquired immunodeficiency syndrome;
 KW chemotherapy; radiation treatment; lung infection; cystic fibrosis;
 KW digestion; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2002081701-A1.
 XX
 PD 27-JUN-2002.


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PR      17-MAY-2000; 2000US-0204769P.
XX
PA      (NICO/) NICOLAIDES N C.
PA      (SAS/) SASS P W.
PA      (GRAS/) GRASSO L.
PA      (VOGE/) VOGELSTEIN B.
PA      (KINZ/) KINZLER K W.
XX
PI      Nicolaides NC, Sass PM, Grasso L, Vogelstein B, Kinzler KW;
XX
WPI; 2002-499469/53.
XX
PT      Generating a mutation in a gene using a dominant negative allele of a
PT      mismatch repair gene which results in mismatch repair deficiency in cells
PT      containing the allele is useful in gene and drug target discovery and
PT      recombinant technology.
XX
PS      Example 5; Fig 7; 25pp; English.
XX
CC      The invention relates to methods for generating a mutation in a gene of
CC      interesting using a dominant negative allele of a mismatch repair gene (D
CC      -MMR) under control of an inducible transcriptional regulatory element
CC      (TRE). The invention is useful to provide new cell lines that can be
CC      used for gene discovery, drug target discovery, recombinant gene
CC      mutagenesis or recombinant protein production. The present sequence is a
CC      polyNP (putative phosphorylase) out-of-frame polya tract DNA
XX
SQ      Sequence 26 BP; 22 A; 1 C; 2 G; 1 T; 0 U; 0 Other;
XX
Query Match          0.3%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred.No.2e+02;
Matches   23; Conservative    0; Mismatches    2; Indels     0; Gaps     0
XX
CY      4464 TTTTTTTTTTTTTTTTGTCTT 4488
DB      25 TTTTTTTTTTTTTTTTTTGCCAT 1
XX
RESULT 100
AAD43853
ID      AAD43853 standard; DNA; 26 BP.
XX
AC      AAD43853;
DT      14-NOV-2002 (first entry)
DE      Primer #2 used to illustrate the method of the invention.
XX
KW      Single stranded polynucleotide tag; cleavage agent; gene expression;
KW      primer; ss.
XX
OS      Unidentified.
XX
PN      WO200259357-A2.
PD      01-AUG-2002.
XX
PF      24-JAN-2002; 2002WO-DK000052.
XX
PR      24-JAN-2001; 2001DK-00000126.
PR      12-FEB-2001; 2001US-0267704P.
XX
PA      (GENO-) GENOMIC EXPRESSION APS.
XX
PI      Pedersen ML;
XX
WPI; 2002-636542/68.
XX
DR      Obtaining single stranded polynucleotide tags from a biological sample,
PT      for analyzing gene expression or diagnosing clinical conditions,
PT      comprises employing nicking endonucleases that cleave complementary
PT      strands.
XX

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PS      Example; Page 294; 302pp; English.
XX
CC      The invention relates to a method for obtaining a single stranded
CC      polynucleotide tag from a biological sample by cleaving one of the
CC      complementary strands of a double stranded polynucleotide with a cleavage
CC      agent capable of recognising a double stranded polynucleotide comprising
CC      complementary strands and cleaving only one of the strands of the
CC      polynucleotide in the process of generating a single stranded
CC      polynucleotide tag. The method is useful for separating, analysing,
CC      quantifying or obtaining single stranded polynucleotides comprising tags
CC      originating partly, and preferably wholly from a source of DNA and/or RNA
CC      in a sample comprising biological cells. The method is particularly for
CC      analysing gene expression (expression profiling or differential gene
CC      expression), or in diagnosing clinical conditions. The present sequence
CC      is a primer used in the exemplification of the invention
CC
SQ      Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;
QY      Query Match          0.3%; Score 21.8; DB 1; Length 26;
      Best Local Similarity 92.0%; Pred. No. 2e+02;
      Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
      4464 TTTTTTTTTTTTTTTTTTTGCTT 4468
      Db      1 TTTTTTTTTTTTTTTTTTTT 25
RESULT 101
ABX93461
ID      ABX93461 standard; DNA; 26 BP.
XX
XX      ABX93461;
XX
XX      27-MAY-2003 (first entry)
DE      L5147-specific polynucleotide sequencing related universal primer #1.
XX
XX      L5147; cancer; lung cancer; gene therapy; cytostatic; ss; sequencing;
KM      primer; EST clone; expressed sequence tag clone.
XX
XX      Synthetic.
OS
XX      US2002186114-A1.
XX
XX      12-DEC-2002.
PD
XX
XX      05-JUN-1998; 98US-00092296.
PF
XX
XX      05-JUN-1997; 97US-0048810P.
PR
XX
XX      (BILL/) BILLINGEL P.
PA
XX      (COHE/) COHEN M.
PA
XX      (COLP/) COLPITTS T L.
PA
XX      (FRIE/) FRIEDMAN P N.
PA
XX      (KLAS/) KLAAS M R.
PA
XX      (RUSSE/) RUSSELL J C.
PA
XX      (STROU/) STROUPE S.
XX
XX      Billingsel P, Cohen M, Colpitts TL, Friedman PN, Kلاس MR,
PI      Russell JC, Stroupe S;
PI
XX      WPI; 2003-341045/32.
DR
XX
XX      New L5147 polypeptide, useful for preparing a composition for treating
PT      e.g., lung cancer.
PT
XX
XX      Example 2; Page 39; 47pp; English.
CC
CC      The invention describes a purified polypeptide or its fragment derived
CC      from the L5147 gene capable of selectively hybridising to the nucleic
CC      acid of the gene and has at least 50% identity with the polynucleotide.
CC      The L5147 polypeptide is useful for preparing a composition for treating
CC      cancer, e.g. lung cancer using gene therapy. This sequence represents a

```

```
CC universal primer used to sequence LS147 expressed sequence tag (EST) -
CC clones
CC
XX
SQ Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
Query Match 0.3%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4464 TTTTGTGCTT 4488
DB 1 TTTTGTGCTT 25
RESULT 102
ABZ24784
ID ABZ24784 standard; DNA; 26 BP.
XX
AC ABZ24784;
XX
DT 07-APR-2003 (first entry)
XX
DE Oligodeoxynucleic acid molecule ODN 24.
XX
KM Immunostimulant; oligodeoxynucleic acid; ODN; vaccine; DNA-RNA hybrid;
KM ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..26
FT /tag= a
FT /mod_base= OTHER
FT /note= "thiophosphate backbone"
XX
XX WO200295027-A2.
XX
XX 28-NOV-2002.
XX
XX 17-MAY-2002; 2002WO-EP005448.
XX
XX 21-MAY-2001; 2001AT-0000805.
XX
XX (INTE-) INTERCELL BIOMEDIZINISCHE FORSCHUNGS.
XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
XX Lingnau K, Schellack C, Schmidt W;
XX WPI; 2003-183880/18.
XX
XX New oligodeoxynucleic acid molecules useful for the preparation of
XX vaccine.
XX
XX Example 8; Page 32; 57pp; English.
XX
XX The present sequence is that of a thiosubstituted oligodeoxynucleic acid
XX (ODN) molecule, ODN 24, including deoxyuridine monophosphates. The
XX invention is based on the discovery that ODNs containing deoxyuridine
XX residues (U-ODNs) have an immunostimulatory effect comparable to, or in
XX many instances greater than, ODNs containing Cpg motifs, producing higher
XX numbers of specific T cells to a given antigen. The U-ODNs do not induce
XX the systemic production of pro-inflammatory cytokines and, in contrast to
XX Cpg ODNs, are not dependent on a specific motif or a palindromic
XX sequence. Use of a U-ODN for the preparation of a vaccine is claimed.
XX Combining the U-ODN with an antigen strongly increases the potential of
XX the antigen to raise the protection/immune response of a vaccinated
XX individual. An example of the invention demonstrated the generation of a
XX specific immune response against a melanoma-derived peptide (see
XX APP58360) by injection of mice with the peptide in combination with ODN
XX 24
XX Sequence 26 BP; 0 A; 0 C; 0 G; 1 T; 25 U; 0 Other;
```

```
Query Match 0.3%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 2e+02;
Matches 0; Conservative 23; Mismatches 2; Indels 0; Gaps 0;
QY 4464 TTTTGTGCTT 4488
DB 1 TTTTGTGCTT 25
RESULT 103
ABX93599
ID ABX93599 standard; DNA; 26 BP.
XX
AC ABX93599;
XX
DT 28-MAY-2003 (first entry)
XX
DE Human zsig63 PCR/sequencing primer ZC7764a.
XX
XX ss; PCR; zsig63; adhesion; salivary gland; dental carries;
XX periodontal disease; thrush; gastrointestinal disease; epithelial wound;
XX urinary tract infection; vaginal infection; skin infection; primer;
XX pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS;
XX lung infection; cystic fibrosis; lung dysfunction; digestive;
XX salivary gland carcinoma; Pneumocystis carinii infection; emphysema;
XX chronic bronchitis; prostate dysfunction; prostate adenocarcinoma;
XX cell culture media; gene therapy; human chromosome 4q12-4q13;
XX dentinogenesis imperfecta; dentin dysplasia type II.
XX
XX Synthetic.
XX
XX US2002173027-A1.
XX
XX 21-NOV-2002.
XX
XX 03-AUG-2001; 2001US-00922469.
XX
XX 17-MAR-1999; 99US-0124820P.
XX 17-MAR-2000; 2000US-00527345.
XX
XX (ADLE/) ADLER D A.
XX (SHEP/) SHEPPARD P O.
XX
XX Adler DA, Sheppard PO;
XX WPI; 2003-328428/31.
XX
XX Novel isolated zsig63 polypeptide, member of the adhesion family, useful
XX for treating dental carries, periodontal disease, thrush,
XX gastrointestinal disease, urinary tract infections, vaginal infections,
XX skin infections.
XX
XX Example 1; Page 29; 32pp; English.
XX
XX The invention relates to an isolated zsig63 polypeptide comprising at
XX least 90% identity to an amino acid sequence which comprises domain 1 of
XX zsig63, domain 2, domain 3, mature zsig63 and full length zsig63. Also
XX included are the polynucleotide encoding zsig63, a zsig63 expression
XX vector, a cultured cell comprising the vector and expressing the protein,
XX a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37, 38-
XX 126, 127-219 or 16-219 of zsig63 and an additional protein), using a
XX zsig63 reporter gene construct to identify zsig63 agonists, and producing
XX an anti-zsig63 antibody using zsig63 immunogenic peptides. Zsig63 is
XX useful for detecting in a test sample, the presence of antagonist of
XX zsig63 protein activity. Zsig63 has antimicrobial activity and since
XX exhibits high expression in salivary gland, can be used for treating
XX dental carries, periodontal disease, thrush, and gastrointestinal
XX disease, urinary tract infections, vaginal infections, skin infections
XX and other epithelial wounds. The polypeptides can be used to establish
XX normal microflora and protect against pathogenic colonization and
XX invasion. Zsig63 can also be used for providing pro-inflammatory activity
XX for treating chronic, tissue damage particularly in areas having limited
XX or damaged vascular system, e.g. in diabetes, and for treating
```



```

PI      Duck P, Bender R, Crosby W, Robertson JG;
XX      WPI; 1987-186567/27.
XX
XX      Synthetic nucleic acid probes - comprising two nucleic acid sequences
XX      linked by a scissile linkage.
XX
XX      Example; p29; 46pp; English.
XX
XX      The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
XX      NA2 are noncomplementary nucleic acid sequences; --S--- = a scissile
XX      linkage; n= 1 or 1,000, which is used for the detection of specific DNA
XX      or RNA sequences in a test soln. The scissile link probes may be PL
XX      (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
XX      Support). The differential liability of DNA and RNA may be exploited in a
XX      heterogeneous system when the scissile linkage is an RNA molecule. In the
XX      examples, counter probe molecules 9 through 16 were used to determine
XX      suitable hybridisation conditions. (updated on 03-OCT-2002 to add missing
XX      OS field.)
XX
XX      Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 2 U; 0 Other;
XX
XX      Query March 0.3%; Score 21.8; DB 1; Length 27;
XX      Best Local Similarity 84.0%; Pred. No. 2.1e+02;
XX      Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX      4464 TTTTTTTTTTTTTTTTTTTTGCCTT 4488
XX      1 TTTTTTTTTTTTTTTUUTTTTTTTT 25
XX
XX      RESULT 106
XX      AAN70274
XX      ID AAN70274 standard; DNA; 27 BP.
XX
XX      AAN70274;
XX
XX      03-OCT-2002 (revised)
XX      DT 26-MAY-1991 (first entry)
XX
XX      Sequence of scissile link probe MRC046 (PL).
XX
XX      Hybridisation; probe; ss.
XX
XX      Synthetic.
XX
XX      EP227976-A.
XX
XX      08-JUL-1987.
XX
XX      04-DEC-1986; 86EP-00116906.
XX
XX      05-DEC-1985; 85US-00805279.
XX
XX      (MEIO-) MEIOGENICS INC.
XX
XX      Duck P, Bender R, Crosby W, Robertson JG;
XX      WPI; 1987-186567/27.
XX
XX      Synthetic nucleic acid probes - comprising two nucleic acid sequences
XX      linked by a scissile linkage.
XX
XX      Example; p29; 46pp; English.
XX
XX      The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
XX      NA2 are noncomplementary nucleic acid sequences; --S--- = a scissile
XX      linkage; n= 1 or 1,000, which is used for the detection of specific DNA
XX      or RNA sequences in a test soln. The scissile link probes may be PL
XX      (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
XX      Support). The differential liability of DNA and RNA may be exploited in a
XX      heterogeneous system when the scissile linkage is an RNA molecule. In the
XX      examples, counter probe molecules 9 through 16 were used to determine

```

CC	suitable hybridisation conditions.	(Updated on 03-OCT-2002 to add missing OS field.)
CC	OS field.)	
XX	!	
XX	Sequence 27 BP; 0 A; 0 C; 0 G; 21 T; 6 U; 0 Other;	
SQ		
	Query Match	0.3%; Score 21.8; DB 1; Length 27;
	Best Local Similarity	68.0%; Pred.No.2.1e+02;
	Matches 17; Conservative	6; Mismatches 2; Indels 0; Gaps 0
OY	4464	TTTTTTTTTTTTTTTTTGTCTT 4488 ::: TTTTTTTTUUUUUUUUUUUUUUU 25
Dd	1	
	RESULT 107	
ID	AAN92240	
XX	AAN92240 standard; DNA; 27 BP.	
AC	AAN92240;	
XX		
DT	25-MAR-2003 (revised)	
DT	31-OCT-2002 (revised)	
DT	25-APR-1990 (first entry)	
XX		
DE	SS probe MRCO46.	
XX		
KW	Probe MRCO46; solid support; ribonuclease.	
XX		
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	misc_feature	1..10
FT		/*tag= a
FT		/note= "deoxyribonucleotides."
FT	misc_feature	11..16
FT		/*tag= b
FT		/note= "ribonucleotides."
FT	misc_feature	17..27
FT		/*tag= c
FT		/note= "deoxyribonucleotides."
PN	WO8910415-A.	
PD		
PD	02-NOV-1989.	
XX		
PE	29-APR-1988; 88US-00187814.	
XX		
PR	29-APR-1988; 88US-00187814.	
XX		
PA	(MEIO-) MEIOGENICS INC.	
XX		
Pt	Duck P, Bender R;	
DR	WI; 1989-339977/46.	
PT		
PT	Detecting target nucleic acid molecules - using excess complementary nucleic acid probes and nicking to complete a cycling sequence.	
XX		
PS	Disclosure; Page 24; 34pp; English.	
XX		
CC	Probe MRCO46 is bound by a permanent linkage to a solid support at its 3' end. It is used by reacting excess probe with a target nucleic acid; nicking hybridised probe at least once within a predetermined sequence to form 2 or more probe fragments hybridised to the target sequence, which results in the probe fragments becoming hybridised to another probe; and identifying probe fragments, so detecting the target sequence. The probe can react with target sequence to complete a cycling sequence. Using this system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg Bse H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)	
CC	(Updated on 25-MAR-2003 to correct PR field.)	
XX		
SQ	Sequence 27 BP; 0 A; 0 C; 0 G; 21 T; 6 U; 0 Other;	

[illegible]

```
CC determining if the extent of binding is less than the extent of binding  
CC between the polypeptide and the protein complex in the absence of the  
CC candidate compound. The ARCAP DNA is useful for determining if a sample  
CC contains cancerous cells which involves providing a sample from a human  
CC patient and detecting ARCAP expression in the sample. The sequences are  
CC useful for determining whether a sample contains liver tumour cells. This  
CC sequence represents a 5'RACE PCR primer used to amplify human ARCAP DNA  
XX
```

```
SQ      Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;  
  
Query Match          0.3%; Score 21.8; DB 1; Length 27;  
Best Local Similarity    92.0%; Pred.No. 2.1e+02;  
Matches   23; Conservative     0; Mismatches    2; Indels       0; Gaps        0
```

```
Gy      4464 TTTTTCCTTTTTTTTGCTT 4488  
Db              |||||  
            1 TTTTTCCTTTTTTTTGCTT 25
```

```
RESULT_114  
ABSS4324  
ID ABSS4324 standard; DNA; 27 BP.  
AC  
XX ABS54324;  
XX  
DT 10-DEC-2002 (first entry)  
DX  
XX Human ARCAP associated 5' RACE PCR primer.  
DE  
XX Human; androgen receptor complex-coupled protein; ARCAP; PCR; primer; ss.  
KW  
XX Homo sapiens.  
OS  
PN JP2002262871-A.  
PD 17-SEP-2002.  
PP 28-FEB-2001; 2001JP-00055192.  
PR 12-FEB-2001; 2001US-00781693.  
PA (VETE-) VETERANS GEN HOSPITAL.  
PI Yai-Jay C,  
DR WPI; 2002-676576/73.
```

Novel substantially pure androgen receptor (AR) complex-associated protein which binds to AR and increases ability of AR to transactivate androgen-responsive gene, useful as drug target for treating liver cancer.

Example; Page 15; 18pp; Japanese.

The present invention relates to the isolation of human androgen receptor complex-coupled protein (ARCAP), and the polynucleotide sequence encoding it. The ARCAP polypeptide complexes with an androgen receptor to increase the activity of the androgen receptor, transactivating the androgen responsive gene. The invention also describes a vector containing the ARCAP polynucleotide sequence, and a host cell containing the ARCAP polynucleotide sequence. The ARCAP polypeptide can be used as a treating agent. The present sequence represents a PCR primer used in the example of the present invention

```
SQ      Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;  
  
Query Match          0.3%; Score 21.8; DB 1; Length 27;  
Best Local Similarity    92.0%; Pred.No. 2.1e+02;  
Matches   23; Conservative     0; Mismatches    2; Indels       0; Gaps        0
```

```
Gy      4464 TTTTTCCTTTTTTTTGCTT 4488  
Db              |||||  
            1 TTTTTCCTTTTTTTTGCTT 25
```

```

RESULT 115
ID ABX79828 standard; cDNA; 27 BP.
XX
AC ABX79828;
XX
DT 17-APR-2003 (first entry)
XX
DE EST polymorphic DNA repeat polynucleotide #153.
XX
KM EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KM polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KM Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KM Haw River syndrome; Huntington's disease; fragile-X syndrome;
KM Friedrich's ataxis; myotonic dystrophy; hyperandrogenemia;
KM spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS Homo sapiens.
XX
US6472154-B1.
XX
PD 29-OCT-2002.
XX
PF 31-DEC-1999; 99US-00475947.
XX
PR 31-DEC-1999; 99US-00475947.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Garner HR, Wren JD, Minna JD, Fondon JW;
XX
PI WPI; 2003-208818/20.
XX
PT Identifying a candidate polymorphic repeat within a coding sequence, for
PT understanding or treating genetic disease, comprises detecting tandem
PT repeats in a target coding sequence and scoring the repeats for
PT polymorphic probability.
XX
PS Example; Col 717; 588bp; English.
XX
CC The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a
CC candidate polymorphic repeat. The computational methods (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxis,
CC myotonic dystrophy, hyperandrogenemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC the polymorphic repeats identified for a search of human ESTs
XX
SQ Sequence 27 BP; 1 A; 0 C; 0 G; 26 T; 0 U; 0 Other;
OY
Query Match 0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 2.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0
Db 4464 TTTTTTTTTTTTTTTTTTTTGTCTT 4488
2 TTTTTTTTTTTTTTTTTTTTATT 26

```

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AC  ACH03245;
DT  25-SEP-2003 (first entry)
DE  Immunostimulatory nucleic acid #880.
KW  Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW  antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
KW  psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW  inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
OS  Synthetic.
XX  US2003050268-A1.
PD  13-MAR-2003.
XX  29-MAR-2002; 2002US-00112653.
PF  29-MAR-2001; 2001US-0279642P.
PR  29-MAR-2001; 2001US-0279642P.
XX  (KRIE/) KRIEG A M.
PA  (BERG/) BERG D J.
XX  Krieg AM, Berg DJ;
PI  WPI; 2003-521815/49.
DR  Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
XX  allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT  disease by administering an immunostimulatory nucleic acid.
XX  Disclosure; Page 32; 229pp; English.
PS  The invention describes a method of treating non-allergic inflammatory
XX  disease comprising administering to a subject having or at risk of
CC  developing a non-allergic inflammatory disease an immunostimulatory
CC  nucleic acid for prevention or treatment of the disease. The method is
CC  useful for treating non-allergic inflammatory diseases, such as
CC  psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC  inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC  This sequence represents an immunostimulatory nucleic acid
SQ  Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;
QY  Query Match 0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 2.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DB  4464 TTTTTTTTTTTTTTTTTTGCTT 4488
1 TTTTTTTTTTTTTTTTTTTTTTTT 25
RESULT 117
ADBS37208
ID  ADB37208 standard; DNA; 27 BP.
XX  ADB37208;
AC  04-DEC-2003 (first entry)
DT  Immunostimulatory nucleic acid #822.
DE  ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW  hypo-responsive subject; immunostimulatory.
XX  Synthetic.
OS  US2003087848-A1.
PN  08-MAY-2003.
XX  08-MAY-2003.
PD  08-MAY-2003.

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PE 02-FEB-2001; 2001US-00776479.
XX
XX 03-FEB-2000; 2000US-0179991P.
XX
XX (BRAT/) BRATZLER R L.
XX PA (PETE/) PETERSEN D M.
XX PA (FOUR/) FOURON Y.
XX
XX Bratzler RL, Petersen DM, Fouron Y,
XX
XX WPI; 2003-657977/62.
XX
XX Treating and/or preventing allergy or asthma using an immunostimulatory
XX PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
XX
XX Disclosure; Page 17; 221pp; English.
XX
XX The invention relates to a method of treating or preventing allergy or
XX CC asthma which comprises administering to a subject a poly-G nucleic acid
XX CC in an aerosol formulation. The methods and compositions of the present
XX CC invention are useful for diagnosing and/or treating asthma and allergy
XX CC especially in a hypo-responsive subject. The present sequence represents
XX CC an immunostimulatory nucleic acid of the invention.
XX
XX
XX Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.3%; Score 21.8; DB 1; Length 27;
XX Best Local Similarity 92.0%; Pred. No. 2.1e+02;
XX Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
XX 4464 TTTTTTTTTTTTTTTTTTGTCTT 4488
XX 1 TTTTTTTTTTTTTTTTTTTTTT 25
XX
XX
XX RESULT 118
XX AAAS7855/C
XX ID AAAS7855 standard; DNA; 28 BP.
XX
XX AAAS7855;
XX
XX 11-OCT-2000 (first entry)
XX
XX Deoxy-A22-tagged substrate oligonucleotide.
XX DE
XX Ribozyme; catalytic RNA; analyte detection; effector molecule;
XX KW nucleic acid substrate; in vitro selection; ribozyme ligase;
XX KW conformation dependent activity; allosteric activation; ss.
XX
XX Synthetic.
XX OS
XX
XX Key Location/Qualifiers
XX FH 23..28
XX FT misc_RNA /*tag= a
XX FT 24..28
XX FT misc_binding /*tag= b
XX FT /bound_molecy= "Bases 13-17 of N90 RNA pool (AAAS7851)"
XX
XX MO200024931-A2.
XX
XX 04-MAY-2000.
XX
XX 22-OCT-1999; 99WO-IL000557.
XX PF
XX 23-OCT-1998; 98IL-00126731.
XX PR
XX (INTE-) INTELLIGENE LTD.
XX PA
XX Nathan A, Ellington A;
XX PI
XX WPI; 2000-350763/30.
XX
XX Detecting an analyte in a sample comprises providing nucleic acid
XX PT

```

PT	sequence which is catalytically active in presence of analyte, contacting
FT	catalytic nucleic acid with substrate and amplifying catalytic product.
XX	
XX	
PS	Disclosure; Page; 36pp; English.
XX	
CC	The invention relates to a method of detecting an analyte in a sample.
CC	The method comprises providing a nucleic acid sequence which is initially
CC	catalytically inactive, but which becomes catalytically active in the
CC	presence of an analyte (the effector); providing a nucleic acid substrate
CC	for the catalytic activity of the nucleic acid sequence; and contacting
CC	the nucleic acid sequence and the substrate with the sample under
CC	conditions allowing catalytic activity of nucleic acid sequences. The
CC	catalytic nucleic acid sequence will be able to convert the nucleic acid
CC	substrate into a nucleic acid product only if the analyte of interest is
CC	present. The nucleic acid catalytic product is then amplified, and a
CC	significant increase in the amount of product indicates the presence of
CC	the analyte in the sample. The method is useful for the qualitative or
CC	quantitative determination of an analyte in a sample in diagnostic
CC	assays. The invention describes the in vitro selection of a ribozyme
CC	ligase (L1, AAAS7859, AAAS7860) which is catalytically active only in the
CC	presence of an oligonucleotide effector (AAAS7854). The L1 ribozyme
CC	ligase was selected from a pool of RNA molecules comprising a central
CC	randomised region 90 nucleotides in length flanked on both sides by
CC	constant sequence regions (the N90 RNA pool, AAAS7851). In the presence
CC	of the effector, selection was performed using one of the tagged
CC	substrate molecules AAAS7855-A57857. RNAs with ligase activity (i.e.,
CC	those which have become ligated to the substrate molecule) were reverse
CC	transcribed using the effector oligo, and then PCR amplified using the
CC	effector and a DNA primer identical in sequence to the substrate used for
CC	the selection. A ribozyme ligase, L1, was selected via this procedure. L1
CC	can only adopt its active conformation (AAAS7859) in the presence of the
CC	effector oligo (analyte). In the absence of the effector, L1 adopts an
CC	inactive conformation (AAAS7860). The present sequence represents the
CC	deoxy-A22-tagged substrate oligonucleotide. The da22 tag enables
CC	successfully ligated products to be isolated using oligo(dT)12-18
CC	cellulose. Note: The present sequence is not given in the specification,
CC	but is created from the information given on page 11
XX	
SQ	Sequence 28 BP; 23 A; 2 C; 1 G; 0 T; 2 U; 0 Other;
OY	Query Match 0.3%; Score 21.8; DB 1; Length 28; Best Local Similarity 92.0%; Pred. No. 2.2e+02; Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0
DG	4459 TGCACCTTTTTTTTTTTTTTTT 4483 26 TGCAATTTTTTTTTTTTTTTT 2
ID	RESULT 119 AAL43065/C
XX	AAL43065 standard; RNA; 28 BP.
NC	AAL43065;
DT	25-SEP-2002 (first entry)
XX	
DE	Regulatable, catalytically active nucleic acid substrate #1.
XX	
KW	Regulatable catalytically active nucleic acid; RCANA; ribozyme;
KM	gene therapy; ss.
XX	
OS	Synthetic.
FH	Key Location/Qualifiers
FT	modified_base 1
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "5; biotinylated"
XX	
PV	WO200196559-A2.
XX	
PD	20-DEC-2001.

XX 14-JUN-2001; 2001MO-US019302.
PF 15-JUN-2000; 2000US-0212097P.
PR (TEXA) UNIV TEXAS SYSTEM.
XX
XX Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L,
PI Davidson E, Cox JC, Reidel T,
DR WPI; 2002-122216/16.
XX
XX New regulatable, catalytically active nucleic acids (RCANA), useful in
PT gene therapy (particularly for regulating gene expression), or in assays
PT for detecting the presence of ligands or activation of an effector of
PT RCANA.
XX
XX Example 6; Page 75; 126pp; English.
XX
XX The present invention relates to regulatable, catalytically active
CC nucleic acids (RCANAs) which are regulated by polypeptides. These are
CC useful for regulating gene expression, in assays for detecting the
CC presence of ligands, for activation of an effector of RCANA, and in gene
CC therapy. The present sequence is an oligonucleotide substrate used in the
CC construction of an RCANA
XX
SQ Sequence 28 BP; 23 A; 2 C; 1 G; 0 T; 2 U; 0 Other;
XX
XX
XX Query Match 0.3%; Score 21.8; DB 1; Length 28;
Best Local Similarity 92.0%; Pred. No. 2.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
DB 26 TGCATTTTTTTTTTTTTTTTTTTT 2
XX
XX
XX RESULT 120
AD39569/C
ID ADA39569 standard; RNA; 28 BP.
XX
XX ADA39569;
AC
XX
DT 20-NOV-2003 (first entry)
XX
XX Substrate RNA related oligonucleotide SEQ ID NO:25.
XX
XX regulatable catalytically active nucleic acid; RCANA; catalytic domain;
KM regulation; screening; gene therapy; biological pathway regulation;
KM regulatory element; metabolic pathway; ribozyme; ss.
XX
XX Synthetic.
XX
XX PN MO2003027310-A2.
XX
XX PD 03-APR-2003.
XX
XX PF 24-SEP-2002; 2002MO-US030458.
XX
XX PR 24-SEP-2001; 2001US-0324715P.
XX
XX (ARCH-) ARCHEMITX CORP.
XX
XX Wilson C, Cload ST, Keefe AD;
XX
XX WPI; 2003-354657/33.
XX
XX
XX Regulating production of a product in a cell, comprises inserting a
PT regulatable catalytically active nucleic acid into a gene that produces
PT the product or regulates the production of the product in the cell.
XX
XX Example 6; Page 76; 128pp; English.

CC The present invention describes a method for regulating production of a
CC product in a cell. The method comprises inserting a regulatable
CC catalytically active nucleic acid (RCANA) into a gene that produces the
CC product or regulates the production of the product in the cell, where the
CC RCANA comprises a catalytic domain which modifies a transcript to alter
CC its coding potential and a regulatory domain that recognises an effector
CC that alters the function of the catalytic domain, and contacting the
CC regulatory domain with an effector to regulate production of the product.
CC Also described: (1) regulating a biological pathway in cell; and (2)
CC screening a population of cells for a cell that produces a bioproduct.
CC The methods are useful for regulating a biological pathway in cell, or
CC regulating production of a product in a cell. The RCANAs are useful as
CC regulatory elements to control the expression of genes in a metabolic
CC pathway, or as regulated selectable markers to increase a selective
CC pressure favouring or disfavouring production of a targeted bioproduct.
CC The RCANAs are also useful for in vitro or in vivo sensing or detection,
CC and in gene therapy. The present sequence represents an RNA substrate
CC oligonucleotide, which is used in an example from the present invention.
XX
SQ Sequence 28 BP; 23 A; 2 C; 1 G; 0 T; 2 U; 0 Other;
XX
XX
XX Query Match 0.3%; Score 21.8; DB 1; Length 28;
Best Local Similarity 92.0%; Pred. No. 2.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
DB 26 TGCATTTTTTTTTTTTTTTTTTTT 2
XX
XX
XX RESULT 121
AA005003
ID AA005003 standard; DNA; 29 BP.
XX
XX AA005003;
AC
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-1990 (first entry)
XX
XX Sequence binding to and inhibiting the GSTpi gene.
XX
XX C-myc; cancer; HIV-1; AIDS; collagenase; Alzheimer's disease; EGF;
KM epidermal growth factor; GSTpi; HMGCoA; thalassaemia;
KM Herpes simplex virus; nerve growth factor receptor; globin; ss.
XX
XX Synthetic.
XX
XX PN BP375408-A.
XX
XX PD 27-JUN-1990.
XX
XX PF 20-DEC-1989; 89EP-00313391.
XX
XX PR 20-DEC-1988; 88US-00287359.
XX
XX (BAYU) BAYTOR COLLEGE MEDICINE.
XX
XX (HOGA/) HOGAN M E.
XX
XX Hogan ME, Kessler DJ;
XX
XX WPI; 1990-195509/26.
XX
XX
XX Synthetic oligo-nucleotide(s) which bind target duplex DNA - forming co-
PT linear triplex to control transcription process in gene-specific fashion.
XX
XX Claim 39; Page 30; 40pp; English.
XX
XX Sequence forms triplex with the double stranded target sequence with G
CC binding to G-C and T to A-T. The strand runs 3' to 5' in an antiparallel
CC orientation and when targeted to a specific sequence will deactivate it.
CC This allows for growth inhibition in cancerous cells; manipulation of
CC cellular structural protein content; inhibition of IL-2 chain receptor;
CC disbursting plaque formation in Alzheimer's disease; inhibiting BGF gene;

CC	Mycobacterium complex nucleic acid sequence. The detection method uses
CC	visual detection of a change in the hybridization without aid of
CC	instrumentation. Multiple copies of a target nucleic acid sequence are
CC	mixed with first and second detectable probes under hybridizing
CC	conditions favouring particle agglutination via a bridging molecule
CC	allowing for visual detection of the target nucleic acid sequence. The
CC	bridging molecule enhances or inhibits formation of a hybridization
CC	complex
XX	
SQ	Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;
	Query Match 0.3%; Score 21.8; DB 1; Length 30;
	Best Local Similarity 92.0%; Pred. No. 2.4e+02;
	Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0
Oy	4464 TTTTTTTTTTTTTTTTGCTT 4468
Db	1 TTTTTTTTTTTTTTTTTTTTTT 25
RESULT 127	
AAF99889/C	
ID	AAF99889 standard; DNA; 30 BP.
XX	
AC	AAF99889;
XX	
DT	12-JUN-2001 (first entry)
XX	
DE	Immunostimulatory nucleic acid #1005.
XX	
KW	Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KM	immunostimulatory; tumour; viral infection; bacterial infection;
KW	fungal infection; parasitic infection; cancer; asthma;
OS	infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX	
SY	Synthetic.
XX	
PN	WO200122972-A2.
PD	
XX	05-APR-2001..
PF	25-SEP-2000; 200OWO-US026383.
XX	
FR	25-SEP-1999; 99US-0156113P.
PR	27-SEP-1999; 99US-0156135P.
XX	
PA	23-AUG-2000; 200OUS-0227436P.
XX	
PA	(IOWA) UNIV IOWA RES FOUND.
XX	(COLE-) COLEY PHARM GMBH.
PI	
XX	Krieg AM, Schetter C, Vollmer J;
DR	WPI, 2001-273485/28.
PT	
XX	Vaccinating against tumors, infectious diseases, allergies and asthma
PS	using immunostimulatory Py-rich and TG nucleic acids.
XX	
XX	Example 6; Page 60; 338pp; English.
CC	The present invention relates to a method for stimulating an immune
CC	response. The method comprises administering an immunostimulatory nucleic
CC	acid to a non-rodent subject in sufficient quantity to stimulate an
CC	immune response. The present sequence is one such immunostimulatory
CC	nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC	(py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC	against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC	and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC	haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC	staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC	also useful for preventing cancer, asthma, infectious disease, allergy or
CC	immune deficiency. The present sequence can also be used to redirect a
CC	T _H 2 to a Th1 immune response and to activate immune cells. Note: The
CC	present sequence may have a phosphorothioate backbone

XX	Sequence	30 BP	30 A	0 C	0 G	0 T	0 U	0 Other
XX	Query Match		0.3%	Score 21.8	DB 1	Length 30		
XX	Best Local Similarity		92.0%	Pred. No. 2.4e+02				
XX	Matches	23	Conservative	0	Mismatches	2	Indels	0
QY	4464	TTTTTTTTTTTTTTTTTTTTTGTCTT	4488					
DB	30	TTTTTTTTTTTTTTTTTTTTTTT	6					
XX	RESULT 128							
XX	AAFG9888							
XX	ID	AAFG9888	standard; DNA;	30 BP.				
XX	AC	AAFG9888;						
XX	DT	12-JUN-2001	(first entry)					
XX	DE	Immunostimulatory nucleic acid #1004.						
XX	DE	Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;						
XX	KW	immunostimulatory; tumour; viral infection; bacterial infection;						
XX	KW	fungal infection; parasitic infection; cancer; asthma;						
XX	KX	infectious disease; allergy; immune deficiency; phosphorothioate; ss.						
XX	OS	Synthetic.						
XX	PN	MO200122972-A2.						
XX	PD	05-APR-2001.						
XX	PF	25-SEP-2000; 2000WO-US026383.						
XX	PR	25-SEP-1999; 99US-0156113P.						
XX	PR	27-SEP-1999; 99US-0156135P.						
XX	PR	23-AUG-2000; 2000US-0227436P.						
XX	PA	(IOWA) UNIV IOWA RES FOUND.						
XX	PA	(COLE) COLEY PHARM GMBH.						
XX	PI	Krieg AM, Schetter C, Vollmer J;						
XX	DR	WPI; 2001-273485/28.						
XX	PT	Vaccinating against tumors, infectious diseases, allergies and asthma						
XX	PT	using immunostimulatory Py-rich and TG nucleic acids.						
XX	PS	Example 6; Page 60; 338pp; English.						
XX	CC	The present invention relates to a method for stimulating an immune						
XX	CC	response. The method comprises administering an immunostimulatory nucleic						
XX	CC	acid to a non-rodent subject in sufficient quantity to stimulate an						
XX	CC	immune response. The present sequence is one such immunostimulatory						
XX	CC	nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich						
XX	CC	(py-rich) or thymidine (T) rich. The method is used to vaccinate subjects						
XX	CC	against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae						
XX	CC	and/or orthonyoviridae), bacterial antigens (e.g. toxoplasma,						
XX	CC	haemophilus, campylobacter, clostridium, Escherichia coli and/or						
XX	CC	staphylococcus), fungal antigens and/or parasitic antigens. The method is						
XX	CC	also useful for preventing cancer, asthma, infectious disease, allergy or						
XX	CC	immune deficiency. The present sequence can also be used to redirect a						
XX	CC	Th2 to a Th1 immune response and to activate immune cells. Note: the						
XX	CC	present sequence may have a phosphorothioate backbone						
XX	SQ	Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;						
XX	Query Match		0.3%	Score 21.8	DB 1	Length 30		
XX	Best Local Similarity		92.0%	Pred. No. 2.4e+02				
XX	Matches	23	Conservative	0	Mismatches	2	Indels	0
QY	4464	TTTTTTTTTTTTTTTTTTGTCTT	4488					

Db 1 ||||| 25
 TTTT

RESULT 129
 ABRK10416/c
 ID ABRK10416 standard; DNA; 30 BP.
 XX
 AC ABRK10416;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Synthetic primer sequence 5'-A30-3'.
 XX
 KW ss; 5'-A30-3'; double stranded DNA generation; promiscuous base;
 KM target molecule; primer.
 XX
 OS Synthetic.
 XX
 PN US6326143-B1.
 XX
 PD 04-DEC-2001.
 XX
 PF 22-MAY-1998; 98US-00083123.
 XX
 PR 22-NOV-1996; 96MO-EP005149.
 XX
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 XX
 PI Orum H, Seeger C;
 XX
 DR WPI; 2002-214947/27.
 XX
 PT Determining an analyte in a sample, for generating multiple double
 PT stranded nucleic acids, comprises employing a single primer sequence with
 PT a nucleobase sequence having affinity to the sequence contained in a
 PT target nucleic acid.
 XX
 PS Example 1; Col 14; 25pp; English.
 XX
 CC The invention relates to determining an analyte in a sample comprising
 CC (a) providing a target nucleic acid comprising a region A, a nucleobase
 CC sequence B, and a sequence I linked to the 5' terminus of the nucleobase
 CC sequence B, where the nucleobase sequence B is not specific for the
 CC analyte, and the region A specifically binds to the analyte, (b) binding
 CC the target nucleic acid to the analyte, separating the analyte bound to
 CC the target nucleic acid from the remaining part of the sample, (d)
 CC hybridizing a primer to the target nucleic acid, where the primer
 CC comprises a nucleobase sequence B', and the nucleobase sequence B'
 CC hybridizes to the nucleobase sequence B, (e) elongating the hybridised
 CC primer to produce an elongation product E using the target nucleic acid
 CC as a template and using nucleotides, where at least 30 % of the
 CC nucleotides contain at least one promiscuous base which is capable of
 CC base pairing with each of adenine, guanine, cytosine, and thymine, (f)
 CC separating the target nucleic acid from the elongation product E, (g)
 CC hybridizing a further primer which comprises the nucleobase sequence B'
 CC to the elongation product E, where the elongation product E is capable of
 CC acting as a template for the elongation of the further primer, (h)
 CC elongating the hybridised further primer of step (g) to produce an
 CC elongation product B', using the elongation product E as a template and
 CC using nucleotides, where at least 30 % of the nucleotides contain at
 CC least one promiscuous base, (i) separating the elongation product E from
 CC the elongation product B', (j) hybridizing a further primer comprising a
 CC nucleobase sequence B' to the target nucleic acid or the elongation
 CC product B, (k) elongating the further primer of step (j) to produce
 CC another elongation product B using the target nucleic acid or elongation
 CC product B as a template and using nucleotides, where at least 30 % of the
 CC nucleotides contain at least one promiscuous base, (l) separating product
 CC B of step (k) from the target nucleic acid or elongation product B', (m)
 CC optionally repeating steps (g) - (l) a sufficient number of times to
 CC generate a desired amount of double stranded nucleic acids and (n)
 CC determining the elongation product B and/or elongation product B' as a
 CC measure of the presence or amount of the analyte, where the lengths of

CC the sequence I and the nucleobase sequence B are chosen such that, when
 CC the further primer hybridizes to the elongation product B in step (g),
 CC the further primer spans a sequence formed by elongation of the
 CC hybridised primer of step (e) and overlaps at least a part of the 3'
 CC region of the hybridized primer of step (e) by an overlap length. The
 CC method is useful for determining an analyte in a sample. In particular, the
 CC method is useful for generating multiple double stranded nucleic acids.
 CC The present sequence is a primer molecule used to exemplify the method of
 CC the invention
 XX
 SQ Sequence 30 BP; 30 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 XX
 QY 4464 TTTTGTCTT 4488
 Db 30 TTTT 6

Query Match 0.3%; Score 21.8; DB 1; Length 30;
 Best Local Similarity 92.0%; Pred. No. 2.4e+02;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 130
 ABRK10412
 ID ABRK10412 standard; DNA; 30 BP.
 XX
 AC ABRK10412;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Synthetic primer sequence 5'-T30-3'.
 XX
 KW ss; 5'-T30-3'; double stranded DNA generation; promiscuous base;
 KM target molecule; primer.
 XX
 OS Synthetic.
 XX
 PN US6326143-B1.
 XX
 PD 04-DEC-2001.
 XX
 PF 22-MAY-1998; 98US-00083123.
 XX
 PR 22-NOV-1996; 96MO-EP005149.
 XX
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 XX
 PI Orum H, Seeger C;
 XX
 DR WPI; 2002-214947/27.
 XX
 PT Determining an analyte in a sample, for generating multiple double
 PT stranded nucleic acids, comprises employing a single primer sequence with
 PT a nucleobase sequence having affinity to the sequence contained in a
 PT target nucleic acid.
 XX
 PS Example 1; Col 14; 25pp; English.
 XX
 CC The invention relates to determining an analyte in a sample comprising
 CC (a) providing a target nucleic acid comprising a region A, a nucleobase
 CC sequence B, and a sequence I linked to the 5' terminus of the nucleobase
 CC sequence B, where the nucleobase sequence B is not specific for the
 CC analyte, and the region A specifically binds to the analyte, (b) binding
 CC the target nucleic acid to the analyte, separating the analyte bound to
 CC the target nucleic acid from the remaining part of the sample, (d)
 CC hybridizing a primer to the target nucleic acid, where the primer
 CC comprises a nucleobase sequence B', and the nucleobase sequence B'
 CC hybridizes to the nucleobase sequence B, (e) elongating the hybridised
 CC primer to produce an elongation product B using the target nucleic acid
 CC as a template and using nucleotides, where at least 30 % of the
 CC nucleotides contain at least one promiscuous base which is capable of
 CC base pairing with each of adenine, guanine, cytosine, and thymine, (f)
 CC separating the target nucleic acid from the elongation product B, (g)
 CC hybridizing a further primer which comprises the nucleobase sequence B'


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RESULT 135
AD33445
ID ADC33445 standard; DNA; 32 BP.
XX
XX
AC ADC33445;
XX
XX
DT 18-DEC-2003 (first entry)
XX
DE Template oligonucleotide #SEQ ID 2.
XX
XX
KW Binding; tandem repeat; label; analyte detection; ss.
XX
XX
OS Synthetic.
XX
XX
PN WO2003072721-A2.
XX
XX
PD 04-SEP-2003.
XX
XX
PF 20-FEB-2003; 2003WO-US005301.
XX
XX
PR 21-FEB-2002; 2002US-0359223P.
XX
XX
PR 08-MAY-2002; 2002US-0379360P.
XX
XX
PA (DISC-) DISCOVERX INC.
XX
XX
PI Wu M, Ullman E;
XX
XX
DR WPI; 2003-712717/67.
XX
XX
PT Detecting a label comprising employing (as the label) a reagent having a
PT 3' extendable terminus hybridized to a tandem repeat template in
PT combination with a DNA polymerase and dNTPs necessary for repetitively
PT replicating the tandem repeat.
XX
XX
PS Example; SEQ ID NO 2; 38pp; English.
XX
XX
CC The invention relates to a method for detecting a label, comprising
CC employing (as the label) a reagent having a 3' extendable terminus
CC hybridized to a tandem repeat template in combination with a DNA
CC polymerase and dNTPs necessary for repetitively replicating the tandem
CC repeat. The method involves detecting a binding event between first and
CC second binding members, employing a label to determine the occurrence of
CC the binding event. The tandem repeating units are polyT. The method of
CC the invention is useful in detecting an analyte using repetitive
CC extension along a tandem repeat. The extended nucleic acid may be used
CC for detecting a moiety, particularly involved in a binding event
CC employing a reagent. The current sequence represents a template member
CC oligonucleotide containing a polyT tandem repeat that binds to the
CC extendable oligonucleotide given in ADC33444.
XX
XX
SQ Sequence 32 BP; 0 A; 0 C; 0 G; 32 T; 0 U; 0 Other;
XX
XX
Query Match 0.3%; Score 21.8; DB 1; Length 33;
Best Local Similarity 92.0%; Pred. No. 2.6e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

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XX
XX
OS Small round structured virus.
XX
XX
PN WO200079280-A1.
XX
XX
PD 28-DEC-2000.
XX
XX
PF 22-JUN-2000; 2000WO-JP004095.
XX
XX
PR 22-JUN-1999; 99JP-00175928.
XX
XX
PA (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
XX
XX
PA (DENK-) DENKA SEIKEN KK.
XX
XX
PI Takeda N, Natori K, Miyamura T, Kamata K, Sato T, Sato S;
XX
XX
DR WPI; 2001-080848/09.
XX
XX
PT Kit for the detection and typing of small round-structured virus (SRSV)
PT strains for investigation of food poisoning outbreaks, contains
PT antibodies.
XX
XX
PS Example 1; Page 75; 84pp; Japanese.
XX
XX
CC This invention relates to a kit for the detection and typing of small
CC round structured virus (SRSV) strains. The kit contains antibodies
CC directed against peptides represented in sequences AAB49700 - AAB49710,
CC which are each SRSV strain specific. Polynucleotide sequences AAF20141 -
CC AAF20151 represent cDNA encoding the strain specific proteins. The kit is
CC used for detecting and typing strains of SRSV in order to prevent the
CC spread of infection and to examine the epidemiology of outbreaks. PCR
CC primers AAF29152 - AAF29163 are used to amplify SRSV strain specific cDNA
CC sequences
XX
XX
SQ Sequence 33 BP; 0 A; 0 C; 0 G; 33 T; 0 U; 0 Other;
XX
XX
Query Match 0.3%; Score 21.8; DB 1; Length 33;
Best Local Similarity 92.0%; Pred. No. 2.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

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RESULT 136
AAF29153
ID AAF29153 standard; DNA; 33 BP.
XX
XX
AC AAF29153;
XX
XX
DT 04-APR-2001 (first entry)
XX
XX
DE PCR primer SEQ ID 24 used to amplify SRSV specific cDNA.
XX
XX
KW Small round structured virus; SRSV; food poisoning; PCR primer; ss.

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RESULT 137
AAK77343
ID AAK77343 standard; DNA; 30 BP.
XX
XX
AC AAK77343;
XX
XX
XX
XX
DT 09-AUG-1999 (first entry)
XX
XX
DE Sindbis virus mRNA amplifying RT-PCR 3' primer.
XX
XX
KW Nucleic acid identification; exogenous protein; gene sorting;
KW growth factor; membrane receptor; sindbis virus; RT-PCR; primer; ss.
XX
XX
OS Synthetic.
XX
XX
PN WO9925876-A1.
XX
XX
PD 27-MAY-1999.
XX
XX
PF 17-NOV-1998; 98WO-US024520.
XX
XX
PR 17-NOV-1997; 97US-00972218.
XX
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
XX
XX
PI Bailey JE, Renner WA, Orberger GH, Koller D;

```

DR WPI; 1999-357620/30.
XX Isolating genes encoding proteins with selected properties, useful for
PT identifying therapeutic agents or targets.
XX
PS Disclosure; Page 66; 136pp; English.
XX
CC The invention relates to the identification of a recombinant nucleic acid
CC encoding an exogenous protein having a selected property. The method
CC comprises preparing a population of eukaryotic host cells, culturing the
CC cells under suitable conditions and identifying cells that contain the
CC recombinant nucleic acid. The method is used to sort genes according to
CC the type of proteins they express, and also to identify new ligand/
CC receptor interactions. Typical applications of the nucleic acid and the
CC exogenous protein are in isolation of new growth factors, cytokines,
CC membrane receptors, cytoplasmic, organelle or nuclear proteins, all of
CC which may be useful as therapeutic agents or therapeutic targets, e.g.
CC apoptosis-promoting or tumour suppressing proteins, regulators of cell
CC proliferation or metabolic processes etc. The protein can also be used to
CC screen for specific modulators. The nucleic acid can also be used as
CC sources of therapeutic antisense or ribozyme sequences. The method allows
CC the protein (rather than a partial DNA sequence) to be isolated and,
CC since a wide range of cells can be used, they can be expressed with the
CC correct glycosylation pattern
XX
SQ Sequence 30 BP; 0 A; 5 C; 5 G; 20 T; 0 U; 0 Other;

Query Match 0.3%; Score 21.6; DB 1; Length 30;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4456 GCATGACCTTTTCTTTTCTTTTCTTTT 4483
DB 3 GCGGCGCCCTTTTCTTTTCTTTTCTTTT 30

RESULT 138
AAA90394
ID AAA90394 standard; DNA; 30 BP.
XX
AC AAA90394;
XX
DT 10-JAN-2001 (first entry)
XX
DE Sindbis virus 3' RT-PCR primer.
XX
XX Nucleic acid identification; exogenous protein; drug screening;
KM recombinant expression; psireps vector; mammalian expression system;
KM reverse transcription-PCR; RT-PCR primer; ss.
XX
XX Sindbis virus.
OS Synthetic.
OS
PN JP2000189173-A.
XX
PD 11-JUL-2000.
XX
PF 23-AUG-1999; 99JP-00236220.
XX
PR 17-NOV-1998; 98US-00193707.
PR 17-NOV-1998; 98MO-US024520.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
PA
PA WPI; 2000-551637/51.
XX
DR
XX
PT Identifying a recombinant nucleic acid to identify and isolate various
PT cellular proteins, comprises culturing a composition comprising
PT eukaryotic host cells and identifying a cell comprising recombinant
PT nucleic acid.
XX
PS Example; Page 35; 56pp; Japanese.
XX

CC The invention relates to the identification of a recombinant nucleic acid
CC encoding an exogenous protein having a selected property. The method
CC comprises preparing populations of eukaryotic host cells, where each cell
CC comprises an expression vector encoding a different exogenous protein.
CC The host cells are cultured under suitable conditions and the nucleic
CC acid which encodes the exogenous protein is identified. The method is
CC useful for the identification and isolation of proteins with a selected
CC property. Typical applications of the nucleic acid and the exogenous
CC protein are in isolation of new growth factors, cytokines, membrane
CC receptors, cytoplasmic, organelle or nuclear proteins, all of which may
CC be useful as therapeutic agents or therapeutic targets, e.g., pro-
CC apoptotic or tumour suppressing proteins, regulators of cell
CC proliferation or of metabolic processes. The protein can also be used to
CC screen for ligands and specific modulators of activity. The method of the
CC invention allows the direct cloning of full length cDNAs in one step. It
CC facilitates direct expression of the protein without the need to perform
CC further procedures such as subcloning and establishment of a cell line
CC for protein production. The method allows a protein of interest (rather
CC than a partial DNA sequence) to be isolated and, since a wide range of
CC cell types can be used, they can be expressed in a correctly folded and
CC glycosylated form. Sequences AAA90394-A90395 represent Sindbis virus
CC reverse transcription-PCR (RT-PCR) primers used in the exemplifications
CC of the invention. This patent is related to WO9925876
XX
SQ Sequence 30 BP; 0 A; 5 C; 5 G; 20 T; 0 U; 0 Other;

Query Match 0.3%; Score 21.6; DB 1; Length 30;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4456 GCATGACCTTTTCTTTTCTTTTCTTTT 4483
DB 3 GCGGCGCCCTTTTCTTTTCTTTTCTTTT 30

RESULT 139
AAF26221/C
ID AAF26221 standard; DNA; 30 BP.
XX
AC AAF26221;
XX
DT 26-APR-2001 (first entry)
XX
DE APC binding protein associated primer ON-AT+ SEQ ID 6.
XX
XX APC binding protein; cell proliferation; adenomatous polyposis coli;
KM tumor cell detection; primer; ss.
XX
XX Unidentified.
OS
XX DE19933237-A1.
PN
PD 18-JAN-2001.
XX
PF 15-JUL-1999; 99DE-0103237.
XX
PR 15-JUL-1999; 99DE-0103237.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PI Mueller O;
XX
DR WPI; 2001-148321/16.
XX
XX
PT Determining proliferative capacity of cells, useful e.g. for detecting
PT tumor cells, by measuring concentration and subcellular localization of
PT adenomatous polyposis coli protein.
XX
XX Claim 10; Page 12; 26pp; German.
XX
XX This invention describes a novel method for determining the proliferative
CC activity of cells, comprising detecting, in a sample, the concentration
CC and/or subcellular localization of APC (adenomatous polyposis coli)

CC protein (1). The invention also describes (1) determining function of (1)
 CC in a sample by detecting presence of the C-terminal, DNA-binding domain
 CC of (1); (2) detecting mutations in (1)-encoding nucleic acid by detecting
 CC the DNA-binding domain of (1); (3) purifying, enriching and/or detecting
 CC (1) or its fragments by reaction with a probe; (4) double-stranded DNA
 CC (11) that contains the sequence GGCCGA_{2-3G} (S1) and/or GATCCT_{2-3GC}
 CC (S2); (5) peptide fragment of (1) containing at least the DNA-binding
 CC domain; (6) antibodies (Ab) directed against an epitope of positions 1340
 CC -1901, 2219-2580 or 2581-2843 of (1); (7) set of two or more antibodies,
 CC one of which is Ab and the other directed against the N-terminal region
 CC (1-1299) of (1); and (8) kit for detecting DNA-binding capacity of (1) or
 CC its fragments in a sample consisting of (11), Ab or the set of (7). The
 CC method is used to detect proliferative, especially tumor (precursor),
 CC cells, to detect function of (1) and mutations in (1), and to purify
 CC and/or enrich (1), or its fragments, from a sample. The method allows
 CC simple, rapid and reliable detection of proliferation, without the need
 CC for polymerase chain reaction or sequencing

SQ Sequence 30 BP; 23 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 21.6; DB 1; Length 30;
 Best Local Similarity 85.7%; Pred. No. 2.6e+02;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4466 TTTTCTTTTCTTCTGCTGAGAC 4493
 Db 29 TTTTCTTTTCTTCTTCTTCTGCGC 2

RESULT 140
 ABX79809
 ID ABX79809 standard; cDNA; 24 BP.

AC ABX79809;
 XX 17-APR-2003 (first entry)

DE EST polymorphic DNA repeat polynucleotide #134.

XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 KM polymorphic marker prediction of ubiquitous simple sequences; POWPOUS;
 KM Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 KM Haw River syndrome; Huntington's disease; fragile-X syndrome;
 KM Friedreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
 KM spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

XX Homo sapiens.

OS Homo sapiens.

PN US6472154-B1.

XX 29-OCT-2002.

PD 31-DEC-1999; 99US-00475947.

XX 31-DEC-1999; 99US-00475947.

PR (TEXA) UNIV TEXAS SYSTEM.

XX Garner HR, Wren JD, Minna JD, Fondon JW;

PI WPI; 2003-208818/20.

XX Identifying a candidate polymorphic repeat within a coding sequence, for

PT understanding or treating genetic disease, comprises detecting tandem

PT repeats in a target coding sequence and scoring the repeats for

PT polymorphic probability.

XX Example; Col 579; 589pp; English.

XX The invention discloses a method for identifying a candidate polymorphic

CC repeat within a coding sequence (expressed sequence tag, EST), which

CC comprises detecting tandem repeats in a target coding sequence, scoring

CC the repeats for polymorphic probability and generating a dataset

CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic
 CC marker prediction of ubiquitous simple sequences, POWPOUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to understand, treat or eliminate genetic
 CC diseases, predispositions or adverse drug-treatment reactions. Examples
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79675-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs

SQ Sequence 24 BP; 0 A; 1 C; 0 G; 23 T; 0 U; 0 Other;

Query Match 0.3%; Score 21.4; DB 1; Length 24;
 Best Local Similarity 95.7%; Pred. No. 2e+02;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTCTTCTTCTGTC 4486
 Db 2 TTTTCTTTTCTTCTTCTTCTTCTTC 24

RESULT 141
 AAX84260
 ID AAX84260 standard; DNA; 25 BP.

XX AAX84260;

AC 08-SEP-1999 (first entry)

XX PCR primer for human Nck associated protein 1 coding sequence.

DE Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;

XX therapy; PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9931239-A1.

PN 24-JUN-1999.

XX 14-DEC-1998; 98WO-UP005646.

PF 15-DEC-1997; 97JP-00363183.

XX (KYOM) KYOMA HAKKO KOGYO KK.

PA (SARA/) SAKAKI Y.

XX Sakaki Y;

PI WPI; 1999-395181/33.

XX Protein inhibiting apoptosis, useful in the diagnosis and treatment of

PT Alzheimer's disease.

XX Disclosure; Page 77; 90pp; Japanese.

XX This sequence represents a PCR primer used to isolate DNA encoding the

CC human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits

CC apoptosis. The protein can be used in the investigation, diagnosis and

CC treatment (e.g. by gene therapy) of Alzheimer's disease

XX Sequence 25 BP; 0 A; 1 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.3%; Score 21.4; DB 1; Length 25;
 Best Local Similarity 95.7%; Pred. No. 2.2e+02;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTCTTCTTCTGTC 4486
 Db 3 TTTTCTTTTCTTCTTCTTCTTCTTC 25


```

RESULT 142
AAD34264/c
ID AAD34264 standard; DNA; 25 BP.
XX
AC AAD34264;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human CYP2D6 gene polymorphic site 385 detecting sense 5' oligo.
XX
KM Human: Cytochrome P450 2D6; CYP2D6; enzyme: detection; xenobiotic;
XX 1ligase-based sequenced determination; drug metabolism; chromosome 22; ss.
XX
OS Homo sapiens.
XX
PN WO200218638-A2.
XX
PD 07-MAR-2002.
XX
PF 27-AUG-2001; 2001WO-IB001544.
XX
PR 30-AUG-2000; 2000GB-00021286.
XX
PA (GEMT-) GEMINI GENOMICS PLC.
XX
PI Risinger C, Andersson MK, Lewander T, Olsson E;
XX
DR WPI; 2002-329785/36.
XX
PT New sequence determination oligonucleotides, useful for detecting
PT polymorphic sites in a 5' flanking region of a CYP2D6 gene, as
PT hybridization probes, as components of diagnostic assays, or in ligase-
PT based sequence determination.
XX
PS Claim 2; Page 23; 63pp; English.
XX
CC The invention relates to sequence determination oligonucleotides for
CC detecting polymorphic sites in a 5' flanking region of cytochrome P450
CC 2D6 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many
CC different xenobiotics. Human CYP2D6 gene is located on chromosome 22. The
CC oligonucleotides may be used as in situ hybridization probes, in ligase-
CC based sequenced determination, as components of diagnostic assays, as
CC probes in sequence determination methods based on mismatches, as
CC hybridization-based diagnostic assays, and as components of diagnostic
CC microarray. CYP2D6 is useful to predict variations in an individual's
CC ability to metabolise certain drugs. The present sequence is a sense
CC oligonucleotide used for detecting of human CYP2D6 gene 5' flanking
CC region single nucleotide polymorphism (SNP)
XX
SQ Sequence 25 BP; 22 A; 2 C; 1 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 2.2e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4463 CTTTCTTTTCTTTTCTTTTGT 4485
Db 25 CTTTCTTTTCTTTTCTTTTGT 3

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XX
OS Homo sapiens.
XX
PN WO200161051-A1.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005305.
XX
PR 16-FEB-2000; 2000US-0182983P.
XX
PA (SEQU-) SEQUEL GENETICS INC.
XX
PI Jarvik JM;
XX
DR WPI; 2001-514778/56.
XX
PT Transcript, genetic, and especially nucleic acid sequence analysis
PT comprises analysis of hybrid peptide products.
XX
PS Example 11; Page 30; 48pp; English.
XX
CC The invention relates to a method of peptide-based transcript or genetic
CC analysis comprising: (a) providing multiple polynucleotides (I) derived
CC from mRNAs from a biological sample, where (I) has homology to a known
CC reference sequence (II); (b) expressing (I); and (c) assessing a physical
CC property of the expression products to determine the sequences of (I) by
CC comparison with the predicted properties of polypeptides encoded by (II).
CC The method is useful for transcript or genetic analysis, especially
CC nucleic acid analysis where the method comprises expressing polypeptides
CC from two or more reading frames and determining the masses to create a
CC peptide mass signature characteristic of the nucleic acid molecule. The
CC peptide is considerably smaller than the DNA molecule that encodes it
CC (individual amino acids averages about 110 Daltons each whereas the
CC trinucleotides (triplets) that encode them average N Daltons each). Also,
CC the peptides are much more diverse in composition than nucleic acids, as
CC they are composed of combinations of 20 different amino acids instead of
CC combinations of 4 different nucleotides, e.g., two random DNA fragments
CC of identical composition (e.g., with 10 adenines, 10 thymines, 15
CC guanines, and 15 cytosines) are extremely unlikely to encode peptides of
CC identical composition. This means that whereas the two nucleic acids have
CC identical masses and cannot be distinguished on the basis of mass, the
CC peptides that they encode will, except in statistically very rare cases,
CC have different masses and can be readily distinguished in the basis of
CC mass. The present sequence represents the coding sequence of human
CC haemoglobin alpha 2 transcript (extreme 3' end) used in an example to
CC demonstrate the method of the invention
XX
SQ Sequence 28 BP; 23 A; 2 C; 3 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 21.4; DB 1; Length 28;
Best Local Similarity 95.7%; Pred. No. 2.6e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4464 TTTTCTTTTCTTTTCTTTTGTGC 4486
Db 25 TTTTCTTTTCTTTTCTTTTGTGC 3

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RESULT 144
AAF26222
ID AAF26222 standard; DNA; 30 BP.
XX
AC AAF26222;
XX
DT 26-APR-2001 (first entry)
XX
DE ABC binding protein associated primer ON-AT- SEQ ID 7.
XX
KM APC binding protein; cell proliferation; adenomatous polyposis coli;
XX tumor cell detection; primer; ss.
XX
OS Unidentified.

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XX  DE1933237-A1.
PN  18-JAN-2001.
XX  15-JUL-1999; 99DE-01033237.
XX  15-JUL-1999; 99DE-01033237.
XX  (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX  Mueller O;
XX  WPI; 2001-148321/16.
XX  Determining proliferative capacity of cells, useful e.g. for detecting
PT  tumor cells, by measuring concentration and subcellular localization of
PT  adenomatous polypsis coli protein.
XX  Claim 10; Page 13; 26pp; German.
XX  This invention describes a novel method for determining the proliferative
CC  activity of cells, comprising detecting, in a sample, the concentration
CC  and/or subcellular localization of APC (adenomatous polypsis coli)
CC  protein (I). The invention also describes (1) determining function of (I)
CC  in a sample by detecting presence of the C-terminal, DNA-binding domain
CC  of (I); (2) detecting mutations in (I)-encoding nucleic acid by detecting
CC  the DNA-binding domain of (I); (3) purifying, enriching and/or detecting
CC  (I) or its fragments by reaction with a probe; (4) double-stranded DNA
CC  (II) that contains the sequence GGCCGCA 2_3G (S1) and/or GATCCT 2_3GC
CC  (S2); (5) peptide fragment of (I) containing at least the DNA-binding
CC  domain; (6) antibodies (Ab) directed against an epitope of positions 1340
CC  -1901, 2219-2580 or 2581-2843 of (I); (7) set of two or more antibodies,
CC  one of which is Ab and the other directed against the N-terminal region
CC  (1-1299) of (I); and (8) kit for detecting DNA-binding capacity of (I) or
CC  its fragments in a sample consisting of (II), Ab or the set of (7). The
CC  method is used to detect proliferative, especially tumor (precursor),
CC  cells, to detect function of (I) and mutations in (I), and to purify
CC  and/or enrich (I), or its fragments, from a sample. The method allows
CC  simple, rapid and reliable detection of proliferation, without the need
CC  for polymerase chain reaction or sequencing
XX  SQ Sequence 30 BP; 1 A; 3 C; 2 G; 24 T; 0 U; 0 Other;
XX  Query Match 0.3%; Score 21.4; DB 1; Length 30;
XX  Best Local Similarity 95.7%; Pred. No. 2.8e+02;
XX  Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX  Qy 4463 CTTTTTTTTTTTTTTTTTGT 4485
XX  ||||| ||||| ||||| ||||| |||||
XX  5 CTTTTTTTTTTTTTTTTTTTTT 27
XX  Db
XX  RESULT 145
XX  ABSS5182/C
XX  ID ABSS5182 standard; DNA; 31 BP.
XX  AC ABSS5182;
XX  12-DEC-2002 (first entry)
XX  Tumour-suppressor gene associated oligonucleotide.
XX  Tumour-suppressor; cancer; ss.
XX  Unidentified.
XX  KR2001061173-A.
XX  07-JUL-2001.
XX  28-DEC-1999; 99KR-00063661.
XX  PT

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PR  28-DEC-1999; 99KR-00063661.
XX  (CHAE/) CHAE J H.
XX  (CHOI/) CHOI W H.
XX  (JUNG/) JUNG T J.
XX  (JUNG/) JUNG H J.
XX  (KIMC/) KIM C G.
XX  (KIMH/) KIM H G.
XX  (PARK/) PARK C I.
XX  (PARK/) PARK J H.
XX  Chae JH, Choi WH, Chung TJ, Jung HJ, Kim CG, Kim HG, Park CI,
PI  Park JH;
XX  WPI; 2002-016333/02.
XX  Vector containing polymerase chain reaction primers of tumor-suppressor
PT  gene, useful for diagnosis of cancer.
XX  Disclosure; Page 11; 19pp; Korean.
XX  CC The present invention relates to a new vector comprising polymerase chain
CC  reaction (PCR) primers of tumor-suppressor gene. The invention can be
CC  useful for the diagnosis of cancer. The present nucleic acid sequence
CC  represents an oligonucleotide as described in the invention
XX  SQ Sequence 31 BP; 22 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
XX  Query Match 0.3%; Score 21.4; DB 1; Length 31;
XX  Best Local Similarity 80.6%; Pred. No. 3e+02;
XX  Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX  Qy 4465 TTTTTTTTTTTTTTTGCTTGAGACAT 4495
XX  ||||| ||||| ||||| ||||| |||||
XX  31 TTTTTTTTTTTTTCATATTCACCAT 1
XX  Db
XX  RESULT 146
XX  ID AAH48764
XX  AAH48764 standard; DNA; 32 BP.
XX  AC AAH48764;
XX  16-NOV-2001 (first entry)
XX  DE Murine liver CDNA library CDNA synthesis associated primer.
XX  Murine; liver; gene library; amino acid synthesis; binding protein;
XX  cell metabolism; energy metabolism; fatty acid metabolism; synthesis;
XX  phospholipid metabolism; purine; pyrimidine; nucleoside; nucleotide;
XX  replication; transcription; translation; transport protein; primer; ss.
XX  Mus musculus.
XX  OS
XX  Key Location/Qualifiers
XX  FH modified_base 1
XX  FT /*tag= a
XX  FT /mod_base= OTHER
XX  FT /note= "5'-biotinylated"
XX  DE20103510-U1.
XX  07-JUN-2001.
XX  28-FEB-2001; 2001DE-02003510.
XX  28-FEB-2001; 2001DE-02003510.
XX  PR (LION-) LION BIOSCIENCE AG.
XX  PA
XX  DR WPI; 2001-368570/39.
XX  PT Gene library containing sequences with specific 3'-ends and no polyA

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PT tail, encoding proteins involved in a wide range of cellular processes.
 XX
 XX Example; Page 7; 251pp; German.
 XX
 CC This invention describes a novel gene library (A) comprising a gene
 CC sequence (or its part) encoding a protein involved in amino acid
 CC synthesis, cellular/energy metabolism, metabolism of fatty
 CC acids/phospholipids, synthesis or breakdown of
 CC purines/pyrimidines/nucleosides/nucleotides, DNA
 CC replication/transcription/translation, or is a transport/binding protein.
 CC (A) are produced that correspond to the 3'-end of mRNA but without the
 CC polyA tail. They can be prepared more efficiently and with less effort
 CC than conventional libraries. This sequence represents a primer involved
 CC in the generation of the gene library described in the method of the
 CC invention
 XX
 SQ Sequence 32 BP; 3 A; 1 C; 4 G; 22 T; 0 U; 2 Other;
 XX
 Query Match 0.3%; Score 21.4; DB 1; Length 32;
 Best Local Similarity 95.7%; Pred. No. 3.1e+02;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4459 TGGACTTTT TTTT TTTT TTTT TTTT 4481
 DB 8 TGGATTTT TTTT TTTT TTTT TTTT 30
 XX
 RESULT 147
 ABV76931
 ID ABV76931 standard; DNA; 32 BP.
 XX
 AC ABV76931;
 XX
 DT 03-MAR-2003 (first entry)
 XX
 DE Oligonucleotide used to reverse transcribe murine cDNA.
 XX
 KM Nucleic acid synthesis; blocking agent; polymerase; DNA library; ss.
 XX
 OS Mus sp.
 XX
 PN BP1253205-A1.
 XX
 PD 30-OCT-2002.
 XX
 PF 24-APR-2001; 2001EP-00109971.
 XX
 PR 24-APR-2001; 2001EP-00109971.
 XX
 PA (LION-) LION BIOSCIENCE AG.
 XX
 PI Hoefer M, Kranz H, Klink M;
 XX
 DR WPI; 2003-077619/08.
 XX
 PT Preferential nucleic acid synthesis reaction of selected regions of
 PT target nucleic acids, by using a blocking agent which preferentially
 PT binds templates which are not desirable when amplifying the nucleic
 PT acids.
 XX
 PS Example 2; Page 6; 20pp; English.
 XX
 CC The specification describes a nucleic acid synthesis reaction of selected
 CC regions of target nucleic acids from a group of two different target
 CC nucleic acids. The method comprises combining in a reaction mixture, two
 CC different target nucleic acids, polymerase, additionally combining a
 CC blocking agent capable of binding a nucleic acid template molecule so
 CC that the polymerase is not able to utilize bound target nucleic acids as
 CC a template, and exposing the reaction mixture to a temperature at which
 CC nucleic acids are synthesized by the polymerase. The method is useful for
 CC nucleic acid synthesis reactions, and is especially useful for creating
 CC DNA libraries. The present oligonucleotide was used to produce cDNA, for
 CC use in the method of the invention

XX
 SQ Sequence 32 BP; 3 A; 1 C; 5 G; 21 T; 0 U; 2 Other;
 XX
 Query Match 0.3%; Score 21.4; DB 1; Length 32;
 Best Local Similarity 95.7%; Pred. No. 3.1e+02;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4459 TGGACTTTT TTTT TTTT TTTT TTTT 4481
 DB 8 TGGAGTTT TTTT TTTT TTTT TTTT 30
 XX
 RESULT 148
 AAV12482/C
 ID AAV12482 standard; DNA; 26 BP.
 XX
 AC AAV12482;
 XX
 DT 15-MAY-1998 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO:5 from US5174320 Example 2.
 XX
 KM Synthesis; selection; amplification; circular oligonucleotide;
 KM rolling circle synthesis; diagnosis; therapeutic agent; ss.
 XX
 OS Synthetic.
 XX
 PN US5714320-A.
 XX
 PD 03-FEB-1998.
 XX
 PF 23-FEB-1995; 95US-00393439.
 XX
 PR 15-APR-1993; 93US-00047860.
 XX
 PA (UYRP) UNIV ROCHESTER.
 XX
 PI Kool ET;
 XX
 DR WPI; 1998-144278/13.
 XX
 PT Rolling circle synthesis of oligo:nucleotide(s) - using primed circular
 PT template to produce oligonucleotide multimer for cleavage.
 XX
 PS Example 2; Col 45; 38pp; English.
 XX
 CC The present sequence represents an oligonucleotide used in an example of
 CC the present invention. The present invention describes a method for
 CC synthesising a selected oligonucleotide (I) having well defined ends. The
 CC method comprises: (a) annealing a primer to a single-stranded (ss)
 CC circular template to yield a primed circular template, where the template
 CC comprises: (i) at least one nucleotide sequence complementary to (I); and
 CC (ii) at least one nucleotide effective to produce a cleavage site in the
 CC oligonucleotide multimer; (b) combining the primed circular template with
 CC at least two types of nucleotide triphosphates and a polymerase enzyme
 CC without the addition of auxiliary proteins to yield a ss oligonucleotide
 CC multimer complementary to the circular oligonucleotide template,
 CC comprising multiple copies of (I); and (c) cleaving the oligonucleotide
 CC multimer at the cleavage site to produce (I) having well defined ends.
 CC The method is used for the large-scale synthesis of DNA and RNA oligomers
 CC for use, e.g. as probes and diagnostic agents and/or therapeutic agents
 XX
 SQ Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
 XX
 Query Match 0.3%; Score 21.2; DB 1; Length 26;
 Best Local Similarity 88.5%; Pred. No. 2.5e+02;
 Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4489
 DB 26 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

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RESULT 149
AAV59215/c
ID AAV59215 standard; DNA; 26 BP.
XX
XX AAV59215;
AC
XX
XX 14-DEC-1998 (first entry)
DT
XX
XX Circular template for linear oligomer dt12.
DE
XX
XX ss; circular; cyclic; RNA oligonucleotide; probe; standard; diagnostic;
XX therapeutic agent.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_binding 1
FT /*tag= a
FT /note= "Position 1 optionally bound to position 26"
FT 26
FT misc_binding 26
FT /*tag= b
FT /note= "Position 26 optionally bound to position 1"
XX
XX WO9838300-A1.
XX
XX 03-SEP-1998.
XX
XX 26-FEB-1998; 98WO-US003784.
XX
XX 26-FEB-1997; 97US-00805631.
XX
XX (UVRP ) UNIV ROCHESTER.
XX
XX PA
XX PI
XX Kool ET;
XX
XX WPI; 1998-481202/41.
XX
XX DR
XX
XX PT Synthesis of oligo:nucleotide(s) - using a single-stranded circular
XX oligo:nucleotide template ribonucleotide triphosphate(s) and a
XX polymerase to form multimer(s) which can be cleaved.
XX
XX PS Example 2; Page 36; 100pp; English.
XX
XX CC The circular template was used for the synthesis of the oligomer dt12 in
XX an example of the method of the invention for synthesizing an RNA
XX oligonucleotide, comprising combining a single-stranded circular
XX oligonucleotide template comprising at least one copy of a nucleotide
XX sequence complementary to the sequence of the desired RNA oligonucleotide
XX with at least 2 types of ribonucleotide triphosphate and a polymerase
XX enzyme to yield a single-stranded RNA oligonucleotide multimer
XX complementary to the circular oligonucleotide template, where the RNA
XX oligonucleotide multimer comprises multiple copies of the desired RNA
XX oligonucleotide. The methods can be used for producing RNA
XX oligonucleotides having a specific sequence and well defined ends. The
XX RNA oligonucleotides produced can be used as probes, standards and
XX diagnostic or therapeutic agents. They can be used for modifying the
XX structure or function of a target molecule. They can also be used to
XX cleave disease-associated RNA, DNA or protein
XX
XX SQ Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 21.2; DB 1; Length 26;
XX Best Local Similarity 88.5%; Pred. No. 2.5e+02;
XX Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 4464 TTTTGTGTTTGTGTTTGTGTTG 4489
XX |||||
XX 26 TTTTGTGTTTGTGTTTGTGTTTGTG 1
XX
XX RESULT 150
XX AAX30018/c
XX ID AAX30018 standard; DNA; 26 BP.

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XX
XX AAX30018;
AC
XX
XX 16-JUN-1999 (first entry)
DT
XX
XX Precircle DNA oligonucleotide SEQ ID NO:5.
DE
XX
XX Multimer; probe; diagnosis; synthesis; detection; polymerase; ss.
XX
XX Synthetic.
OS
XX
XX WO9909216-A2.
XX
XX 25-FEB-1999.
XX
XX 13-AUG-1998; 98WO-US016776.
XX
XX 13-AUG-1997; 97US-00910632.
XX
XX (UVRP ) UNIV ROCHESTER.
XX
XX PA
XX PI
XX Kool ET;
XX
XX WPI; 1999-181062/15.
XX
XX DR
XX
XX PT New detectably labelled oligonucleotide multimer, comprising multiple
XX contiguous copies of a repeated oligonucleotide - useful for detecting
XX target molecules in diagnosis and medicinal applications.
XX
XX PS Example 2; Page 41; 103pp; English.
XX
XX CC The present invention describes a detectably labelled oligonucleotide
XX multimer, comprising multiple contiguous copies of a repeated
XX oligonucleotide. The detectably labelled oligonucleotide multimer is
XX useful for detecting a target molecule. Oligonucleotide multimers may be
XX produced in sufficient quantity to be useful for diagnostic and medical
XX applications. The multimers are useful for affinity labelling of
XX proteins, and for signal amplification in highly sensitive affinity
XX capture and sequence identification applications. The method provides a
XX faster, cheaper and simpler way for large-scale production of DNA and RNA
XX oligomers and multimers. The incorporation of labels enables the
XX oligonucleotide multimers to be useful in diagnostics and medicine. The
XX present sequence represents an oligonucleotide used in an example from
XX the present invention
XX
XX SQ Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 21.2; DB 1; Length 26;
XX Best Local Similarity 88.5%; Pred. No. 2.5e+02;
XX Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 4464 TTTTGTGTTTGTGTTTGTGTTG 4489
XX |||||
XX 26 TTTTGTGTTTGTGTTTGTGTTTGTG 1
XX
XX RESULT 151
XX ADC65872/c
XX ID ADC65872 standard; DNA; 26 BP.
XX
XX AC ADC65872;
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX DNA oligonucleotide #5.
DE
XX
XX RNA oligonucleotide synthesis; ribonucleotide triphosphate; polymerase;
XX electroporation; calcium phosphate treatment; lipid-mediated delivery;
XX cation-mediated delivery; bacterial infection; viral infection;
XX drug resistant infection; double stranded DNA oligomer; ss.
XX
XX OS Synthetic.
XX

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PN US2003087241-A1.
XX
XX 08-MAY-2003.
XX
XX 30-NOV-2001; 2001US-0097931.
XX
XX 15-APR-1993; 93US-00047860.
XX 23-FEB-1995; 95US-00393439.
XX 26-FEB-1997; 97US-00805631.
XX 11-MAY-2000; 2000US-00569344.
XX
XX (UYRP ) UNIV ROCHESTER.
XX
XX KOOL ET;
XX
XX WPI; 2003-755141/71.
XX
XX Synthesizing RNA oligonucleotide involves combining single-stranded
XX circular oligonucleotide, ribonucleotide triphosphate and polymerase
XX enzyme to yield desired RNA complementary to circular oligonucleotide
XX template.
XX
XX Example 2; SEQ ID NO 5; 78bp; English.
XX
XX The invention relates to a method for synthesizing an RNA
XX oligonucleotide, comprising combining a single-stranded circular
XX oligonucleotide template with at least two types of ribonucleotide
XX triphosphate and a polymerase enzyme to yield a single-stranded RNA
XX oligonucleotide multimer complementary to the circular oligonucleotide
XX template, where the RNA oligonucleotide multimer comprises multiple
XX copies of the desired RNA oligonucleotide. The method is useful for
XX synthesizing an RNA oligonucleotide with well-defined ends. The circular
XX oligonucleotide is introduced into the cell using direct injection,
XX electroporation, calcium phosphate treatment, lipid-mediated delivery, or
XX cation-mediated delivery. The method is useful for treating bacterial
XX and/or viral infections in mammals, particularly drug resistant
XX infections, and for producing double stranded DNA oligomers. The method
XX is performed in the absence of an oligonucleotide primer, or without the
XX addition of auxiliary proteins. This sequence represents an
XX oligonucleotide used in the method of the invention.
XX
XX Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 21.2; DB 1; Length 26;
XX Best Local Similarity 88.5%; Pred. No. 2.5e+02;
XX Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 4464 TTTTGTCTG 4489
XX | ||||| ||||| ||||| |||||
XX 26 TTTTGTCTGTTTGTCTG 1
XX
XX RESULT 152
XX ID AAA40358 standard; DNA; 28 BP.
XX AC AAA40358;
XX
XX 10-NOV-2000 (first entry)
XX
XX pbluescriptSK+ phagemid primer SEQ ID NO: 8.
XX
XX Synthetic.
XX OS
XX PN WO200036088-A1.
XX
XX 22-JUN-2000.
XX
XX 17-DEC-1999; 99WO-US030277.
XX
XX 17-DEC-1998; 98US-0021834.

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XX
XX (ROMA/) ROMANTCHIKOV Y.
XX Romanchikov Y;
XX
XX WPI; 2000-442381/38.
XX
XX Inserting a nucleic acid into a circular vector comprising joining their
XX ends, melting, and reannealing ends at two different concentrations,
XX useful for cloning small amounts of nucleic acids and forming genomic
XX libraries.
XX
XX Example 3; Page 67; 71pp; English.
XX
XX This invention describes a novel method (M1) for inserting a nucleic acid
XX (N1) into a circular vector (V1) comprising joining ends of N1 and V1
XX under a first nucleic acid concentration, melting hybridized cohesive
XX circularization ends, and reannealing the ends at a second concentration.
XX The methods are useful for the cloning small amounts of nucleic acids and
XX forming genomic libraries of complex populations of DNA or cDNA. The
XX methods allow the cloning of minute amounts of nucleic acids efficiently
XX and avoids the size selection problems of prior art systems. Larger
XX nucleic acid fragments are just as easily cloned, allowing highly
XX representative libraries to be made. Vector to vector ligation is avoided
XX using the methods. AAA40351-A40366 represents primers used to illustrate
XX the method of the invention.
XX
XX Sequence 28 BP; 1 A; 1 C; 1 G; 25 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 21.2; DB 1; Length 28;
XX Best Local Similarity 88.5%; Pred. No. 2.8e+02;
XX Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 4462 ACTTTTGTCTG 4487
XX | ||||| ||||| ||||| |||||
XX 3 AGTTTGTCTGTTTGTCTG 28
XX
XX RESULT 153
XX ID AAA03952 standard; DNA; 29 BP.
XX AC AAA03952;
XX
XX 22-MAY-2000 (first entry)
XX
XX Polymorphic fragment of hypertension associated gene APOA4.
XX
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
XX polycystic kidney disease; von Willebrand's disease; forensic; human;
XX familial sclerotic; hereditary hemorrhagica telangiectasia;
XX familial colonic polyposis; osteogenesis imperfecta; porphyria;
XX Ehlers-Danlos syndrome; ss.
XX
XX Homo sapiens.
XX
XX BP955382-A2.
XX
XX 10-NOV-1999.
XX
XX 07-MAY-1999; 99EP-00250150.
XX
XX 07-MAY-1998; 98US-0084641P.
XX
XX 03-MAY-1999; 99US-00304232.
XX
XX (AFY-) AFFYMETRIX INC.
XX (UYCA-) UNIV CASE WESTERN RESERVE.
XX
XX Fan JB, Chakravarti A, Haluska MK;
XX
XX WPI; 2000-107928/10.

```

XX Novel nucleic acids containing polymorphisms used in the diagnosis of
 PT hypertension.
 XX
 PS Claim 1, Page 21; 53pp; English.
 XX
 CC The invention provides polymorphic fragments of genes associated with
 CC hypertension. The nucleic acids including the polymorphic sites can be
 CC used as probes or primers for expressing variant proteins. Detection of
 CC the polymorphisms is useful in designing prophylactic and therapeutic
 CC regimens customized to underlying abnormalities. The polymorphisms can be
 CC used for association studies for hypertension, and in hypertension
 CC diagnostic assays. Where the polymorphisms have strong correlation with
 CC hypertension, within a gene, they are likely to have a causative role in
 CC hypertension. This information can be used to find the precise role of a
 CC polymorphism in the disease, and this can be used to identify potential
 CC drugs which combat the disease. The polymorphisms can be tested for
 CC association with other diseases e.g. agammaglobulinemia, diabetes
 CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
 CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
 CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
 CC tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial
 CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
 CC acute intermittent porphyria. The polymorphic forms can also be used in
 CC forensic science to identify individuals
 XX
 SQ Sequence 29 BP; 11 A; 8 C; 9 G; 0 T; 0 U; 1 Other;
 XX
 Query Match 0.3%; Score 21.2; DB 1; Length 29;
 Best Local Similarity 82.1%; Pred. No. 2.9e+02;
 Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 XX
 QY 7405 ACCAATCATCAGCAGCAGCAGCAGCA 7432
 Db 2 AGCAGCAACGACGACGACGAGCAGCAGCA 29
 XX
 RESULT 154
 AAS63442/C
 ID AAS63442 standard; DNA; 31 BP.
 XX
 AC AAS63442;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Oligonucleotide-nanoparticle probe #64.
 XX
 KW Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;
 KW nucleic acid detection; nanostructure; biochip; biofilter; drug delivery;
 KW ss.
 XX
 OS Synthetic.
 XX
 PN WO200173123-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 28-MAR-2001; 2001WO-US010071.
 XX
 PR 28-MAR-2001; 2000US-0192699P.
 PR 26-APR-2001; 2000US-0200161P.
 PR 26-JUN-2001; 2000US-00603830.
 PR 08-DEC-2000; 2000US-021306P.
 PR 11-DEC-2000; 2000US-0254392P.
 PR 12-JAN-2001; 2000US-0255235P.
 PR 12-JAN-2001; 2001US-00760500.
 PR 28-MAR-2001; 2001US-00820279.
 XX
 (NANO-) NANOSPHERE INC.
 XX
 PA Mirtin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghamian R;
 PT Taton JA, Park S, Li Z;
 XX

DR WPI; 2001-656926/75.
 XX
 XX Detecting and separating nucleic acid, useful e.g. for diagnosis,
 PT comprises reaction with nanoparticles that carry oligonucleotides
 PT complementary to parts of the target.
 XX
 PS Example 24; Fig 44; 404pp; English.
 XX
 CC The invention relates to a method for detection of nucleic acid (I)
 CC having at least 2 portions, comprising treatment with nanoparticles that
 CC carry oligonucleotides complementary to at least 2 parts of (I), where
 CC detectable change caused by hybridisation of the oligonucleotide to (I)
 CC is observed. The method is used to detect (or to separate) specific (I),
 CC e.g. for diagnosing a wide variety of diseases, sequencing, in forensic
 CC analysis etc., and generally to detect analytes other than (I). The
 CC oligonucleotide-derivatised nanoparticles are also useful for preparing
 CC nanostructures useful, for example, as biochips, biofilters, mechanical
 CC devices, separation membranes, chemical sensors, in computers, and for
 CC drug delivery. Very stable nanoparticle-oligonucleotide conjugates can be
 CC produced, allowing their direct use (as probes) in polymerase chain
 CC reaction, i.e. they survive multiple heating/cooling cycles so do not
 CC need to be added after amplification. (I) are detected by simple colour
 CC change, without the need for special equipment, making possible rapid
 CC field testing for e.g. pathogens. AAS63374-AAS63448 represent
 CC oligonucleotide-nanoparticle probes, and related sequences, used in the
 CC method of the invention
 XX
 SQ Sequence 31 BP; 21 A; 3 C; 3 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 0.3%; Score 21.2; DB 1; Length 31;
 Best Local Similarity 88.5%; Pred. No. 3.2e+02;
 Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 4457 CATGACCTTTTCTTTTCTTTTCTTTT 4482
 Db 26 CATGACCTTTTCTTTTCTTTTCTTTT 1
 XX
 RESULT 155
 AAS10386/C
 ID AAS10386 standard; DNA; 31 BP.
 XX
 AC AAS10386;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Oligonucleotide-cyclic disulphide linker, c2 #2.
 XX
 KW Nanoparticle; cyclic disulphide-oligonucleotide; DNA detection;
 KW DNA isolation; genetic disease; bacterial disease; viral disease;
 KW forensic science; paternity testing; gene therapy; ss.
 XX
 OS Synthetic.
 XX
 PN WO200151665-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 12-JAN-2001; 2001WO-US001190.
 XX
 PR 13-JAN-2001; 2000US-0176409P.
 PR 26-APR-2001; 2000US-0200161P.
 PR 26-JUN-2001; 2000US-00603830.
 PR 12-JAN-2001; 2001US-00760500.
 XX
 (NANO-) NANOSPHERE INC.
 XX
 PA Mirtin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghamian R;
 PT Taton JA, Park S, Li Z;
 XX

PI Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;
 PI Taton TA, Li Z;
 DR WPI; 2001-451868/48.
 XX
 PT Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or
 PT viral diseases, by contacting the nucleic acid with oligonucleotides
 PT attached to nanoparticles and having sequences complementary a portion of
 PT the nucleic acid.
 XX
 XX
 PS Example 24; Fig 44; 323pp; English.
 XX
 CC The sequence represents a cyclic disulphide linked oligonucleotide which
 CC may be coupled with colloidal gold particles (nanoparticles) and used to
 CC demonstrate the method of the invention. The invention relates to
 CC isolating or detecting a nucleic acid of interest, in a mixture of
 CC nucleic acids, by binding it to 2 or more complementary nucleotides which
 CC have a nanoparticle attached to their 5' ends. The nanoparticles (e.g.
 CC colloidal gold) are used to both isolate and detect (e.g. by linking the
 CC particle to a fluorescent probe) the resultant complex. The methods are
 CC useful for detecting nucleic acids, natural or synthetic, and modified or
 CC unmodified. The methods may also be applied in the diagnosis of genetic,
 CC bacterial and viral diseases, in forensics, in DNA sequencing, for
 CC paternity testing, for cell line authentication, and for monitoring gene
 CC therapy. The methods are further useful in research and analytical
 CC laboratories in DNA sequencing, in the field to detect the presence of
 CC specific pathogens, for quick identification of an infection to assist in
 CC drug prescription, and in homes and health centres for inexpensive first-
 CC line screening. The methods, which are based on observing colour change
 CC with the naked eye, are cheap, fast, simple, robust (reagents are
 CC stable), do not require specialised or expensive equipment, and little or
 CC no instrumentation is required
 CC
 SQ Sequence 31 BP; 21 A; 3 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 0.3%; Score 21.2; DB 1; Length 31;
 Best Local Similarity 88.5%; Pred. No. 3.2e+02;
 Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4457 CATGACCTTTTTTTTTTTTTTTTTTTT 4482
 DB 26 CATAGCTTTTTTTTTTTTTTTTTTTT 1
 RESULT 156
 ABR65049/c
 ID ABR65049 standard; DNA; 31 BP.
 XX
 AC ABR65049;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Nanoparticle-oligonucleotide #69.
 XX
 DE Nanoparticle-oligonucleotide #69.
 KM Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
 KW ss.
 XX
 OS Synthetic.
 XX
 PN WO200218643-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 10-AUG-2001; 2001WO-US025237.
 XX
 PR 11-AUG-2000; 2000US-0224631P.
 PR 08-DEC-2000; 2000US-0254392P.
 PR 11-DEC-2000; 2000US-0255235P.
 PR 12-JAN-2001; 2001US-00760500.
 PR 28-MAR-2001; 2001US-00820279.
 XX
 PA (NANO-) NANOSPHERE INC.
 XX

PI Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;
 PI Taton TA, Garimella V, Li Z, Park S;
 DR WPI; 2002-258024/30.
 XX
 PT Detecting nucleic acid, useful for diagnosis of genetic, viral or
 PT bacterial disease, comprises hybridizing nanoparticles with attached
 PT oligonucleotides to nucleic acid and detecting change brought about by
 PT hybridization.
 XX
 XX
 PS Example 24; Fig 44; 412pp; English.
 XX
 CC The invention relates to a method of detecting a nucleic acid (NA) having
 CC at least 2 portions comprising: (a) providing nanoparticles (NP) with
 CC attached oligonucleotides (OGN), where OGN has a sequence complementary
 CC to the sequence of NA; (b) contacting NA and NP under conditions
 CC effective to allow hybridisation of OGN with NA; and (c) observing a
 CC detectable change brought about by hybridisation of OGN with NA. The
 CC method is useful for detecting a nucleic acid, separating a selected
 CC nucleic acid from others and methods of nanofabrication. Detecting
 CC analytes such as nucleic acids and proteins are useful for the diagnosis
 CC of genetic, bacterial and viral diseases. The OGN-NP conjugates that use
 CC cyclic disulphide linkers improve the sensitivity of diagnostic assays.
 CC In particular assays using OGN-NP conjugates prepared using linkers
 CC comprising a steroid residue attached to a cyclic disulphide have been
 CC found to be approximately 10 times more sensitive than assays employing
 CC conjugates prepared using alkanethiols or acyclic disulphides as the
 CC linker. The OGN-NP conjugates are stable allowing them to be used
 CC directly in PCR solutions. Therefore conjugates added as probes to a DNA
 CC target to be PCR amplified can be carried through the 30 or 40 heating
 CC cooling cycles of the PCR and are still able to detect the amplicons
 CC without opening the tubes and causing contamination. ABR64981-ABR65055
 CC represent nanoparticle-oligonucleotides of the invention
 CC
 SQ Sequence 31 BP; 21 A; 3 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 0.3%; Score 21.2; DB 1; Length 31;
 Best Local Similarity 88.5%; Pred. No. 3.2e+02;
 Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4457 CATGACCTTTTTTTTTTTTTTTTTTTT 4482
 DB 26 CATAGCTTTTTTTTTTTTTTTTTTTT 1
 RESULT 157
 ABS64687/c
 ID ABS64687 standard; DNA; 31 BP.
 XX
 AC ABS64687;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Nucleic acid detection method associated polynucleotide #69.
 XX
 DE Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
 KM nanoparticle; viral RNA detection; bacterial DNA detection;
 KM fungal DNA detection; nanoprobe conjugate; ss.
 XX
 OS Synthetic.
 XX
 PN WO200246472-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 07-DEC-2001; 2001WO-US046418.
 XX
 PR 08-DEC-2000; 2000US-0254392P.
 PR 08-DEC-2000; 2000US-0254418P.
 PR 11-DEC-2000; 2000US-0255235P.
 PR 11-DEC-2000; 2000US-0255236P.
 PR 12-JAN-2001; 2001US-00760500.
 PR 28-MAR-2001; 2001US-00820279.
 XX

PS Disclosure; Page 47; 101pp; English.

XX CC The sequence is that of an oligonucleotide, I, which is able to form a

CC triple helix with a duplex nucleic acid (dsNA) contg. a target sequence

CC which comprises at least one pyrimidine tract, and at least one adjacent

CC purine tract. It is useful for therapeutic or diagnostic control of gene

CC expression, e.g. suppression of mRNA synthesis from a target gene. A

CC specified application is targeting of RNA in the HIV-1 genome. When

CC appropriately labelled it may also be used as a probe. Attachment of

CC cleavage agents caused permanent inactivation of the target by site-

CC specific cleavage. (Updated on 25-MAR-2003 to correct PN field.)

XX

SO Sequence 32 BP; 8 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

QY Query Match 0.3%; Score 21.2; DB 1; Length 32;

Best Local Similarity 88.5%; Pred. No. 3.4e+02;

Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 4462 ACTTTTGTGCT 4487

7 AATTTTGTGCT 32

RESULT 160

ABS53433

ID ABS53433 standard; DNA; 32 BP.

XX

AC ABS53433;

XX

DT 29-NOV-2002 (first entry)

XX

DE First strand synthesis - first primer.

XX

KW Terminal continuation; TC; ss; second strand cDNA synthesis; primer.

XX

OS Synthetic.

XX

PN WO200265093-A2.

XX

PD 22-AUG-2002.

XX

PF 14-FEB-2002; 2002WO-US005713.

XX

PR 14-FEB-2001; 2001US-0268645P.

PR 14-FEB-2001; 2001US-0268646P.

PR 18-JUL-2001; 2001US-0306216P.

PR 07-NOV-2001; 2001US-0344557P.

PR 07-NOV-2001; 2001US-0348242P.

PR 09-NOV-2001; 2001US-0350176P.

XX

PA (BAYU) BAYLOR COLLEGE MEDICINE.

PA (REME-) RES FOUND MENTAL HYGIENE INC.

XX

PI Ginsberg SD, Che S;

XX

DR WPI; 2002-567050/60.

XX

PT Increasing efficiency of second strand cDNA synthesis using terminal

PT continuation model before performing further RNA amplification by RNA

PT transcription.

XX

PS Example 4; Page 78; 128pp; English.

XX

CC This invention relates to a novel method for increasing the efficiency of

CC second strand cDNA synthesis through a mechanism of terminal

CC continuation. In the method an RNA molecule is obtained and a first

CC primer is added that comprises a region that hybridises to a

CC complementary region of the molecule before a second primer is added

CC comprising at least one riboguanine at the 3' end of the primer. A first

CC complementary nucleic acid molecule is synthesised, the RNA molecule and

CC second primer are removed and a second complementary nucleic acid

CC molecule is synthesised to form a second hybrid with an extension product

CC of the third primer bound to the first complementary molecule. The method

CC of the invention is useful for increasing the efficiency of second strand

CC cDNA synthesis and may be used for linear amplification of genetic

CC signals from histologically stained tissue. The present sequence

CC represents a first strand synthesis - first primer used in the method of

CC the invention

XX

SO Sequence 32 BP; 3 A; 4 C; 1 G; 22 T; 0 U; 2 Other;

QY Query Match 0.3%; Score 21.2; DB 1; Length 32;

Best Local Similarity 95.5%; Pred. No. 3.4e+02;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 4463 CTTTGTGCT 4484

10 CTTTGTGCT 31

RESULT 161

AAQ75653

ID AAQ75653 standard; DNA; 21 BP.

XX

AC AAQ75653;

XX

DT 04-AUG-1995 (first entry)

XX

DE Reverse transcription primer used in cDNA analysis technique.

XX

KW Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

XX

OS Synthetic.

XX

FN JP06303997-A.

XX

PD 01-NOV-1994.

XX

PF 16-APR-1993; 93JP-00112515.

XX

PR 16-APR-1993; 93JP-00112515.

XX

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX

DR WPI; 1995-018287/03.

XX

PT Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.

XX

PS Disclosure; Page 6; 11pp; Japanese.

XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c) the

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX

SO Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

QY Query Match 0.3%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4467 TTTTGTGCT 4487

1 TTTTGTGCT 21

RESULT 162

AAAX17962/c

ID AAAX17962 standard; cDNA; 21 BP.

XX

AC AAX17962;
 XX
 DT 11-MAY-1999 (first entry)
 XX
 DE Triplet repeat sequence PCR primer #12.
 XX
 KW Primer; PCR; amplification; triplet repeat; spinobulbar atrophy;
 KM myotonic dystrophy; spinocerebellar ataxia; Huntington's disease;
 KM fragile X syndrome; Behcet's disease; diagnosis; ss.
 XX
 OS Synthetic.
 XX
 PN WO9856950-A1.
 XX
 PD 17-DEC-1998.
 XX
 PF 10-JUN-1998; 98WO-FR001187.
 XX
 PR 11-JUN-1997; 97FR-00007225.
 XX
 PA (DAUS-) FOND DAUSSET-CEPH JEAN.
 XX
 PI Neri C, Cann HM;
 XX
 DR WPI; 1999-070334/06.
 XX
 PT DNA sequences rich in repeated nucleotide triplets - used for the
 PT diagnosis and prognosis of diseases associated with trinucleotide
 PT repeats.
 XX
 PS Claim 5; Page 14; 30pp; French.
 XX
 CC Primers AAX17951-X17974 are used to PCR amplify sequences containing the
 CC triplet repeat sequences CAG/CTG or CCG/GCC. The amplified sequences can
 CC be compared to sequences from a patient to determine presence of
 CC additional trinucleotide repeats (TNR), specifically for assessing the
 CC risk of developing a TNR-related disease (e.g. spinobulbar atrophy;
 CC myotonic dystrophy; spinocerebellar ataxia; Huntington's disease; fragile
 CC X syndrome or Behcet's disease). The method is especially useful for
 CC early diagnosis or specific monitoring, but if the disease is associated
 CC with a relatively small variation in the number of repeats, it may also
 CC be used to predict the onset of disease and/or its severity
 CC
 SQ Sequence 21 BP; 8 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
 XX
 QY
 Db 7440 TCTGTGTTTATTAAGACAAC 7460
 21 TCTGTGTTTATTAAGACAAC 1
 XX
 RESULT 163
 AAF99580/c
 ID AAF99580 standard; DNA; 21 BP.
 XX
 AC AAF99580;
 XX
 DT 12-JUN-2001 (first entry)
 XX
 DE Immunostimulatory nucleic acid #696.
 XX
 KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 KM immunostimulatory; tumour; viral infection; bacterial infection;
 KM fungal infection; parasitic infection; cancer; asthma;
 KM infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 PN WO200122972-A2.
 XX

PD 05-APR-2001.
 XX
 PF 25-SEP-2000; 2000WO-US026383.
 XX
 PR 25-SEP-1999; 99US-0156113P.
 XX
 PR 27-SEP-1999; 99US-0156135P.
 XX
 PR 23-AUG-2000; 2000US-0227436P.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI (COLE-) COLEY PHARM GMBH.
 XX
 PI Kriegl AM, Schetter C, Vollmer J;
 XX
 DR WPI; 2001-273485/28.
 XX
 PT Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids.
 XX
 PS Claim 101; Page 53; 338pp; English.
 XX
 CC The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC stephylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the
 CC present sequence may have a phosphorothioate backbone
 XX
 SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
 XX
 QY
 Db 7413 CAGCAGCAGCAGCAGCAGCAG 7433
 21 CAGCAGCAGCAGCAGCAGCAG 1
 XX
 RESULT 164
 ABK81862/c
 ID ABK81862 standard; DNA; 21 BP.
 XX
 AC ABK81862;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Lung specific gene PCR primer #20.
 XX
 KW Lung specific gene; gene therapy; vaccine; lung cancer; cancer staging;
 KM cancer monitoring; cancer diagnosis; imaging lung cancer; metastases;
 KM PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200218576-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 27-AUG-2001; 2001WO-US026684.
 XX
 PR 28-AUG-2000; 2000US-0228378P.
 XX
 PA (DIAD-) DIADEXUS INC.
 XX
 PI Chen S, Macina RA, Sun Y, Reardon H;
 XX

XX
DR WPI; 2002-434904/46.
XX
PT New lung specific genes and their encoded proteins, useful in gene
PT therapy or as a vaccine for treating lung cancer, as well as for
PT measuring metastases of lung cancer, or staging, monitoring, diagnosing
PT or imaging lung cancer.
XX
PS Example 10; Page 127; 206pp; English.
XX
CC The invention describes a new lung specific gene and it's variants. The
CC lung specific gene proteins and genes are useful in gene therapy or as a
CC vaccine for treating lung cancer. Lung specific genes are also useful for
CC staging, monitoring, diagnosing or imaging lung cancer, as well as for
CC measuring metastases of lung cancer. This sequence represents a PCR
CC primer used in microarray analysis to isolate a lung specific gene
CC thought to be involved in development of lung cancer
XX
SQ Sequence 21 BP; 9 A; 8 C; 1 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5593 TGGATTGCTTAAAGTGTGC 5613
DB 21 TGGATTGCTTAAAGTGTGC 1
XX
RESULT 165
ABST8296/C
ID ABST8296 standard; DNA; 21 BP.
XX
AC ABST8296;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #780.
XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
XX diabetic retinopathy; retinopathy of prematurity; macular degeneration;
XX corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
XX rubecosis; Osler-Webber Syndrome; myocardial angiogenesis;
XX plaque neovascularisation; telangiectasia; haemophilic joint;
XX angiodioma; wound granulation; intestinal adhesion; atherosclerosis;
XX scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLB-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
XX Claim 2; Page 33; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject

CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubecosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophilic joints, angiodioma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma, and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7413 CAGCAGCAGCAGCAGCAG 7433
DB 21 CAGCAGCAGCAGCAGCAG 1
XX
RESULT 166
ABL38849/C
ID ABL38849 standard; DNA; 21 BP.
XX
AC ABL38849;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 240.
XX
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
XX angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..21
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note="phosphorothioate backbone"
XX
PN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020154.
XX
PR 22-JUN-2000; 2000US-0213346P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
PS Disclosure; Page 156; 312pp; English.
XX
XX The present invention relates to methods for treating or preventing
XX cancer, involving administering to a subject having or at risk of
XX developing cancer immunostimulatory nucleic acids that induce expression
XX of cell surface antigens and antibodies. The methods are useful for
XX treating or preventing cancer such as basal cell carcinoma, bladder
XX cancer, bone cancer, brain and central nervous system (CNS) cancer,
XX breast cancer, cervical cancer, colon and rectum cancer, connective
XX tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
XX cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-

CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention

SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 21; Conservative 0; Indels 0;

QY 7413 CAGCAGCAGCAGCAGCAGCAG 7433

Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 167
ABK10202/c
ID ABK10202 standard; DNA; 21 BP.

XX ABK10202;

XX 21-MAY-2002 (first entry)

XX Double stranded DNA isolation (CTG) 7 repeat sequence.

XX Single stranded DNA isolation; DNA purification; CTG repeat; ds.

XX Synthetic.

XX Key Location/Qualifiers

FT repeat_region 1..21

FT repeat_unit /rpt_type= TANDEM

FT /tag= b

FT /note= "CTG type repeat"

XX WO200210182-A2.

XX 07-FEB-2002.

XX 18-JUL-2001; 2001WO-US022782.

XX 02-AUG-2000; 2000US-0222866P.

XX (PEKE) PE CORP NY.

XX Chiesse C, Schroth GP, Egholm M;

XX WPI; 2002-188719/24.

PT Isolating one strand of double-stranded nucleic acid, by contacting
PT double stranded nucleic acid having first and second strands with
PT competitor oligo to form first strand-oligo complex and isolating the
PT complex.

PS Disclosure; Page 12; 61pp; English.

XX This invention relates to a novel method for isolating one strand of
XX double-stranded target nucleic acid. The method comprises contacting a
XX double stranded target DNA molecule with a competitor oligonucleotide
XX capable of hybridizing to the first strand of the double stranded
XX molecule. The method is performed under conditions in which the first
XX strand dissociates from the second and hybridizes with the competitor
XX oligonucleotide to form a heteroduplex. The method of the invention is
XX useful for separating a strand from a double-stranded target nucleic
XX acid. The method is rapid, efficient and specific for isolating a single
XX strand from a double-stranded nucleic acid. Because the method provides
XX easy and efficient recovery of the single stranded DNA, the method is
XX advantageously used to purify a first strand from a double-stranded
XX nucleic acid that is a polymerase chain reaction (PCR) amplification

CC product from a pool of related or unrelated sequences in high yield for
CC subsequent use. The method also permits capture and/or recovery of the
CC first strand of a double-stranded target nucleic acid from biological
CC samples or other samples containing large molecule contaminants. The
CC present sequence represents a double stranded (CTG) 7 DNA molecule used to
CC isolate double stranded DNA molecules in an example of a similar method
CC to that of the invention

SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 21; Conservative 0; Indels 0;

QY 7413 CAGCAGCAGCAGCAGCAGCAG 7433

Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 168
ACH03118/c
ID ACH03118 standard; DNA; 21 BP.

XX ACH03118;

XX 25-SEP-2003 (first entry)

XX Immunostimulatory nucleic acid #753.

XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
XX antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
XX psoriasis; eczema; allergic contact dermatitis; latex dermatitis;

XX inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX Synthetic.

XX US2003050268-A1.

XX 13-MAR-2003.

XX 29-MAR-2002; 2002US-00112653.

XX 29-MAR-2001; 2001US-0279642P.

XX (KRIE/) KRIEG A M.

XX (BERG/) BERG D J.

XX Krieg AM, Berg DJ;

XX WPI; 2003-521815/49.

PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.

PS Disclosure; Page 29; 229pp; English.

XX The invention describes a method of treating non-allergic inflammatory
XX disease comprising administering to a subject having or at risk of
XX developing a non-allergic inflammatory disease an immunostimulatory
XX nucleic acid for prevention or treatment of the disease. The method is
XX useful for treating non-allergic inflammatory diseases, such as
XX psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
XX inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
XX This sequence represents an immunostimulatory nucleic acid

SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 21; Conservative 0; Indels 0;

QY 7413 CAGCAGCAGCAGCAGCAGCAG 7433


```

FT      misc_feature      11..12
FT      /tag= d
FT      /note= "o-xyloso dimer synthon linkage"
FT      misc_feature      12..23
FT      /tag= c
FT      /label= inverted_polarity_region
FT      /note= "see comments"
FT      modified_base     23
FT      /tag= b
FT      /mod_base= OTHER
FT      /note= "OTHER= N4 N4 ethanocytosine"
XX
XX      WO9209705-A1.
XX
XX      11-JUN-1992.
XX
XX      25-NOV-1991; 91WO-US008811.
XX
XX      23-NOV-1990; 90US-00617907.
XX      18-JAN-1991; 91US-00643382.
XX      08-APR-1991; 91US-00683420.
XX      17-APR-1991; 91US-00685444.
XX      17-APR-1991; 91US-00685446.
XX      17-APR-1991; 91US-00685447.
XX      27-SEP-1991; 91US-00766733.
XX
XX      (GILE-) GILEAD SCI INC.
XX
XX      Froehler B, Krawczyk S, Matteucci MD, Milligan J;
XX      WPI; 1992-217083/26.
XX
XX      New oligomers contg. modified bases - which form a triplex with G-C
XX      doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
XX      herpes malignancy and inflammation.
XX
XX      Claim 12; Page 71; 77pp; English.
XX
XX      The synthetic oligomer is capable of forming a triplex at physiological
XX      pH with a purine rich target sequence by coupling into the major groove
XX      of the duplex. The specific target sequence of this oligomer is the human
XX      interleukin 6 gene untranslated sequence contg. a purine rich sequence
XX      concd. on one strand of the duplex. The oligomer, and others like it are
XX      useful in diagnosis and therapy of diseases characterised by specific DNA
XX      duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant
XX      tumours and inflammation. The triple helices form under mild conditions
XX      thus assays may be carried out without subjecting the test specimen to
XX      harsh conditions. The oligomer contains an inverted polarity region
XX      formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
XX      (nucleotides have the 3' positions of xylene sugars linked via the o-
XX      xylene ring). Two nucleotides are coupled through a xylene residue to
XX      form the dimer synthon. This additional modifications may render the
XX      oligomer stable to nuclease activity. The oligomer is able to inhibit
XX      gene expression, as verified by in vitro systems. See also AAQ25452-25501
XX      and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX      Sequence 23 BP; 0 A; 2 C; 0 G; 21 T; 0 U; 0 Other;
SQ
Query Match      0.3%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2,2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4463 CTTTTTTTTTTTTTTTTT 4483
Db      1 CTTTTTTTTTTTTTTTTT 21
RESULT 172
AAQ30431
ID      AAQ30431 standard; DNA; 23 BP.
XX      AAQ30431;
XX

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DT      25-MAR-2003 (revised)
DT      07-DEC-1992 (first entry)
XX
XX      Oligomer IL6804 for forming triplex with HUMIL6 target duplex.
DE      Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;
XX      malignancy; hepatitis; inflammation; ss.
XX
XX      Synthetic.
OS
XX
XX      Key      Location/Qualifiers
FH      modified_base     1
FH      /tag= a
FH      /mod_base= OTHER
FH      /note= "OTHER= N4 N4 ethanocytosine"
FT      misc_feature      11..12
FT      /tag= d
FT      /note= "o-xyloso dimer synthon linkage"
FT      misc_feature      12..23
FT      /tag= c
FT      /label= inverted_polarity_region
FT      /note= "see comments"
FT      modified_base     23
FT      /tag= b
FT      /mod_base= OTHER
FT      /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
XX      WO9209705-A1.
XX
XX      11-JUN-1992.
XX
XX      25-NOV-1991; 91WO-US008811.
XX
XX      23-NOV-1990; 90US-00617907.
XX      18-JAN-1991; 91US-00643382.
XX      08-APR-1991; 91US-00683420.
XX      17-APR-1991; 91US-00685444.
XX      17-APR-1991; 91US-00685446.
XX      17-APR-1991; 91US-00685447.
XX      27-SEP-1991; 91US-00766733.
XX
XX      (GILE-) GILEAD SCI INC.
XX
XX      Froehler B, Krawczyk S, Matteucci MD, Milligan J;
XX      WPI; 1992-217083/26.
XX
XX      New oligomers contg. modified bases - which form a triplex with G-C
XX      doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
XX      herpes malignancy and inflammation.
XX
XX      Claim 12; Page 71; 77pp; English.
XX
XX      The synthetic oligomer is capable of forming a triplex at physiological
XX      pH with a purine rich target sequence by coupling into the major groove
XX      of the duplex. The specific target sequence of this oligomer is the human
XX      interleukin 6 gene untranslated sequence contg. a purine rich sequence
XX      concd. on one strand of the duplex. The oligomer, and others like it are
XX      useful in diagnosis and therapy of diseases characterised by specific DNA
XX      duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant
XX      tumours and inflammation. The triple helices form under mild conditions
XX      thus assays may be carried out without subjecting the test specimen to
XX      harsh conditions. The oligomer contains an inverted polarity region
XX      formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
XX      (nucleotides have the 3' positions of xylene sugars linked via the o-
XX      xylene ring). Two nucleotides are coupled through a xylene residue to
XX      form the dimer synthon. This additional modifications may render the
XX      oligomer stable to nuclease activity. The oligomer is able to inhibit
XX      gene expression, as verified by in vitro systems. See also AAQ25452-25501
XX      and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX      Sequence 23 BP; 1 A; 1 C; 0 G; 21 T; 0 U; 0 Other;
SQ

```

	Query Match	0.3%;	Score 21;	DB 1;	Length 23;	
	Best Local Similarity	100.0%;	Pred. No.	2.2e+02;		
	Matches	21;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0
Oy	4463 CTTTCTTTTTTTTTTTTTTTT	4463				
Db	1 CTTTTTTTTTTTTTTTTTTT	21				
	RESULT 173					
ID	AAAS7856 standard; DNA; 28 BP.					
XX	AAAS7856;					
AC						
XX						
DT	11-OCT-2000 (first entry)					
XX						
DE	Deoxy-TT2-tagged substrate oligonucleotide.					
XX						
KW	Ribozyme; catalytic RNA; analyte detection; effector molecule;					
KM	nucleic acid substrate; in vitro selection; ribozyme ligase;					
KV	conformation dependent activity; allosteric activation; ss.					
XX						
OS	Synthetic.					
XX						
FH	Key	Location/Qualifiers				
FT	misc_RNA	23..28				
FT		/tag= a				
FT	misc_binding	24..28				
FT		/tag= b				
FT		/bound_moiety= "Bases 13-17 of N90 RNA pool (AAAS7851)"				
FN						
MO	WO200024931-AZ.					
PD						
XX	04-MAY-2000.					
XX						
PE	22-OCT-1999; 99WO-IL000557.					
PR						
XX	23-OCT-1998; 98IL-00126731.					
PA	(INTE-) INTELIGENE LTD.					
Nathan A,	Ellington A;					
DR	WPI; 2000-350763/30.					
PT	Detecting an analyte in a sample comprises providing nucleic acid					
FT	sequence which is catalytically active in presence of analyte, contacting					
PS	sealytic nucleic acid with substrate and amplifying catalytic product.					
XX						
PS	Disclosure; Page; 36pp; English.					
CC						
CC	The invention relates to a method of detecting an analyte in a sample.					
CC	The method comprises providing a nucleic acid sequence which is initially					
CC	catalytically inactive, but which becomes catalytically active in the					
CC	presence of an analyte (the effector); providing a nucleic acid substrate					
CC	for the catalytic activity of the nucleic acid sequence; and contacting					
CC	the nucleic acid sequence and the substrate with the sample under					
CC	conditions allowing catalytic activity of nucleic acid sequences. The					
CC	catalytic nucleic acid sequence will be able to convert the nucleic acid					
CC	substrate into a nucleic acid product only if the analyte of interest is					
CC	present. The nucleic acid catalytic product is then amplified, and a					
CC	significant increase in the amount of product indicates the presence of					
CC	the analyte in the sample. The method is useful for the qualitative or					
CC	quantitative determination of an analyte in a sample in diagnostic					
CC	assays. The invention describes the in vitro selection of a ribozyme					
CC	ligase (Il), AAAS7859, AAAS7860) which is catalytically active only in the					
CC	presence of an oligonucleotide effector (AAAS7854). The Il ribozyme					
CC	ligase was selected from a pool of RNA molecules comprising a central					
CC	randomised region 90 nucleotides in length flanked on both sides by					
CC	constant sequence regions (the N90 RNA pool; AAAS7851). In the presence					
CC	of the effector, selection was performed using one of the tagged					
CC	substrate molecules AAAS7855-AA7857. RNAs with ligase activity (i.e.,					

CC	those which have become ligated to the substrate molecule) were reverse
CC	transcribed using the effector oligo, and then PCR amplified using the
CC	effector and a DNA primer identical in sequence to the substrate used for
CC	the selection. A ribozyme ligase, Ll, was selected via this procedure. Ll
CC	can only adopt its active conformation (AAAs7859) in the presence of the
CC	effector oligo (analyte). In the absence of the effector, Ll adopts an
CC	inactive conformation (AAAs7860). The present sequence represents the
CC	deoxy-722-tagged substrate oligonucleotide. The dr22 tag enables
CC	successfully ligated products to be isolated using oligo(dA) cellulose
CC	Type 7. Note: The present sequence is not given in the specification, but
CC	is created from the information given on page 11
SQ	Sequence 28 BP; 1 A; 2 C; 1 G; 22 T; 2 U; 0 Other;
OY	Query Match 0.3%; Score 21; DB 1; Length 28; Best Local Similarity 95.2%; Pred. No. 3e+02; Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0
DB	4464 TTTTTCCTTTTTTTTTTTTTTG 4484 4 TTTTTCCTTTTTTTTTTTUG 24
XX	RESULT 174
XX	AAQ68614/C
XX	ID AAQ68614 standard; cDNA; 29 BP.
XX	AC AAQ68614;
XX	MT 25-MAR-2003 (revised)
XX	DT 19-JAN-1995 (first entry)
XX	DE tRNApolyU reverse crna primer.
KM	cDNA; RNA template; reverse-transcriptase; primer; tRNApolyU;
KM	tRNA template; pUC18; ss.
OS	Synthetic.
PN	WO9413669-A1.
PD	23-JUN-1994.
XX	PF 09-DEC-1993; 93WO-US012029.
PR	XX 09-DEC-1992; 92US-00989851.
PA	(MILL/) MILLER J E.
PI	Miller JE;
DR	WPI; 1994-217796/26.
PT	In vivo cDNA synthesis - by using synthetic polynucleotide(s) which bind
PT	in vivo to RNA templates as primers for reverse transcriptase.
PS	Example 1; Page 33; 102pp; English.
CC	DNA encoding the modified crna primer: tRNApolyU (AAQ68616), was obtained
CC	using the primer pair given in AAQ68612-13. The DNA was cloned in pUC18.
CC	PCR was used to amplify a promoter-crna-polyU fragment and to define the
CC	end of the tRNApolyU coding template. A reverse crna primer (AAQ68614)
CC	was used. The 5' base of this primer was also the last 3' base of the
CC	encoded tRNApolyU template, as shown in AAQ68617. For in vitro production
CC	of tRNApolyU, a DraI-sensitive T7-tRNApolyU cassette was linearized and
CC	used as template for in vitro transcription using oligomers AAQ68612 and
CC	AAQ68515. The crna primer is used for in vivo cDNA synthesis. (Updated on
CC	25-MAR-2003 to correct PN field.)
SQ	Sequence 29 BP; 22 A; 3 C; 4 G; 0 T; 0 U; 0 Other;
OY	Query Match 0.3%; Score 21; DB 1; Length 29; Best Local Similarity 100.0%; Pred. No. 3.2e+02;

PT polymorphic probability.
XX
PS Example; Col 1163; 588pp; English.
XX
CC The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a
CC candidate polymorphic repeat. The computational method (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX19676-ABX80022 are
CC the polymorphic repeats identified for a search of human ESTs
XX
SQ Sequence 30 BP; 1 A; 9 C; 20 G; 0 T; 0 U; 0 Other;
XX
QY Query Match 0.3%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 3.3e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
DB 52 GGGCGGCAAGGAGGCTGGCGGCGGCGG 80
1 GGGCGCGCGCGCGCGCGCGCGGCGGCGG 29
XX
RESULT 184
AAL61658/c
ID AAL61658 standard; DNA; 30 BP.
XX
AC AAL61658;
XX
DT 22-SEP-2003 (first entry)
XX
DE Oligonucleotide #19 used in the nucleic acid detection method.
XX
KW Nucleic acid detection; fabrication; ss.
XX
OS Unidentified.
XX
PN WO2003035829-A2.
XX
PD 01-MAY-2003.
XX
PF 08-OCT-2002; 2002WO-US032088.
XX
PR 09-OCT-2001; 2001US-0327864P.
XX
PR 07-DEC-2001; 2001US-00008978.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Park S, Taton TA, Mirkin CA;
XX
DR WPI; 2003-430409/40.
XX
PT Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change.
XX
PS Example 24; Fig 44; 467pp; English.
XX
CC The invention relates to a method of detecting a nucleic acid having two
CC portions. The method involves providing nanoparticles having
CC oligonucleotides attached to it which has a sequence complementary to
CC sequence of two portions of nucleic acid, contacting nucleic acid and
CC nanoparticles to allow hybridisation of oligonucleotides with two or more
CC portions of nucleic acid and observing a detectable change brought about
CC by hybridisation. The method and aggregate probes are useful for

CC detecting two or more nucleic acids (from a biological source) having at
CC least two portions such as viral RNA, bacterial or fungal DNA, a gene
CC associated with a disease, synthetic or structurally modified natural or
CC synthetic RNA or DNA, or a product of a polymerase chain reaction
CC amplification. The invention is useful for preparing a nanoprobe
CC conjugate for detecting an analyte and for detecting a nucleic acid bound
CC to an electrode surface. It is also useful for fabrication and for
CC separating a selected nucleic acid having two portions from other nucleic
CC acids. The present sequence is an oligo used to illustrate the method of
CC the invention
XX
SQ Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
XX
QY Query Match 0.3%; Score 21; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
DB 4463 CTTTCTTTCTTTCTTTCTTTCTTTT 4463
21 CTTTCTTTCTTTCTTTCTTTCTTTT 1
XX
RESULT 185
ABX89953
ID ABX89953 standard; DNA; 30 BP.
XX
AC ABX89953;
XX
DT 30-APR-2003 (first entry)
XX
DE PolYA adapter DNA.
XX
KW Probe; detection; genotyping; cell status; chromosomal resistance gene;
XX array; ss.
XX
OS Synthetic.
XX
PN DE10117857-A1.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2001; 2001DE-01017857.
XX
PR 10-APR-2001; 2001DE-01017857.
XX
PA (CLON-) CLONDIAG CHIP TECHNOLOGIES GMBH.
XX
PI Ellinger T, Ehrlich R, Wagenhaus A, Ermantraut E;
XX
DR WPI; 2003-068801/07.
XX
PT Detecting specific interactions between molecular targets and probes,
PT useful for determining genotypic and physiological status of cells, by
PT attaching an markable adapter to the target.
XX
PS Example 1; Page 8; 25pp; German.
XX
CC This invention describes a novel method for detecting the specific
CC interaction between a target sequence, especially a nucleic acid, and a
CC probe on an array, in which adapter molecules are fixed to the target,
CC forming a continuous sequence. Labeling of the target is independently
CC mediated by interaction of the adapter molecule with a label. The method
CC is used to investigate the genotypic and physiological status of cells,
CC e.g. to detect chromosomal resistance genes in *Staphylococcus aureus*. The
CC method provides a modular, specific and sensitive system for quantitative
CC or qualitative detection of a specific target. It provides efficient,
CC homogeneous and parallel labeling of a target, before, during or after
CC interaction with the probe array, and both DNA and RNA can be labeled.
CC The detection signal may be amplified and only low concentrations of
CC label (particularly 0.1-1 micro M) are used, so non-specific signals are
CC minimised. This sequence represents a polYA adapter used in the method
CC described in the invention
XX

SO Sequence 30 BP; 5 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.3%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 3.3e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTGCTTGAGA 4492
1 TTTTCTTTTCTTTTCTTTATATATA 29

RESULT 186

AAI29951
ID AAI29951 standard; DNA; 31 BP.

AC AAI29951;

DT 18-OCT-2001 (first entry)

DE Human single nucleotide polymorphism (SNP) SATB1 3.

KM Human; resequence; genotype; disease; forensic; paternity testing;

XX single nucleotide polymorphism; SNP; ss.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Variation replace(16,G)

FT /*tag= a /standard_name= "single nucleotide polymorphism"

PN WO200166800-A2.

XX 13-SEP-2001.

PD 07-MAR-2001; 2001WO-US007268.

PF 07-MAR-2000; 2000US-0187510P.

PR 22-MAY-2000; 2000US-0206129P.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX Cargill M, Ireland JS, Lander ES;

XX DR WPI; 2001-522952/57.

PT Nucleic acid molecules from the human genome which include polymorphic sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype.

XX Claim 1; Page 58; 145pp; English.

XX The invention relates to the identification of nucleic acid molecules (AAI29513-AAI3114) from the human genome which include polymorphic sites which can predispose individuals to disease. Various genes from a number of individuals were resequenced and single nucleotide polymorphisms (SNPs) in these genes discovered. The method is useful for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype. The nucleic acids containing the polymorphic sites may be useful in forensics and paternity testing

XX Sequence 31 BP; 8 A; 13 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 21; DB 1; Length 31;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7413 CAGCAGCAGCAGCAGCAGCAG 7433

DB 1 CAGCAGCAGCAGCAGCAGCAG 21

RESULT 187

AAV03988
ID AAV03988 standard; DNA; 32 BP.

AC AAV03988;

DT 13-MAY-1998 (first entry)

DE Primer B for Non-A non-B hepatitis viral peptide coding sequence.

KM Non-A non-B hepatitis virus; antibody production; infection diagnosis;

XX PCR primer; amplify; ss.

XX Synthetic.

XX Hepatitis virus.

XX JP04084887-A.

PD 18-MAR-1992.

PF 25-JUL-1990; 90JP-00198588.

PR 25-JUL-1990; 90JP-00198588.

XX (KAGA) KAGAKU OYOBI KESSEI RYOHO.

XX WPI; 1992-145501/18.

PT Nucleic acid fragment coding peptide of non-A non-B hepatitis virus - for the early diagnosis of non-A non-B hepatitis by ELISA or agglutination methods.

XX Example 2; Page 7; 12pp; Japanese.

XX This sequence represents a primer for the coding sequence for a non-A non-B hepatitis virus peptide. The protein encoded by the amplified sequence can be used to prepare an antibody specific for non-A non-B hepatitis

XX CC virus. The peptide and antibody can be used in both ELISA and agglutination methods and is useful in the early diagnosis of non-A non-B hepatitis

XX Sequence 32 BP; 1 A; 5 C; 5 G; 21 T; 0 U; 0 Other;

Query Match 0.3%; Score 21; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4463 CTTTCTTTTCTTTTCTTTT 4483
12 CTTTCTTTTCTTTTCTTTT 32

RESULT 188

AAI77235
ID AAI77235 standard; DNA; 32 BP.

AC AAI77235;

DT 12-FEB-1998 (first entry)

DE Rat fibroblast growth factor FGF-10 RACE primer X.

KM Fibroblast growth factor; rat; human; recombinant DNA; bone disease;

XX wound healing; cartilage; RACE primer; ss.

XX Synthetic.

XX Rattus rattus.

XX WO9720929-A1.

XX PD 12-JUN-1997.

```

PF 06-DEC-1996; 96WO-JP003579.
XX
PR 07-DEC-1995; 95JP-00345689.
PR 28-MAR-1996; 96JP-00103240.
PR 24-JUL-1996; 96JP-00214378.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
XX
PI Itoh N, Negoro T, Katsumata T, Tagashira S;
XX
DR WPI; 1997-319776/29.
XX
PT Recombinant fibroblast growth factor FGF-10 and related DNA - useful for
XX the treatment of bone disease and for wound healing.
PS Example 1; Page 36; 51pp; Japanese.
XX
CC The present sequence represents a RACE primer involved in the
CC amplification of rat fibroblast growth factor FGF-10. Recombinant FGF-10,
CC vectors, containing the DNA, and host cells, containing the vectors, are
CC useful for the recombinant production of FGF-10. The recombinant FGF-10
CC is useful for the treatment of diseases and injury of bone or cartilage,
CC and as a wound healing promoter.
XX
SQ Sequence 32 BP; 3 A; 4 C; 4 G; 21 T; 0 U; 0 Other;

Query Match          0.3%; Score 21; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4463 CTTTTTTTTTTTTTTTTTTT 4483
DB 12 CTTTTTTTTTTTTTTTTTTT 32

RESULT 189
AAF60568
ID AAF60568 standard; DNA; 32 BP.
XX
AC AAF60568;
XX
DT 27-APR-2001 (first entry)
XX
DE Neuraminidase PCR primer #6.
XX
KM PCR primer; virucide; vaccine; gene therapy; neuraminidase; vaccine;
XX immune response; ss.
XX
OS Influenza virus.
XX
PN WO200109291-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-GB002933.
XX
PR 30-JUL-1999; 99GB-00017981.
PR 30-JUL-1999; 99US-0146145P.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Brownlee GG, Fodor E, Poon L;
XX
DR WPI; 2001-159859/16.
XX
PT New negative-sense single stranded RNA virus, e.g. influenza virus,
XX attenuated by replacing the poly U track with a poly A track, useful as a
XX vaccine and in gene therapy.
PS Example 7; Page 28; 49pp; English.
XX
CC The present invention relates to an attenuated influenza virus. The virus
CC is attenuated by replacement of the poly U track in a genomic nucleic

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```

CC acid by a poly A track capable of being copied to provide a poly U tail
CC for mRNA transcribed from the nucleic acid. The attenuated virus is
CC useful as a vaccine, for immunisation against diseases caused by the
CC equivalent wild type viruses. The present sequence is a PCR primer used
CC to generate the virus of the present invention
XX
SQ Sequence 32 BP; 1 A; 6 C; 4 G; 21 T; 0 U; 0 Other;

Query Match          0.3%; Score 21; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4463 CTTTTTTTTTTTTTTTTTTT 4483
DB 12 CTTTTTTTTTTTTTTTTTTT 32

RESULT 190
AAF60569/C
ID AAF60569 standard; DNA; 32 BP.
XX
AC AAF60569;
XX
DT 27-APR-2001 (first entry)
XX
DE Neuraminidase PCR primer #7.
XX
KM PCR primer; virucide; vaccine; gene therapy; neuraminidase; vaccine;
XX immune response; ss.
XX
OS Influenza virus.
XX
PN WO200109291-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-GB002933.
XX
PR 30-JUL-1999; 99GB-00017981.
PR 30-JUL-1999; 99US-0146145P.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Brownlee GG, Fodor E, Poon L;
XX
DR WPI; 2001-159859/16.
XX
PT New negative-sense single stranded RNA virus, e.g. influenza virus,
XX attenuated by replacing the poly U track with a poly A track, useful as a
XX vaccine and in gene therapy.
PS Example 7; Page 28; 49pp; English.
XX
CC The present invention relates to an attenuated influenza virus. The virus
CC is attenuated by replacement of the poly U track in a genomic nucleic
CC acid by a poly A track capable of being copied to provide a poly U tail
CC for mRNA transcribed from the nucleic acid. The attenuated virus is
CC useful as a vaccine, for immunisation against diseases caused by the
CC equivalent wild type viruses. The present sequence is a PCR primer used
CC to generate the virus of the present invention
XX
SQ Sequence 32 BP; 21 A; 6 C; 4 G; 1 T; 0 U; 0 Other;

Query Match          0.3%; Score 21; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTTTTTG 4484
DB 32 TTTTTTTTTTTTTTTTTTTG 12

RESULT 191

```

AA	T9	92	86	/C	AA	T9	92	86	standard; DNA; 24	BP.
ID	AA	T9	92	86	standard; DNA; 24	BP.				
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
AC	AA	T9	92	86						
DT	15	-APR	-1998	(first entry)						
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
DE	POLYA, a competitor oligonucleotide for binding human PUR-alpha.									
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
KW	PUR element; human; C-myc; inhibitor; hyperproliferative disease; ss;									
XX	cancer; probe; hybridisation.									
OS	Synthetic.									
XX	Homo sapiens.									
PN	US5672479-A.									
PD	30-SEP-1997.									
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
PF	07-JUN-1995; 95US-00486421.									
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
PR	28-AUG-1992; 92US-00938189.									
PR	02-FEB-1993; 93US-0004943.									
PR	06-JUN-1995; 95US-00470911.									
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
PA	(MOUN) MOUNT SINAI SCHOOL MEDICINE.									
PI	Bergemann AD, Johnson EM;									
DR	WPI, 1997-48859/45.									
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
PT	Assays for PUR protein ligands or modulators - using immobilised PUR									
XX	protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.									
PS	Example; Col 33; 64pp; English.									
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
CC	The oligonucleotides AAT9279-T99286 were used as competitor									
CC	oligonucleotides for the binding of PUR protein to DNA. The PUR sequence									
CC	can be used to identify chemical or biological compounds that bind to PUR									
CC	or binding fragments of PUR. Inhibitors of PUR activity may be used to									
XX	treat hyperproliferative diseases such as cancer									
SO	Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;									
QY	4464 TTTT	TTTT	TTTT	TTTT	TTTT	TGCT	4487			
DB	24 TTTT	TTTT	TTTT	TTTT	TTTT	TTTT	1			
RESULT 192										
AAV31743/C										
ID	AAV31743	standard; DNA; 24	BP.							
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
AC	AAV31743;									
DT	24-SEP-1998	(first entry)								
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
DE	Nucleotide sequence of the oligonucleotide POLYA.									
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
KW	PUR-alpha gene; inhibition; viral infection; cancer; PUR element;									
XX	hyperproliferative disease; ss.									
OS	Synthetic.									
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
PN	US5756684-A.									
PD	26-MAY-1998.									
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
PF	06-JUN-1995; 95US-00470911.									

```

XX XX 28-AUG-1992; 92US-00938189.
PR PR 02-FEB-1993; 93US-00014943.
XX XX
PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX XX
PI Bergemann AD, Johnson EM;
XX XX WPI; 1998-321632/28.
DR DR
PT PUR protein and its fragments - that inhibit PUR protein binding to PUR
PT element or other proteins.
XX XX
PS Example 7.1.1; Col 33; 63pp; English.
CC CC This is the nucleotide sequence of an oligonucleotide used as a
CC competitor with the PUR element in the method of the invention, involving
CC the use of the PUR protein and its fragments, which inhibit PUR protein
CC binding to PUR element or other proteins. Inhibitors of PUR activity may
CC be useful for treating viral infections and hyperproliferative diseases
CC such as cancer
XX XX
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2.6e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT TTTTTTTTTTTTTTTTGTCG 4487
DB 24 TTTTTTTTTTTTTTTTTTTTTT 1

RESULT 193
AAAX04086/c
ID AAAX04086 standard; DNA; 24 BP.
XX AC
XX AAAX04086;
DT 12-APR-1999 (first entry)
XX
DE Oligonucleotide POLYA used in PUR cloning and sequencing.
XX
KW PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
KM monoclonal antibody; identification; characterisation; ss.
OS Synthetic.
OS Homo sapiens.
XX
PN US5869622-A.
PN
PD 09-FEB-1999.
XX
PF 07-JUN-1995; 95US-00486809.
XX
PR 28-AUG-1992; 92US-00938189.
PR 02-FEB-1993; 93US-00014943.
PR 06-JUN-1995; 95US-00470911.
XX
PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
PI Bergemann AD, Johnson EM;
XX
DR WPI; 1999-152881/13.
XX
PT Monoclonal antibody specific for PUR protein - useful for treating
PT cancer.
XX
PS Example; Col 33; 64pp; English.

```


XX	immunostimulatory; tumour; viral infection; bacterial infection;
KW	fungal infection; parasitic infection; cancer; asthma;
XX	infectious disease; allergy; immune deficiency; phosphorothioate; ss.
OS	Synthetic.
XX	
XX	WO200122972-A2.
XX	
XX	05-APR-2001.
XX	
XX	25-SEP-2000; 2000WO-US026383.
XX	
XX	25-SEP-1999; 99US-0156113P.
PR	27-SEP-1999; 99US-0156135P.
PR	23-AUG-2000; 2000US-0227436P.
XX	
PA	(IOWA) UNIV IOWA RES FOUND.
PA	(COLE-) COLEY PHARM GMEH.
XX	
XX	Krieg AM, Schetter C, Vollmer J;
XX	
XX	WPI, 2001-273485/28.
XX	
XX	Vaccinating against tumors, infectious diseases, allergies and asthma
PT	using immunostimulatory Py-rich and TG nucleic acids.
XX	
XX	Claim 101; Page 57; 338pp; English.
XX	
XX	The present invention relates to a method for stimulating an immune
CC	response. The method comprises administering an immunostimulatory nucleic
CC	acid to a non-rodent subject in sufficient quantity to stimulate an
CC	immune response. The present sequence is one such immunostimulatory
CC	nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC	(py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC	against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC	and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC	haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC	staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC	also useful for preventing cancer, asthma, infectious disease, allergy or
CC	immune deficiency. The present sequence can also be used to redirect a
CC	Th2 to a Th1 immune response and to activate immune cells. Note: the
CC	present sequence may have a phosphorothioate backbone
XX	
XX	Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
XX	
XX	
XX	Query Match 0.3%; Score 20.8; DB 1; Length 24;
XX	Best Local Similarity 91.7%; Pred. No. 2.6e+02;
XX	Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX	
Qy	4464 TTTTTTTTTTTTTTTTTTGTCT 4487
DB	1 TTTTTTTTTTTTTTTTTTTTTTTT 24
XX	
XX	RESULT 197
XX	AAFA99304
ID	AAFA99304 standard; DNA; 24 BP.
XX	
AC	AAFA99304;
XX	
DT	12-JUN-2001 (first entry)
XX	
DE	Immunostimulatory nucleic acid #420.
XX	
XX	Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW	immunostimulatory; tumour; viral infection; bacterial infection;
KW	fungal infection; parasitic infection; cancer; asthma;
KW	infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX	
OS	Synthetic.
XX	
XX	WO200122972-A2.
XX	

```

PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-USO26383.
XX
XX   25-SEP-1999;    99US-0156113P.
PR   27-SEP-1999;    99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMSB.
XX
PI   Krieg AM, Schetter C, Volmer J;
XX
XX   WPI; 2001-273485/28.
XX
XX   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Claim 101, Page 46; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
      Query Match          0.3%; Score 20.8; DB 1; Length 24;
      Best Local Similarity 91.7%; Pred. No. 2.6e+02;
      Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY     4464 TTTTTTTTTTTTTTTTTTTGCTCT 4487
DB       1 TTTTTTTTTTTTTTTTTTTTTT 24
RESULT 198
AAF99757/C
ID      AAF99757 standard; DNA; 24 BP.
XX
AC      AAF99757;
XX
DT      12-JUN-2001 (first entry)
DE      Immunostimulatory nucleic acid #873.
XX
XX      Immunostimulatory nucleic acid #873.
XX
XX      Vaccine: cytotoxic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW      immunostimulatory; tumor; viral infection; bacterial infection;
KW      fungal infection; parasitic infection; cancer; asthma;
XX      infectious disease; allergy; immune deficiency; phosphorothioate; ss.
OS      Synthetic.
XX
PN      WO200122972-A2.
XX
PD      05-APR-2001.
XX
PF      25-SEP-2000; 2000WO-USO26383.
XX
XX      25-SEP-1999;    99US-0156113P.
PR      27-SEP-1999;    99US-0156135P.
PR      23-AUG-2000; 2000US-0227436P.
XX
```


CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Weber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophilic joints, angiodiroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention

SO Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2.6e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT GCT 4487
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 24

RESULT 201
ABS77949 standard; DNA; 24 BP.

XX ABS77949;
XX
XX 13-DEC-2002 (first entry)
XX
XX
DE Angiogenesis inhibitory oligonucleotide #433.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
XX diabetic retinopathy; retinopathy of prematurity; macular degeneration;
XX corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
XX rubeosis; Osler-Weber Syndrome; myocardial angiogenesis;
XX plaque neovascularisation; telangiectasia; haemophilic joint;
XX angiodiroma; wound granulation; intestinal adhesion; atherosclerosis;
XX scleroderma; hypertrophic scar.

XX Synthetic.
XX
XX WO200253141-A2.
XX
XX 11-JUL-2002.
XX
XX 14-DEC-2001; 2001WO-US048458.
XX
XX 14-DEC-2000; 2000US-0255534P.
XX
XX (COLE-) COLEY PHARM GROUP INC.
XX
XX Bratzler RL;
XX
XX WPI; 2002-566690/60.
XX
XX Inhibiting angiogenesis in a subject, involves administering at least one
XX antiangiogenic nucleic acid molecule to the subject.

PS Claim 2; Page 27; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising
XX administering at least one antiangiogenic nucleic acid molecule. Also
XX included is a kit comprising a first container housing the antiangiogenic
XX nucleic acids, and instructions for administering them to a subject
XX having a condition characterised by unwanted angiogenesis. The method is
XX useful for inhibiting angiogenesis associated with solid tumour growth,
XX tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
XX diabetic retinopathy, retinopathy of prematurity, macular degeneration,
XX corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
XX rubeosis, Osler-Weber Syndrome, myocardial angiogenesis, plaque
XX neovascularisation, telangiectasia, haemophilic joints, angiodiroma,
XX wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
XX hypertrophic scars. The present sequence is an antiangiogenic nucleic
XX acid of the invention

SO Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.3%; Score 20.8; DB 1; Length 24;

CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention

SO Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2.6e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT GCT 4487
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 24

RESULT 202
ABS78478/C

ID ABS78478 standard; DNA; 24 BP.

XX ABS78478;
XX
XX 13-DEC-2002 (first entry)
XX
XX
DE Angiogenesis inhibitory oligonucleotide #962.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
XX diabetic retinopathy; retinopathy of prematurity; macular degeneration;
XX corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
XX rubeosis; Osler-Weber Syndrome; myocardial angiogenesis;
XX plaque neovascularisation; telangiectasia; haemophilic joint;
XX angiodiroma; wound granulation; intestinal adhesion; atherosclerosis;
XX scleroderma; hypertrophic scar.

XX Synthetic.
XX
XX WO200253141-A2.
XX
XX 11-JUL-2002.
XX
XX 14-DEC-2001; 2001WO-US048458.
XX
XX 14-DEC-2000; 2000US-0255534P.
XX
XX (COLE-) COLEY PHARM GROUP INC.
XX
XX Bratzler RL;
XX
XX WPI; 2002-566690/60.
XX
XX Inhibiting angiogenesis in a subject, involves administering at least one
XX antiangiogenic nucleic acid molecule to the subject.

PS Claim 2; Page 36; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising
XX administering at least one antiangiogenic nucleic acid molecule. Also
XX included is a kit comprising a first container housing the antiangiogenic
XX nucleic acids, and instructions for administering them to a subject
XX having a condition characterised by unwanted angiogenesis. The method is
XX useful for inhibiting angiogenesis associated with solid tumour growth,
XX tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
XX diabetic retinopathy, retinopathy of prematurity, macular degeneration,
XX corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
XX rubeosis, Osler-Weber Syndrome, myocardial angiogenesis, plaque
XX neovascularisation, telangiectasia, haemophilic joints, angiodiroma,
XX wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
XX hypertrophic scars. The present sequence is an antiangiogenic nucleic
XX acid of the invention

SO Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 20.8; DB 1; Length 24;


```

XX 24-JUN-2003.
PD
XX
PF 11-MAY-2001; 2001US-00854317.
XX
XX 11-MAY-2001; 2001US-00854317.
XX
XX 11-MAY-2001; 2001US-00854317.
XX
XX (AFFY-) AFFYMETRIX INC.
XX
XX Su X, Dong H, Ryder TB;
XX
XX WPI; 2003-656427/62.
XX
XX Amplification of nucleic acids, where the promoter is blocked from
XX extension at the 3' end, useful for eliminating multiple step reactions.
XX
XX Disclosure; Fig 2; 9pp; English.
XX
XX The invention relates to a method of amplification of nucleic acid which
XX comprises primer extension by reverse transcriptase and hybridising an
XX oligonucleotide to the single stranded DNA, where the oligonucleotide is
XX blocked from extension at the 3' end. The method is useful for
XX amplification of nucleic acids. In the new method, a promoter is
XX protected from degradation throughout the method. The promoter is
XX constructed so that it does not serve as a primer for extension of a
XX sequence that is complementary to the target sequence, i.e. it is
XX blocked. The method can be combined with other processes to eliminate the
XX need for multiple steps and varying reaction conditions and their
XX associated problems. At least three otherwise separate enzymatic
XX reactions can occur consecutively in one phase (i.e., without organic
XX extraction and precipitation), more preferably in the same reaction
XX vessel. Preferably, cDNA synthesis according to the new method may occur
XX in a modified low salt buffer. The present sequence represents the poly A
XX tract of a mRNA used to illustrate the method of the invention.
XX
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2.6e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 4464 TTTT TTTT TTTT TTTT TTTT TTTT GCT 4487
Db 24 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 214
ADB37258
ID ADB37258 standard; DNA; 24 BP.
XX
XX ADB37258;
XX
XX 04-DEC-2003 (first entry)
XX
XX Immunostimulatory nucleic acid #872.
XX
XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
XX hypo-responsive subject; immunostimulatory.
XX
XX Synthetic.
XX
XX US2003087848-A1.
XX
XX 08-MAY-2003.
XX
XX 02-FEB-2001; 2001US-00776479.
XX
XX 03-FEB-2000; 2000US-0179991P.
XX
XX (BRAT/) BRATZLER R L.
XX (PETE/) PETERSEN D M.
XX (FOUR/) FOURON Y.
XX

```

XX	PI	Bratzler RL, Petersen DM, Fouron Y;
XX	DR	WPI; 2003-657977/62.
XX	PT	Treating and/or preventing allergy or asthma using an immunostimulatory
XX	PT	nucleic acid alone or in combination with an asthma/allergy medicament.
XX	PS	Disclosure; Page 18; 221pp; English.
XX	CC	The invention relates to a method of treating or preventing allergy or
XX	CC	asthma which comprises administering to a subject a poly-G nucleic acid
XX	CC	in an aerosol formulation. The methods and compositions of the present
XX	CC	invention are useful for diagnosing and/or treating asthma and allergy
XX	CC	especially in a hypo-responsive subject. The present sequence represents
XX	CC	an immunostimulatory nucleic acid of the invention.
XX	SEQ	Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
XX	Query Match	0.3%; Score 20.8; DB 1; Length 24;
XX	Best Local Similarity	91.7%; Pred. No. 2.6e+02;
XX	Matches 22; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
XX	QY	4464 TTTT TTTT TTTT TTTT TTTT TTTT GCT 4487
XX	DB	1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 24
XX	RESULT 215	
XX	ADB36806	
XX	ID	ADB36806 standard; DNA; 24 BP.
XX	AC	ADB36806;
XX	DT	04-DEC-2003 (first entry)
XX	DE	Immunostimulatory nucleic acid #420.
XX	XX	de; allergy; asthma; poly-G nucleic acid; aerosol formulation;
XX	XX	hypo-responsive subject; immunostimulatory.
XX	XX	Synthetic.
XX	XX	US2003087848-A1.
XX	XX	08-MAY-2003.
XX	XX	02-FEB-2001; 2001US-00776479.
XX	XX	03-FEB-2000; 2000US-0179991P.
XX	XX	(BRATZLER R L.
XX	XX	(PETE/) PETERSEN D M.
XX	XX	(FOUR/) FOURON Y.
XX	XX	Bratzler RL, Petersen DM, Fouron Y;
XX	XX	WPI; 2003-657977/62.
XX	XX	Treating and/or preventing allergy or asthma using an immunostimulatory
XX	XX	nucleic acid alone or in combination with an asthma/allergy medicament.
XX	XX	Disclosure; Page 11; 221pp; English.
XX	XX	The invention relates to a method of treating or preventing allergy or
XX	XX	asthma which comprises administering to a subject a poly-G nucleic acid
XX	XX	in an aerosol formulation. The methods and compositions of the present
XX	XX	invention are useful for diagnosing and/or treating asthma and allergy
XX	XX	especially in a hypo-responsive subject. The present sequence represents
XX	XX	an immunostimulatory nucleic acid of the invention.
XX	XX	Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
XX	XX	0.3%; Score 20.8; DB 1; Length 24;


```

FT      /mod_base= OTHER
PT      /note= "optional biotin label"
XX
XX
XX      WO2003066817-A2.
XX
XX      14-AUG-2003.
XX
XX      06-FEB-2003; 2003WO-US003533.
XX
XX      06-FEB-2002; 2002US-0355374P.
XX
XX      (AMSH ) AMERSHAM BIOSCIENCES AB.
XX
XX      Xia J;
XX
XX      WPI; 2003-697450/66.
XX
XX      Detecting nucleic acid targets, useful e.g. for diagnosing single
PT      nucleotide polymorphisms, by extension of capture probe complementary to
PT      open circle probe.
XX
XX      Example 1; Fig 5; 66pp; English.
XX
XX      The invention is directed to novel methods of amplifying and detecting
XX      DNA using rolling circle amplification (RCA). The invention relates to
XX      detecting a target sequence (I1), which involves using a capture probe
XX      (CP) that is complementary to an open circle probe and includes a
XX      cleavage site. The method comprises: attaching a capture probe (CP) to a
XX      substrate, at both ends, where the CP includes one domain complementary
XX      to an OCP (open circle probe) and a second domain that contains a
XX      cleavage site (CS), to form a device; treating CP with (I1) and OCP for
XX      form a hybridisation complex (HC); treating HC with a ligase so that OCP
XX      is circularised, forming a second complex (HC2); treating CP with a
XX      cleavage agent, to cut at CS, and adding an extension enzyme (EE) and
XX      nucleotide triphosphates (NTPs) to form an extended CP, which is
XX      detected. The method is used for detecting (I1) that comprises two target
XX      domains (TD1, TD2) and (I1) that comprises two adjacent target domains.
XX      The method is used for detection, genotyping and/or quantification of
XX      target sequences, for research, clinical use, quality control or field
XX      testing, particularly detection of single-nucleotide polymorphisms. The
XX      method permits a high level of multiplexing, and since it provides
XX      localized, product detection, with linear kinetics, is sensitive enough
XX      for direct detection and quantitation of unmodified targets. The present
XX      sequence is that of a single base extension (SBE) probe used in SNP
XX      genotyping with RCA signal amplification to demonstrate the method of the
XX      invention.
XX
XX      Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
SQ
XX
XX      Query Match      0.3%; Score 20.8; DB 1; Length 24;
XX      Best Local Similarity 91.7%; Pred. NO. 2.6e+02;
XX      Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      4464 TTTTTTTTTTTTTTTTTTTTTGTCCT 4487
XX      |||||||
XX      1 TTTTTTTTTTTTTTTTTTTTTTTT 24
XX
XX      RESULT 219
XX      AAX84259
XX      ID AAX84259 standard; DNA; 25 BP.
XX
XX      AAX84259;
XX
XX      08-SEP-1999 (first entry)
XX
XX      PCR primer for human Nck associated protein 1 coding sequence.
XX
XX      Nck associated protein 1; Napi; human; apoptosis; Alzheimer's disease;
XX      therapy; PCR primer; ss.
XX
XX      Synthetic.
XX      Homo sapiens
XX

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XX      MN      WO9931239-A1.
XX      PD      24-JUN-1999.
XX
XX      PF      14-DEC-1998;      98WO-JP005646.
XX
XX      PR      15-DEC-1997;      97JP-00363183.
XX
XX      PA      (KYOW ) KYOWA HAKKO KOGYO KK.
XX      PA      (SAKA/) SAKAKI Y.
XX
XX      PI      Sakaki Y;
XX
XX      DR      WPI; 1999-395181/33.
XX
XX      PT      Protein inhibiting apoptosis, useful in the diagnosis and treatment of
XX      PT      Alzheimer's disease.
XX
XX      PS      Disclosure; Page 76; 90pp; Japanese.
XX
XX      CC      This sequence represents a PCR primer used to isolate DNA encoding the
XX      CC      human Nck associated protein 1 (Napi) of the invention. Napi inhibits
XX      CC      apoptosis. The protein can be used in the investigation, diagnosis and
XX      CC      treatment (e.g. by gene therapy) of Alzheimer's disease
XX
XX      SQ      Sequence 25 BP; 1 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
XX
XX      Query Match      0.3%; Score 20.8; DB 1; Length 25;
XX      Best Local Similarity 91.7%; Pred. NO. 2.8e+02;
XX      Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX      QY      4464 TTTTTTTTTTTTTTTTTTGTCT 4487
XX      DB      1 TTTTTTTTTTTTTTTTTTTTTT 24
XX
XX      RESULT 220
XX      AAH38515
XX      ID      AAH38515 standard; DNA; 25 BP.
XX
XX      AC      AAH38515;
XX
XX      DT      14-AUG-2001 (first entry)
XX
XX      DE      SNP specific SNPE primer SEQ ID 1311.
XX
XX      Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX      SNEP; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX      Leech-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX      polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX      acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX      inflammation; forensic investigation; paternity analysis; primer; ss.
XX
XX      OS      Homo sapiens.
XX
XX      PN      WO200129262-A2.
XX
XX      PD      26-APR-2001.
XX
XX      PF      13-OCT-2000; 2000WO-US028436.
XX
XX      PR      15-OCT-1999; 99US-0160096P.
XX
XX      PA      (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX      PI      Picoult-Newburg L, Pohl M;
XX
XX      DR      WPI; 2001-290930/30.
XX
XX      New genotyping oligonucleotide, useful for detecting the presence,
XX      PT      absence or identity of single polymnucleotide polymorphism in a nucleic
XX      PT      acid sample.

```

XX Claim 1; Page 56; 83pp; English.

PS
XX
CC Sequences AAH37205 - AAH0944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence

XX
SQ Sequence 25 BP; 1 A; 1 C; 0 G; 23 T; 0 U; 0 Other;

Query Match 0.3%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 2.8e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4462 ACTTTTCTTTTCTTTTCTTTTCTT 4485
DB 2 ATTTTCTTTTCTTTTCTTTTCTT 25

RESULT 221
ACF79235
ID ACF79235 standard; DNA; 25 BP.

XX
AC ACF79235;
XX
DT 04-DBC-2003 (first entry)

XX
DE Calix(a)arene-oligonucleotide hybrid.

XX
KM Calix(4)arene; triplex; gene therapy; DNA sensor; ss.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT stem_loop 1..25
FT /*tag= a
FT modified_base 13
FT /mod_base= OTHER
FT /note= "OTHER= calix(4)arene nucleoside"

XX
XX WO2003059925-A1.
XX
XX 24-JUL-2003.
XX
XX 19-JUN-2002; 2002WO-KR001160.
XX
XX 15-JAN-2002; 2002KR-00002316.
XX
XX (POST-) POSTECH FOUND.
XX
XX Kim BH, Kim SJ,
XX
XX

DR WPI; 2003-627375/59.

XX
XX
PT New calix(4)arene-nucleoside hybrid useful in gene therapy has at least
PT one nucleoside attached to a calix(4)arene group through amide bonding,
PT and is derived from a calix(4)arene having amino groups.

XX
XX
PS Claim 7; Page 20; 16pp; English.

XX
CC The present sequence is that of a calix(4)arene-oligonucleotide hybrid of
CC the invention, which includes a calix(4)arene-nucleoside (preferably
CC thymidine) derivative. The calix(4)arene-oligonucleotide hybrid functions
CC as a DNA hairpin structure mimic. It effectively recognises DNA or RNA
CC through triplex formation by bonding between the calix(4)arene-containing
CC cavity and a biologically active substance. The hybrid has a certain
CC level of both rigidity and flexibility, is stable in vivo, has high cell
CC permeability and can be mass-produced. It can be used as a DNA sensor or
CC for gene therapy

XX
SQ Sequence 25 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 1 Other;

Query Match 0.3%; Score 20.8; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 2.8e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTTCTT 4488
DB 1 TTTTCTTTTCTTTTCTTTTCTT 25

RESULT 222
AAL44903
ID AAL44903 standard; DNA; 29 BP.

XX
AC AAL44903;
XX
DT 05-AUG-2002 (first entry)

XX
DE Triplex forming oligonucleotide #4.

XX
KM Cancer; cytostatic; gene therapy; triplex forming oligonucleotide; ds.

XX
OS Unidentified.

XX
OS KR2001086830-A.

XX
PD 15-SEP-2001.

XX
XX 03-MAR-2000; 2000KR-00010744.

XX
XX 03-MAR-2000; 2000KR-00010744.

XX
XX (KOCH-) KOREA CHUNGANG EDUCATIONAL FOUND.

XX
PA Choi JG, Lee DH, Lee GY, Park GH, Park MG, Son JW,
PI WPI; 2002-233771/29.

XX
XX Novel triplex forming synthetic oligonucleotide, useful for gene therapy
PT of tumor.

XX
PS Claim 4; Page 11; 13pp; Korean.

XX
CC The present invention relates to a triplex forming oligonucleotide which
CC specifically binds to a specific gene. This is useful for the gene
CC therapy of cancer by binding itself to Auger electron emitters. The
CC present sequence is a triplex forming oligonucleotide of the invention

XX
SQ Sequence 29 BP; 0 A; 1 C; 3 G; 25 T; 0 U; 0 Other;

Query Match 0.3%; Score 20.8; DB 1; Length 29;
Best Local Similarity 91.7%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4465 TTTTGTGCTT 4488
DB 2 TTTTGTGCTT 25

RESULT 223

ID ADCl6682 standard; DNA; 30 BP.

AC ADCl6682;

DT 18-DEC-2003 (first entry)

DE Aminoacylation RNA molecule related DNA oligo. p3-2.

KW ribozyme; aminoacylate; tRNA; non-cognate; catalytic RNA molecule; cis;

KM aminoacylation; trans; proteomic; ds.

OS Unidentified.

PN WO2003070740-A1.

PD 28-AUG-2003.

PF 18-FEB-2003; 2003WO-US005007.

PR 15-FEB-2002; 2002US-0357424P.

PA (UNYNY) UNIV NEW YORK STATE RES FOUND.

PI Suga H, Murakami H, Saito H;

DR WPI; 2003-748198/70.

PT New polynucleotide, useful for preparing peptides containing non-cognate amino acids, encodes ribozyme that can aminoacylate tRNA with such amino acids.

PS Example 3; SEQ ID NO 42; 85bp; English.

XX The invention relates to a novel polynucleotide comprising a sequence encoding a ribozyme that can aminoacylate tRNA with a non-cognate amino acid. Ribozymes encoded by the polynucleotide of the invention are used to prepare polypeptides that contain non-cognate, including non-natural, amino acids. The invention more specifically provides catalytic RNA molecules having cis aminoacylation activity with a catalytic and aminoacylation domain, or an RNA molecule with trans aminoacylation activity with only a catalytic domain. The products of the invention are potentially useful for biomedical and therapeutic use, e.g. for probing the structure and function of proteins; preparation of peptide libraries and in proteomics. This polynucleotide sequence represents a DNA oligo CC relating to the RNA molecule with aminoacylation activity of the CC invention.

SO Sequence 30 BP; 3 A; 5 C; 1 G; 21 T; 0 U; 0 Other;

Query Match 0.3%; Score 20.8; DB 1; Length 30;

Best Local Similarity 91.7%; Pred. No. 3.6e+02;

Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTGCTT 4487
DB 1 TTTTGTGCTT 24

RESULT 224

ID AA130723 standard; DNA; 31 BP.

AC AA130723;

DT 18-OCT-2001 (first entry)

DE Human single nucleotide polymorphism (SNP) 175.

KW Human; resequence; genotype; disease; forensic; paternity testing;

OS Homo sapiens.

Key Location/Qualifiers
FT Variation replace(16,C)
FT FT /tag= a
XX /standard_name= "single nucleotide polymorphism"

PN WO200166800-A2.

PD 13-SEP-2001.

PF 07-MAR-2001; 2001WO-US007268.

PR 07-MAR-2000; 2000US-0187510P.

PR 22-MAY-2000; 2000US-0206129P.

PA (WHED) WHITEHEAD INST BIOMEDICAL RES.

PI Cargill M, Ireland JS, Lander ES;

DR WPI; 2001-522952/57.

PT Nucleic acid molecules from the human genome which include polymorphic sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype.

PS Claim 1; Page 103; 145pp; English.

XX The invention relates to the identification of nucleic acid molecules CC (AA199513-AA13114) from the human genome which include polymorphic sites CC which can predispose individuals to disease. Various genes from a number CC of individuals were resequenced and single nucleotide polymorphisms CC (SNPs) in these genes discovered. The method is useful for predicting the CC presence, absence or severity of a particular phenotype or disorder (e.g. CC diabetes) associated with a particular genotype. The nucleic acids CC containing the polymorphic sites may be useful in forensics and paternity CC testing

SO Sequence 31 BP; 3 A; 9 C; 12 G; 7 T; 0 U; 0 Other;

Query Match 0.3%; Score 20.8; DB 1; Length 31;

Best Local Similarity 91.7%; Pred. No. 3.8e+02;

Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7413 CAGCAGCAGCAGCAGCAGCAGCAGC 7436
DB 30 CAGCAGCAGCAGCAGCAGCAGCAGC 7

RESULT 225

ID AA43798 standard; DNA; 32 BP.

AC AA43798;

DT 30-OCT-1998 (first entry)

DE RT-PCR primer used in the course of the invention.

KW Gene expression; cloning vector; restriction endonuclease; RT-PCR;

OS Synthetic.

PN WO9831838-A1.

PD 23-UTL-1998.

XX 15-JAN-1998; 98WO-US000965.
 PF
 XX
 PR 15-JAN-1997; 97US-00784208.
 XX
 PA (CHUS) CHUGAI PHARM CO LTD.
 XX
 PI Spinella DG, Sajjadi FG;
 XX
 DR WPI; 1998-427566/36.
 XX
 PT Identifying gene expression patterns - by preparing cDNA from a mRNA
 PT population, cleaving with restriction endonuclease(s), inserting into
 PT hosts, amplification and obtaining tags.
 XX
 PS Disclosure; Page 21; 74pp; English.
 XX
 CC This primer is used in the method of the invention of identifying gene
 CC expression patterns in a population of mRNA. The method comprises
 CC preparing a population of double stranded (ds) cDNA from a population of
 CC mRNA using a primer, cleaving the ds cDNA with a first restriction
 CC endonuclease (RE) which cleaves at a site within the cDNA and not within
 CC the primer, to obtain a population of cDNA inserts. The cDNA inserts are
 CC inserted into insertion sites of cloning vectors to obtain DNA
 CC constructs, where each cloning vector comprises a second RE recognition
 CC sequence (RERS) located 5' to the insertion site, and a third RERS
 CC located 5' to or overlapping with the second RERS. The DNA constructs in
 CC a host cell are amplified and are digested with a second RE such that
 CC digestion of the DNA constructs with second RE cleaves the DNA constructs
 CC at sites within the cDNA inserts. The amplified DNA constructs are
 CC digested with a third RE to obtain tags and a nucleotide sequence of the
 CC tags is obtained to identify gene expression patterns in the population
 CC of mRNA. The method can be used for identifying gene expression patterns
 CC in cells and tissues. It can also be used to identify differential gene
 CC expression at different stages of development in the same cell-type or
 CC tissue-type, and to identify changes in gene expression patterns in
 CC diseased or abnormal cells. It can also be used to detect changes in gene
 CC expression patterns due to changes in environmental conditions or to
 CC treatment with drugs
 XX
 SQ Sequence 32 BP; 1 A; 5 C; 6 G; 20 T; 0 U; 0 Other;
 Query Match 0.3%; Score 20.8; DB 1; Length 32;
 Best Local Similarity 78.1%; Pred. No. 3.9e+02;
 Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 4465 TTTT TTTT TTTT TTTT TTTT GCTT GAGACATG 4496
 DB 1 TTTT TTTT TTTT TTTT TTTT TCGCGGCGCATG 32
 RESULT 226
 ID AB224036 standard; DNA; 32 BP.
 XX
 AC AB224036;
 XX
 DT 31-MAR-2003 (first entry)
 XX
 DE DNA sequence of a single mismatch oligonucleotide substrate 1B.
 XX
 KW Primer extension; transferase; single nucleotide polymorphism; SNP;
 KW nucleic acid synthesis; ss.
 XX
 OS Synthetic.
 XX
 PN WO200297109-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 23-MAY-2002; 2002WO-US016063.
 XX
 PR 25-MAY-2001; 2001US-0293182P.

XX (INVIT-) INVITROGEN CORP.
 PA
 XX
 PI Kort TF, Astakke M;
 XX
 DR WPI; 2003-140482/13.
 XX
 PT Composition useful for extending a primer, comprises a polypeptide
 PT capable of extending a mismatched primer over a fully complementary
 PT primer.
 XX
 PS Example; Page 32; 47pp; English.
 XX
 CC The invention relates to a composition (I) for primer extension which
 CC comprises a polypeptide capable of extending a 3'-hydroxyl terminus of
 CC the primer, where the polypeptide preferentially extends a mismatched
 CC primer over a fully complementary primer. (I) is useful for extending a
 CC primer molecule, by: (a) mixing a nucleic acid primer with a template;
 CC (b) adding one or more polypeptides of (I) to form a mixture; and (c)
 CC incubating the mixture under conditions sufficient to extend the nucleic
 CC acid molecule at the 3' hydroxyl terminus. The synthesis is accomplished
 CC in the presence of a component chosen from one or more nucleotides and
 CC one or more primers. The substrates are double-stranded nucleic acid
 CC template/primer complex, single-stranded template/primer complex, and a
 CC single stranded/double stranded nucleic acid template/primer complex. The
 CC nucleic acid is RNA or DNA and is immobilized. An isolated and purified
 CC terminal transferase is useful for extending a nucleic acid molecule. A
 CC new method for identifying a single nucleotide polymorphisms (SNP) in a
 CC target nucleic acid is also provided. The terminal transferase and/or synthesis
 CC of nucleic acids, in particular for the detection of SNPs. The present
 CC sequence represents the nucleotide sequence of a single mismatched
 CC substrate used in the assays of the invention
 XX
 SQ Sequence 32 BP; 3 A; 13 C; 14 G; 2 T; 0 U; 0 Other;
 Query Match 0.3%; Score 20.8; DB 1; Length 32;
 Best Local Similarity 78.1%; Pred. No. 3.9e+02;
 Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 42 GCTCGCGCGCGCGCGCAACGAGCTGCGGG 73
 DB 1 GCTCGCGAGCGGACGCGAGGCTGCGCGG 32
 RESULT 227
 ID ABK48140 standard; DNA; 24 BP.
 XX
 AC ABK48140;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Aspergillus niger aminopeptidase RT-PCR primer poly-T.
 XX
 KW Aminopeptidase; primer; ss; food composition; dough; flavour enhancer;
 KW baked product; cheese; poly-T; reverse transcriptase PCR.
 XX
 OS Synthetic.
 XX
 PN WO200216618-A1.
 XX
 PD 28-FEB-2002.
 XX
 PF 22-AUG-2001; 2001WO-EP009925.
 XX
 PR 23-AUG-2000; 2000EP-00202995.
 XX
 PA (STAM) DSM NV.
 XX
 PI Baeten D, Dekker PJT, Schuurhuizen PW, Schaap PJ, Visser J;
 XX
 DR WPI; 2002-257917/30.

XX WP1: 2000-664908/64.

XX Detaching nucleic acid molecule comprising unconventional nucleotide

XX incorporated at predetermined site from a solid support involves cleaving

XX the nucleic acid molecule at the site of unconventional nucleotide.

XX

XX Disclosure, Page 16; 47pp; English.

XX

XX The present invention is concerned with the cleavage of nucleic acids

XX from solid supports. This is carried out by adding a non-conventional

XX nucleotide into the nucleic acid attached to the support, so that it is

XX recognised and cleaved by a specific DNA glycosylase and the sequence is

XX released. This is useful in many molecular biological procedures such as

XX sequencing, in vitro amplifications, cDNA and template preparation, DNA-

XX based assays, mutagenesis procedures, nucleic acid purification and

XX affinity chromatography. The present sequence is an oligonucleotide used

XX in assays to demonstrate the methods of the invention

XX

XX Sequence 23 BP; 0 A; 0 C; 0 G; 22 T; 1 U; 0 Other;

XX

XX

XX Query Match 0.3%; Score 20.4; DB 1; Length 23;

XX Best Local Similarity 95.5%; Pred. No.2,9e+02;

XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX

XX 4464 TTTTTTTTTTTTTTTTTTGT 4485

XX |||||

XX 1 TTTTTTTTTTTTTTTTTTTT 22

XX

XX RESULT 232

XX AAC62451

XX ID AAC62451 standard; RNA; 23 BP.

XX

XX AAC62451;

XX

XX 07-FEB-2001 (first entry)

XX

XX Cleavage of nucleic acids from solid supports assay oligonucleotide #2.

XX

XX Nucleic acid cleavage; solid support; affinity chromatography;

XX sequencing; mutagenesis; DNA preparation; nucleic acid purification; ss.

XX

XX Synthetic.

XX

XX WO200058329-A1.

XX

XX 05-OCT-2000.

XX

XX 28-MAR-2000; 2000WO-GB001190.

XX

XX 29-MAR-1999; 99GB-00007245.

XX

XX (GOLD/) GOLDSBOROUGH A.

XX

XX WP1: 2000-664908/64.

XX

XX Detaching nucleic acid molecule comprising unconventional nucleotide

XX incorporated at predetermined site from a solid support involves cleaving

XX the nucleic acid molecule at the site of unconventional nucleotide.

XX

XX Example 1; Page 32; 47pp; English.

XX

XX The present invention is concerned with the cleavage of nucleic acids

XX from solid supports. This is carried out by adding a non-conventional

XX nucleotide into the nucleic acid attached to the support, so that it is

XX recognised and cleaved by a specific DNA glycosylase and the sequence is

XX released. This is useful in many molecular biological procedures such as

XX sequencing, in vitro amplifications, cDNA and template preparation, DNA-

XX based assays, mutagenesis procedures, nucleic acid purification and

XX affinity chromatography. The present sequence is an oligonucleotide used

XX in assays to demonstrate the methods of the invention

XX

[illegible]

XX	Arabidopsis thaliana, aconitase; exon; intron; probe; melon; Zea mays;
KX	Cucumis melo; maize; plant metabolism; Krebs cycle; glyoxylate cycle;
KW	citrate; acetyl CoA; catabolism; polysaccharide; lipase; chimeric;
KW	resistance marker; hormone; enzyme; primer; PCR; amplification; ss.
OS	Synthetic.
XX	
PN	W09520046-A1.
PD	27-JUL-1995.
XX	
PF	25-JAN-1995; 95WO-EP000263.
XX	
PR	25-JAN-1994; 94FR-00000787.
PA	(BIOC-) BIOCEM SA.
XX	
PI	Peyret P, Alric M, Perez P;
DR	WPI; 1995-269459/35.
XX	
PT	New plant aconitase, its fragments and related nucleic acid - also
PT	chimeric genes, transgenic plants, antibodies etc., used to modify plant
PT	metabolism by regulating carboxylic acid prodn.
XX	
PS	Example 7; Page 55; 122pp; French.
XX	
CC	Primers AAT02374-78 were used to isolate the gene encoding the
CC	Arabidopsis thaliana aconitase (AAT02364). This primer is complementary
CC	to the anchor primer (AAT02375) for PCR after the first strand cDNA
CC	synthesis in a RACE (rapid amplification of cDNA ends) technique to
CC	determine the transcriptional start site of the Arabidopsis aconitase
CC	gene. The aconitase genes can be used to modify plant metabolism by
CC	overexpression of aconitase. This leads to overproduction of acids in the
CC	Krebs and glyoxylate cycles, esp. citrate. Fragments of the genes can be
CC	used to inhibit the expression of aconitase, resulting in overproduction
CC	of acetyl CoA, and alterations of metabolism/catabolism of
CC	polysaccharides, lipases, and N cpds. Chimeric genes contg. the aconitase
CC	gene or its promoter, are used to provide controlled expression e.g.
CC	during development, or to express heterologous enzymes, desired traits,
CC	resistance makers, hormones, etc., in plants
XX	
SQ	Sequence 30 BP; 15 A; 9 C; 5 G; 1 T; 0 U; 0 Other;
XX	
Query Match	0.3%; Score 20.4; DB 1; Length 30;
Best Local Similarity	80.0%; Pred. No. 4.2e+02;
Matches 24; Conservative	0; Mismatches 6; Indels 0; Gaps 0.
QY	7403 CAAGCAACATCAGCAGCAGCAGCAGCA 7432
Db	1 CAAGCAAGATCAACAACAGCAGCAACACCA 30
RESULT 237	
AAD25661	
ID	AAD25661 standard; DNA; 30 BP.
XX	
AC	AAD25661;
XX	
DT	26-MAR-2002 (first entry)
XX	
DE	Oligonucleotide #7 related to method for production of RNA viruses.
XX	
KM	Cytostatic; replication defective gene transfer; encapsidated RNA virus;
XX	gene therapy; cancer therapy; ss.
XX	
OS	Unidentified.
XX	
PN	W0200190302-A2.
XX	
PD	29-NOV-2001.
XX	

PF		10-MAY-2001; 2001WO-US015449.
XX		
PR		24-MAY-2000; 2000US-0206997P.
XX		
PA	(FENG// FENG Y.	
PA	(TANG// TANG H.	
XX		
P1	Feng Y, Tang H;	
DR	WPI; 2002-066766/09.	
PT	Producing encapsidated RNA virus by coexpressing RNA virus genomic	
PT	sequence linked to bacteriophage promoter, and coding sequence for	
PT	bacteriophage polymerase linked to poxvirus promoter in eukaryotic cell	
XX		
PS	Cytoplasm.	
XX		
PS	Disclosure; Page 38; 49pp; English.	
XX		
CC	The patent discloses methods to produce RNA viral sequences, recombinant	
CC	RNA viruses, mutants of RNA viruses and RNA virus-derived vectors in cell	
CC	culture and in vitro using non-viable, replication defective helper	
CC	vaccinia recombinants. These methods generate RNA viral genomes and viral	
CC	particles in cell culture and in vitro independent of their natural	
CC	replication pathways, bypassing the limitation of any cellular barriers.	
CC	The invention also relates to a method for producing encapsidated RNA	
CC	virus comprising coexpressing polypeptide coding sequences capable of	
CC	forming capsid and packaging RNA viral genomic sequence in eukaryotic	
CC	cell, a construct comprising RNA viral genomic sequence linked to	
CC	bacteriophage promoter and transcription terminator and bacteriophage	
CC	polymerase coding sequence, which is operably compatible with the	
CC	promoter and is linked to poxvirus promoter. The methods are useful for	
CC	producing infectious or non-infectious, replication-defective,	
CC	encapsidated RNA viruses such as hepatitis virus comprising an RNA genome	
CC	e.g., hepatitis C virus (HCV), immature hepatitis B virus or hepatitis A	
CC	virus, lentivirus, rhinovirus, influenza virus, LCMV, arenavirus,	
CC	parainfluenza virus, reovirus, rotavirus, astrovirus, filiovirus, or	
CC	coronaviruses. They are preferably useful for producing encapsidated human	
CC	immunodeficiency virus (HIV)-1, where the HIV-1 lacks a Rev-response	
CC	element (RRE) or an envelope sequence. Methods of the invention are also	
CC	useful for producing replication defective gene transfer and gene therapy	
CC	vectors, particularly to transfer nucleic acids to human cells in vivo	
CC	and in vitro. The methods can be used for packaging therapeutic sequences	
CC	as gene therapy vector preparations in that are substantially free of helper	
CC	virus and used as pharmaceuticals in e.g. gene replacement therapy, or	
CC	cancer therapy. The present sequence is an oligonucleotide which is	
CC	related to a method for production of RNA viruses	
XX		
SQ	Sequence 30 BP; 6 A; 0 C; 2 G; 22 T; 0 U; 0 Other;	
	Query Match 0.3%; Score 20.4; DB 1; Length 30;	
	Best Local Similarity 80.0%; Pred. No. 4,2e+02;	
Dy	Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	
OY	4465 TTTTTTTTTTTTTTTTTTTGCTTGAGACA 4494	
Db	1 TTTTTTTTTTTTTTTTAGGATTTAATA 30	
RESULT 238		
ID	AA043410 standard; DNA; 31 BP.	
XX	AA043410;	
AC		
XX	AA043410;	
DT	25-MAR-2003 (revised)	
DT	29-OCT-1993 (first entry)	
XX		
DE	Structural production oligonucleotide S-Strand-1.	
XX		
KM	Molecular scaffolding; molecule orientation; orient; juxtaposition;	
KM	functional artificial components; one; two; three; dimensional;	
KM	structure formation; therapeutic; analytical; industrial; ss.	
XX		

OS	Synthetic.
FH	Key Location/Qualifiers
FT	misc_feature .1..15 /*tag= "exposed/exposable sticky end"
FT	/note=
FT	misc_feature 1 /*tag= b /note= "PO4-Cytosine"
FT	/tag= c /note= "Thymine - Teflon based solid support"
FT	
PN	WO9312244-A1.
XX	
PD	24-JUN-1993.
XX	
PF	03-DEC-1992; 92WO-US010431.
XX	
PR	12-DEC-1991; 91US-0080564.
XX	
PA	(UWNY) UNIV NEW YORK STATE.
XX	
PI	Seeman NC, Zhang Y;
DR	WPI; 1993-214185/26.
PT	Prodn. of structure including double stranded polynucleotide - comprises cleavage of loop in core structure of 1st polynucleotide with restriction enzyme and ligation to 2nd polynucleotide, used to orient mols., etc.
PS	Example; Page 34; 58pp; English.
CC	The sequence is that of the oligonucleotide S-Strand-1 which can be used in the formation or modification of one-, two- and three-dimensional structures. It may be used as molecular scaffolding to orient and juxtapose other molecules. It has analytical, industrial or therapeutical potential. (Updated on 25-MAR-2003 to correct PN field.)
SO	Sequence 31 BP; 2 A; 4 C; 2 G; 23 T; 0 U; 0 Other;
OY	Query Match 0.3%; Score 20.4; DB 1; Length 31; Best Local Similarity 95.5%; Pred.No. 4.4e+02; Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0. 4464 TTTTTTTTTTTTTTTTGTG 4485 10 TTTTTTTTTTTTTTTTTT 31
DB	
RESULT 239	
AAL50570	
ID	AAL50570 standard; DNA; 22 BP.
AC	AAL50570;
DT	12-DEC-2002 (first entry)
DE	Molecular array production method-related PCR primer.
KX	
KV	Molecular array; ss; target molecule identification; genetic analysis;
KW	gene expression; SNP detection; haplotyping; sequencing; PCR; primer.
OS	Unidentified.
PN	WO200274988-A2.
PD	
PP	26-SEP-2002.
XX	
PE	18-MAR-2002; 2002MO-GB001245.
XX	
PL	16-MAR-2001; 2001GB-00006635.
PR	02-AUG-2001; 2001GB-00018879.

XX (UYCH-) UNIV CHANCELLOR MASTER & SCHOLARS OXF.
 PA Mir K;
 XX WPI; 2002-732872/79.
 DR
 XX
 PT Producing a molecular array with a plurality of molecules immobilised to
 PT a solid substrate, useful in genetic analysis, gene expression studies or
 PT the detection or typing of single nucleotide polymorphisms in a sample of
 PT nucleic acids.
 XX
 XX Example 15; Page 122; 166pp; English.
 XX
 CC The invention comprises a method for producing a molecular array, the
 CC method involves immobilising molecules to a solid phase at a density
 CC which allows individual immobilised molecules to be individually
 CC resolved. The molecular array produced by the method of the invention is
 CC useful for identifying one or more target molecules in a sample. The
 CC molecular array is also useful in genetic analysis, gene expression
 CC studies, identifying molecules which interact with a target molecule,
 CC detection/typing of single nucleotide polymorphisms, haplotyping and
 CC sequencing. The present DNA sequence represents a PCR primer that was
 CC used in an example of the invention
 CC
 XX Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;
 SQ
 OY Query Match 0.3%; Score 20.2; DB 1; Length 22;
 Db Best Local Similarity 95.2%; Pred.No.2.9e+02;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0
 OY 4464 TTTT TTTT TTTT TTTT TTTT TTTT G 4484
 Db 1 TTTT TTTT TTTT TTTT TTTT TTTT V 21
 RESULT 240
 ABX74887
 ID ABX74887 standard; DNA; 22 BP.
 XX
 AC ABX74887;
 XX
 DT 21-MAR-2003 (first entry)
 XX
 DE Oligo-dT primer used in human CC-RCC invention.
 XX
 XX Microarray; solid surface; immobilised probe; CC-RCC;
 KW differential expression profile; aggressive CC-RCC tumour type;
 KW non-aggressive CC-RCC tumour type; clear cell renal carcinoma;
 KW gene expression profiling; tumour tissue; oligo-dT; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200279411-A2.
 PD 10-OCT-2002.
 XX
 PF 29-MAR-2002; 2002WO-US0009576.
 XX
 PR 29-MAR-2001; 2001US-0279411P.
 XX
 PA (VAND-) VAN ANDEL INST.
 PI Haab B, Rhodes D, Teh BT, Takashi M;
 XX WPI; 2003-040679/03.
 DR
 XX New microarray, comprising a matrix of cDNA probe from a set of probes
 PT immobilized to a solid surface in predetermined order, useful in the
 PT prognosis of patients with clear cell renal carcinoma.
 XX
 PS Example 2; Page 30; 179pp; English.
 XX

ID	ACC48485	standard; DNA; 22 BP.
XX	ACC48485;	
XX	11-AUG-2003	(first entry)
XX	locked nucleic acid anchored oligo(1) primer ON15.	
XX	locked nucleic acid; LNA; gene therapy; primer; ss.	
XX	Synthetic.	
XX	Key	Location/Qualifiers
XX	modified_base	21
XX		/tag= a
XX		/mod_base= OTHER
XX		/note= "OTHER= locked nucleic acid"
XX	modified_base	22
XX		/tag= b
XX		/mod_base= OTHER
XX		/note= "OTHER= Compound 17d"
XX	WO2003020739-A2.	
XX	13-MAR-2003.	
XX	04-SEP-2002; 2002WO-IB003911.	
XX	04-SEP-2001; 2001US-0317034P.	
XX	22-SEP-2001; 2001US-0323967P.	
XX	(EXIQ-) EXIQON AS.	
XX	Wengel J, Kauppinen S;	
XX	WPI; 2003-363021/34.	
XX	Novel nucleic acid comprising a locked nucleic acid unit having a	
XX	modified base that comprises an optionally substituted carbocyclic aryl	
XX	moiety, or modified nucleobase or nucleosidic base other than	
XX	oxazole,imidazole.	
XX	Example 24a; Page 90; 119pp; English.	
XX	The present sequence is that of pyrene-anchored locked nucleic acid (LNA)	
XX	oligo(dT) primer ON15, which was used in first-strand cDNA synthesis from	
XX	eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based	
XX	on an LNA-type 2'-O,4'-C-methylene-beta-d-ribofuranosyl moiety. It is	
XX	one of a set of such primers (see also ACC48482-84) that were used in an	
XX	example from the invention to demonstrate improved reverse transcription	
XX	of mRNA using pyrene-LNA anchored oligo(T) primers. The following results	
XX	were observed: efficient priming on mRNAs with short poly(A) tails;	
XX	efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T	
XX	units resulting in an improved T20-VN anchor primer and thus avoiding	
XX	reverse transcription of long poly(A) tracts; and improved reverse	
XX	transcription of eukaryotic poly(A)+RNA directly from total RNA extracts	
XX	due to increased specificity. The invention relates to modified LNA units	
XX	that comprise unique base groups. Desirable nucleobase and nucleosidic	
XX	base substitutions can mediate universal hybridisation when incorporated	
XX	into nucleic acid strands. The novel LNA compounds can be used e.g. as	
XX	PCR primers, in sequencing, the synthesis of antisense oligonucleotides,	
XX	and in diagnostics	
XX	Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;	

Query Match	0.3%	Score 20.2;	DB 1;	Length 22;
Best Local Similarity	95.2%;	Pred. No. 2.9e+02;		
Matches 20; Conservative	1;	Indels 0;	Gaps 0;	
QY	4464	TTTTTTTTTTTTTTTTTTTG	4484	

DB	I	TTTTTTTTTTTTTTTTTTTV	21
XX	RESULT	243	
XX	ACC48483		
XX	ID	ACC48483	standard; DNA; 22 BP.
AC	ACC48483;		
DT	11-AUG-2003	(first entry)	
XX	locked nucleic acid anchored oligo(1) primer ON13.		
DE	locked nucleic acid; LNA; gene therapy; primer; ss.		
XX	Synthetic.		
OS			
FH	Key	Location/Qualifiers	
FT	modified_base	2	
FT		/tag= a	
FT		/mod_base= OTHER	
FT		/note= "OTHER= locked nucleic acid"	
FT	modified_base	5	
FT		/tag= b	
FT		/mod_base= OTHER	
FT		/note= "OTHER= locked nucleic acid"	
FT	modified_base	8	
FT		/tag= c	
FT		/mod_base= OTHER	
FT		/note= "OTHER= locked nucleic acid"	
FT	modified_base	11	
FT		/tag= d	
FT		/mod_base= OTHER	
FT		/note= "OTHER= locked nucleic acid"	
FT	modified_base	14	
FT		/tag= e	
FT		/mod_base= OTHER	
FT		/note= "OTHER= locked nucleic acid"	
FT	modified_base	17	
FT		/tag= f	
FT		/mod_base= OTHER	
FT		/note= "OTHER= locked nucleic acid"	
FT	modified_base	21	
FT		/tag= g	
FT		/mod_base= OTHER	
FT		/note= "OTHER= locked nucleic acid"	
FT	modified_base	22	
FT		/tag= h	
FT		/mod_base= OTHER	
FT		/note= "OTHER= Compound 17d"	
PN	WO2003020739-A2.		
PD	13-MAR-2003.		
PF	04-SEP-2002; 2002WO-IB003911.		
PR	04-SEP-2001; 2001US-0317034P.		
PR	22-SEP-2001; 2001US-0323967P.		
PA	(EXIQ-) EXIQON AS.		
PI	Wengel J, Kaupinen S;		
DR	WPI; 2003-363021/34.		
PT	Novel nucleic acid comprising a locked nucleic acid unit having a		
PT	modified base that comprises an optionally substituted carbocyclic aryl		
PT	molety, or modified nucleobase or nucleosidic base other than		
PT	oxazole/imidazole.		
PS	Example 24a; Page 90; 119pp; English.		
XX			

CC The present sequence is that of pyrene-anchored locked nucleic acid (LNA)
CC oligo(dT) primer CN13, which was used in first-strand cDNA synthesis from
CC eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based
CC on an LNA-type 2',0,4'-C-methylene-beta-D-ribofuranosyl moiety. It is
CC one of a set of such primers (see also ACC48482-85) that were used in an
CC example from the invention to demonstrate improved reverse transcription
CC of mRNA using pyrene-LNA anchored oligo(T) primers. The following results
CC were observed: efficient priming on mRNAs with short poly(A) tails;
CC efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T
CC units resulting in an improved T20-VN anchor primer and thus avoiding
CC reverse transcription of long poly(A) tracts; and improved reverse
CC transcription of eukaryotic poly(A)+RNA directly from total RNA extracts
CC due to increased specificity. The invention relates to modified LNA units
CC that comprise unique base groups. Desirable nucleobase and nucleosidic
CC base substitutions can mediate universal hybridisation when incorporated
CC into nucleic acid strands. The novel LNA compounds can be used e.g. as
CC PCR primers, in sequencing, the synthesis of antisense oligonucleotides,
CC and in diagnostics

XX
SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

Query Match 0.3%; Score 20.2; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 2.9e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT G 4484
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT V 21

RESULT 244
ID AAD51324 standard; DNA; 22 BP.
XX
AC AAD51324;
XX
DT 16-APR-2003 (first entry)
XX
DE Anchored oligo dT primer used to illustrate the method of the invention.
XX
DS
XX Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis;
XX Gastritis; gastric ulcer; respiratory ailment; fracture; joint disease;
XX musculoskeletal damage; ss.
XX
OS Unidentified.
XX
XX WO200290579-A1.
XX
XX 14-NOV-2002.
XX
XX 03-MAY-2002; 2002WO-AU000553.
XX
XX 04-MAY-2001; 2001AU-00004809.
XX
XX 29-JUN-2001; 2001US-00086941.
XX
XX (GENO-) GENOMICS RES PARTNERS PTY LTD.
XX
XX Brandon RB;
XX
XX WPI; 2003-120558/11.
XX
XX
XX Assessing condition e.g. athletic ability, stage of disease, presence of
XX drugs, response to exercise, response to vaccines, therapies, nutritional
XX states, of performance animal involves analyzing nucleic acid expression.
XX
XX
XX Disclosure; Page 46; 87pp; English.
XX
XX The invention relates to a method for assessing a condition of a
XX performance animal. The method involves determining in sample abundance
XX of expressed target nucleic acid, transmitting digital sample signal to
XX remote diagnostic server; processing digital sample signal at remotely
XX located database to correlate digital signal with digital information and
XX returning report of particular condition of animal. The method is useful

CC for assessing a condition of a performance animal preferably human, dog
CC or camel. The condition can be an athletic ability and a condition that
CC enhances, hinders, impedes or does not change an expected ability of the
CC performance animal; and also normal, pre-clinical, overt progress and/or
CC stage of disease, undiagnosed or unclassified conditions, presence of
CC drug, response to exercise, response to vaccines, therapies, nutritional
CC states and response to environmental conditions. Diseases assessed by the
CC invention include laminitis, lameness, viral or bacterial disease,
CC gastritis, gastric ulcers, respiratory ailments, fractures, epistaxis,
CC musculoskeletal damage or disorders and joint diseases. The present
CC sequence is a primer used to illustrate the method of the invention

XX
SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

Query Match 0.3%; Score 20.2; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 2.9e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT G 4484
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT V 21

RESULT 245
ID ABR13916 standard; DNA; 23 BP.
XX
AC ABR13916;
XX
DT 21-MAY-2002 (first entry)
XX
DE 3'-PCR primer used in method of identifying transcribed genes.
XX
XX Identification of transcribed gene; mRNA profile; gene expression;
XX cellular process; fingerprinting; susceptibility to external factor;
XX development; disease; PCR; primer; ss.
XX
OS Synthetic.
XX
XX WO200208461-A2.
XX
XX 31-JAN-2002.
XX
XX 23-JUL-2001; 2001WO-IB001539.
XX
XX 21-JUL-2000; 2000GB-00018016.
XX
XX 21-JUL-2000; 2000US-0219925P.
XX
XX (GLOB-) GLOBAL GENOMICS AB.
XX
XX
XX Linnarsson S, Ernfors P, Bauren G;
XX
XX WPI; 2002-217065/27.
XX
XX
XX Providing mRNA profile, by generating two independent patterns
XX characteristic of sample mRNA population, analyzing patterns, comparing
XX PT gene expression by cell types under varied conditions, and identifying
XX PT genes.
XX
XX
XX Example 2; Page 45; 67pp; English.
XX
XX
XX The present invention relates to a method for providing a profile of mRNA
XX molecules present in a sample. The method comprises generating two
XX independent patterns characteristic of the population of mRNA molecules
XX expressed in the sample and analysing the patterns using a combinatorial
XX algorithm, comparing gene expression by different or same cell types
XX under different conditions, and identifying genes having a role in
XX various cellular processes. The method is useful for the analysis and
XX identification of transcribed genes, and fingerprinting. The method can
XX be used to identify genes which play a role in determining various
XX cellular processes, including susceptibility to external factors,
XX development, and disease. The present sequence for a PCR primer is used
XX in the methods of the present invention

```

XX SQ Sequence 23 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 3 Other;
Query Match 0.3%; Score 20.2; DB 1; Length 23;
Best Local Similarity 95.2%; Pred. No. 3.1e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTTGTGTTTGTGTTG 4484
DB 1 TTTTGTGTTTGTGTTT 21

RESULT 246
ABK86172
ID ABK86172 standard; DNA; 24 BP.
XX AC ABK86172;
XX DT 24-SEP-2002 (first entry)
XX DE Oligo dt primer #4 used in method to study gene expression.
XX KM Oligo dt primer; gene expression analysis; primer; ss.
XX OS Synthetic.
XX PN WO200236828-A2.
XX PD 10-MAY-2002.
XX PF 01-NOV-2001; 2001WO-US045401.
XX PR 01-NOV-2000; 2000US-0244933P.
XX PA (GENO-) GENOMIC SOLUTIONS INC.
XX PI Kane MD, Dombkowski AA, Nagel AC;
XX DR WPI; 2002-508123/54.
XX PT Identifying and characterizing gene expression in samples, for
PT identifying mRNAs expressed at different levels, comprises employing an
PT identifier having a oligo-dt primer of a specific sequence and a
PT detectable marker at its 5' end.
XX PS Example 1; Page 15; 45pp; English.
XX CC The invention relates to systems for identification and characterisation
CC of gene expression in one or more samples, comprising an identifier having
CC a specific oligo-dt primer sequence, where the identifier comprises a
CC detectable marker at its 5' end. The system is useful for identifying any
CC or all genes expressed in a given in vivo or in vitro RNA sample, as well
CC as the relative differences in mRNA between 2 or more samples, where
CC desired, for supporting discovery of new genes, and for identifying mRNAs
CC that are expressed at different levels between 2 or more samples. The new
CC system or method addresses limitations of prior methods by comprising
CC compositions and systems that incorporate new strategies where molecular
CC or biochemical assay compositions and systems are linked to DNA or RNA
CC sequence databases for optimal resource efficiency in assaying gene
CC expression. The system has the following advantages over existing
CC methods: (a) prior sequence information or clone library construction is
CC not needed to enable the assay; (b) provides immediate sequence
CC information in addition to information concerning changes or differences
CC in mRNA level, to determine mRNA expression level and mRNA identification
CC in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC sample for subsequent investigation by common molecular biology
CC techniques; and (d) does not require prior knowledge of the sequence of
CC the genome of the organism under investigation and can be employed in
CC organisms lacking significant genomic sequence information. The present
CC sequence represents an oligo dt primer used in the method of the
CC invention
XX SQ Sequence 24 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 4 Other;

```

```

Query Match 0.3%; Score 20.2; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 3.3e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 4463 CTTTGTGTTTGTGTTT 4483
DB 4 VTTTGTGTTTGTGTTT 24

RESULT 247
AAC95894
ID AAC95894 standard; DNA; 25 BP.
XX AC AAC95894;
XX DT 26-FEB-2001 (first entry)
XX DE HLA HLA-B gene PCR primer #5.
XX KM DNA sequence analysis; sequencing; protein sequence; protein structure;
XX gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
XX human leukocyte antigen; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200065088-A2.
XX PD 02-NOV-2000.
XX PF 20-APR-2000; 2000WO-BP003636.
XX PR 26-APR-1999; 99EP-00303215.
XX PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX PI Ulfendahl P, Wong K;
XX DR WPI; 2000-679677/66.
XX PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX PS Claim 14; Page 42; 66pp; English.
XX CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC particular
XX SQ Sequence 25 BP; 0 A; 1 C; 5 G; 19 T; 0 U; 0 Other;
Query Match 0.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 3.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 4465 TTTTGTGTTTGTGTTG 4489
DB 1 TTTTGTGTTTGTGTTGTTG 25

RESULT 248
AAC96201
ID AAC96201 standard; DNA; 25 BP.
XX AC AAC96201;
XX DT 26-FEB-2001 (first entry)

```



```

DE    16S rRNA gene PCR primer #168.
XX
XX    DNA sequence analysis; sequencing; protein sequence; protein structure;
KW    gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
KM    human leukocyte antigen; PCR primer; ss.
OS    Homo sapiens.
XX
XX    WO200065088-A2.
XX
XX    02-NOV-2000.
XX
XX    20-APR-2000; 2000WO-EP003636.
XX
XX    26-APR-1999; 99EP-00303215.
XX
XX    (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX    Ulfendahl P, Wong K;
XX
XX    WPI; 2000-679677/66.
XX
XX    Identifying extendible primers for use in identification, or
PT    classification of a nucleic acid of an organism, allele or gene such as
PR    class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT    specific length.
XX
XX    Claim 14; Page 47; 66pp; English.
XX
XX    The present invention provides a method for identifying a set of
CC    extendible primers which can be used in the identification, typing and
CC    classification of genes. This can then be used to predict protein
CC    sequence and structure, in organ donation to match the organ with the
CC    receiver, and to identify bacteria in a sample. The method can be used to
CC    type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC    particular
XX
XX    Sequence 25 BP; 1 A; 3 C; 3 G; 18 T; 0 U; 0 Other;
SQ
Query Match      0.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 3.Se+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy      4467 TTTTTTTTTTTTGTGCTTGAG 4491
          |||||
Db       1 TTTTITTTTTTTTCAGTCTTGCG 25
RESULT 249
AAZ99741
ID      AAZ99741 standard; DNA; 25 BP.
XX
XX      AAZ99741;
XX
XX      12-JUL-2000 (first entry)
XX
XX      Primer used to reverse transcribe barley 17 kDa foam protein mRNA.
DE
XX      Barley; 17 kDa foam protein; foam; prolamin storage protein;
KW      foaming beverage; beer; brewed product; foam head; primer; ss.
XX
XX      Hordeum vulgare.
XX
XX      WO200014237-A2.
XX
XX      16-MAR-2000.
XX
XX      02-SEP-1999; 99WO-IB001597.
XX
XX      03-SEP-1998; 98US-00146703.
XX      13-JAN-1999; 99US-0115756P.
XX

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```

PA (VNA6//) VNA6 P.
PA (BECH//) BECH L M.
PA (CAME//) CAMERON-MILLS V.
PA (SORE//) SORESENSEN M B.
XX
PI Vaag P, Bech LM, Cameron-Mills V, Sorensen MB;
XX
DR WPI; 2000-317103/27.
XX
PT New foam protein from cereals useful for improving foam formation,
PT stability and half-life in foaming products such as beverages and
PT especially beer.
XX
PS Example 6; Page 22; 82pp; English.
XX
XX The present sequence represents a primer used to reverse transcribe mRNA
CC encoding the barley 17 kDa foam protein. The protein has foam enhancing
CC properties, and belongs to the prolamin storage protein family. It is
CC found in the endosperm tissue of mature cereal grain, and is synthesised
CC during grain development. The 17 kDa foam protein can be added to
CC products, e.g. foaming beverages such as beer, to enhance the foaming
CC quality of the product. The protein can be used to produce improved
CC brewed products. The proteins and polynucleotides are especially useful
CC for improving the formation, stability and half-life of the foam head on
CC beer. The antibodies are useful to detect, measure and purify the
CC proteins in samples such as transgenic cells/plants and foaming products
SQ
Sequence 25 BP; 2 A; 2 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 3.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0.

Oy 4458 ATGACCTTTTTTTTTTTTTTTT 4482
||||| |||||||||
Db 1 ATGACCTCTTTTTTTTTTTTTTTT 25

RESULT 250
ADB04573
ID ADB04573 standard; DNA; 25 BP.
AC ADB04573;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5559.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EPI281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

```

```

XX Example 8; SEQ ID NO 5559; 103bp; English.
PS
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring the disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize genes
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 3 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

Query Match      0.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 3.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4470 TTTTCTTTTTCGCTGAGACA 4494
DB 1 TTTCTTTTCTTTTTCGAGACA 25

RESULT 251
AA239941
ID AA239941 standard; DNA; 27 BP.
XX
AC AA239941;
XX
DT 06-JUL-1999 (first entry)
XX
DE Primer #22 for PDZ domain-containing protein gene 5' RACE PCR.
XX
KM PDZ domain; gene expression; human umbilical vascular endothelial cell;
KM HUVEC; stimulation; tumour necrosis factor; TNF; protein binding; PCR;
KM cell; proliferation disorder; cancer; primer; amplification; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO9907846-A1.
XX
PD 18-FEB-1999.
XX
PF 12-AUG-1998; 98WO-JP003603.
XX
PR 12-AUG-1997; 97JP-00230356.
XX
PR 19-JUN-1998; 98JP-00189944.
XX
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI Funahashi S, Miyata S;
XX
DR WPI; 1999-167423/14.
XX
PT Protein containing PDZ domain, whose expression is enhanced by TNF
PT stimulation - plays an important role in protein/protein interactions and
PT is used for screening for proteins for use in treatment of cell
PT proliferation disorders such as cancer.
XX
XX Example 2; Page 30; 240bp; Japanese.
XX
CC This sequence represents a primer used in a 5' RACE PCR reaction to
CC isolate longer clones which encode new proteins containing PDZ domains
CC whose expression in human umbilical vascular endothelial cells (HUVEC)
CC are enhanced by stimulation with tumour necrosis factor (TNF) alpha. The

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CC new protein is used to identify proteins which bind to it (particularly
CC to the PDZ domains) and the genes encoding them, for use in the treatment
CC of cell proliferation disorders such as cancer
XX
SQ Sequence 27 BP; 5 A; 1 C; 15 G; 6 T; 0 U; 0 Other;

Query Match      0.3%; Score 20.2; DB 1; Length 27;
Best Local Similarity 88.0%; Pred. No. 3.9e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3626 TGGGGCTGGAGAGAGCTAGATG 3650
DB 2 TGGGCTGGAGAGAGCTAGATTG 26

RESULT 252
AB259816
ID AB259816 standard; RNA; 28 BP.
XX
AC AB259816;
XX
DT 01-APR-2003 (first entry)
XX
DE Potato gene PCR primer DDT18AN.
XX
KM Potato; plant; mitochondrial carrier protein; elongation factor EF-2;
KM transferrin binding protein; receptor-like protein kinase; helicase;
KM non-long terminal repeat retroelement reverse transcriptase;
KM overwatering; transgenic; reverse transcriptase; PCR; primer; ss.
XX
OS Synthetic.
OS Del0114063-A1.
XX
PD 10-OCT-2002.
XX
PF 22-MAR-2001; 2001DE-01014063.
XX
PR 22-MAR-2001; 2001DE-01014063.
XX
PA (MPEC-) MPE COLOGNE GMBH MOLECULAR PLANT & PROTE.
XX
PI Buelow L, Tscharncke W, Hausenuhl K;
XX
DR WPI; 2003-041808/04.
XX
PT New DNA sequences from potato, useful for producing plants with altered
PT properties, e.g. tolerance of flooding, also related proteins, antibodies
PT and inhibitory sequences.
XX
XX Example 1; Page 8; 26bp; German.
XX
PS
XX
CC The invention relates to DNA sequences (I) that encode six specific plant
CC proteins: (i) a protein (ABP60425) with mitochondrial carrier protein
CC activity (IIa); (ii) a protein (ABP60426) with transferrin binding
CC protein activity (Iib); (iii) a protein (ABP60427) with receptor-like
CC protein kinase activity (Iic); (iv) a protein (ABP60428) with elongation
CC factor EF-2 activity (Iid); (v) a protein (ABP60429) with non-long
CC terminal repeat retroelement reverse transcriptase activity (Iie); or
CC (vi) a protein (ABP60430) with helicase activity (Iif). (I), also related
CC sequences, derived ribozymes and antisense sequences, expression vectors,
CC encoded proteins and antibodies against the proteins, are used to produce
CC plants with altered properties, including tolerance of overwatering. The
CC antibodies are also used for isolation of the proteins and in
CC immunoassays. Also (I) or their primer or probe fragments are used to
CC screen for terminators and constitutively, aerobically or anaerobically
CC inducible plant promoters, specifically for use in potatoes and the
CC sequence that encodes (Iid) is used to alter the translation profile in
CC plants. Since (I) are derived from potato, their promoters and
CC terminators provide high level transgene expression in potato, with
CC improved tissue specificity and inducibility, and can also be used to
CC control endogenous genes. The present sequence is that of a PCR primer
CC used in the first strand synthesis of cDNAs derived from potato

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XX Sequence 28 BP; 3 A; 2 C; 2 G; 20 T; 0 U; 1 Other;
SQ
Query Match
Best Local Similarity 88.0%; Score 20.2; DB 1; Length 28;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4458 ATGACTTTTATTTTATTTTATTTT 4482
DB 2 ATGACTTTTATTTTATTTTATTTT 26

RESULT 253
AAQ93201
ID AAQ93201 standard; DNA; 29 BP.
AC AAQ93201;
XX
XX 24-FEB-1996 (first entry)
DT
XX C. perfringens beta 1 toxin PCR primer BetatoxL.
DE
XX Enterotoxin; beta 1 toxin; food poisoning; faeces; contamination;
KM Clostridium perfringens; polymerase chain reaction; primer; PCR; ss.
XX
OS Synthetic.
XX
XX WO9517521-A2.
XX
XX 29-JUN-1995.
XX
XX 22-DEC-1994; 94MO-EP004292.
XX
XX 22-DEC-1993; 93US-00172026.
XX
XX (INSP ) INST PASTEUR.
PA (CNEV-) CNEVA CENT NAT ETUD VETERINAIRES & ALIME.
XX
XX Fach P, Guillion J, Popoff M;
XX
XX WPI; 1995-240681/31.
XX
XX New primers for amplification of Clostridium perfringens toxin genes -
PT and new beta 2 toxin gene, used to detect and quantify C.perfringens in
PT e.g. food and faecal samples.
PT
XX Example 7; Page 28; 43pp; English.
XX
XX The presence of beta 1 and beta 2 toxin genes was examined by PCR in a
CC series of type B and C Clostridium perfringens strains. For beta 2 gene
CC amplification, primers P319 and P320 (AAQ93199-200) were used; primers
CC BetatoxL and BetatoxR (AAQ93201-02) were used for the beta 1 gene. The 3
CC B strains examined possessed the beta 1 gene. Type C strains had either
CC the beta 2 gene, or the beta 1 gene, or both
XX
XX Sequence 29 BP; 5 A; 0 C; 6 G; 18 T; 0 U; 0 Other;
SQ
Query Match
Best Local Similarity 88.0%; Score 20.2; DB 1; Length 29;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4460 GGACTTTTATTTTATTTTATTTTATTTT 4484
DB 2 GGAGTTTATTTTATTTTATTTTATTTT 26

RESULT 254
AAV59216
ID AAV59216 standard; DNA; 29 BP.
AC AAV59216;
XX
XX 14-DEC-1998 (first entry)
DT

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```

XX
XX Linear multimer produced by rolling circle synthesis.
DE
XX ss; RNA oligonucleotide; probe; standard; diagnostic; therapeutic agent.
XX
XX Synthetic.
OS
XX WO938300-A1.
XX
XX 03-SEP-1998.
XX
XX 26-FEB-1998; 98MO-US003784.
XX
XX 26-FEB-1997; 97US-00805631.
XX
XX (UYRP ) UNIV ROCHESTER.
XX
XX KOOL ET;
XX
XX WPI; 1998-481202/41.
XX
XX Synthesis of oligo:nucleotide(s) - using a single-stranded circular
PT oligo:nucleotide template ribonucleotide triphosphate(s) and a
PT polymerase to form multimer(s) which can be cleaved.
XX
XX Example 2; Page 36; 100pp; English.
XX
XX The linear multimer was produced by rolling circle synthesis in an
CC example of the method of the invention for synthesising an RNA
CC oligonucleotide, comprising combining a single-stranded circular
CC oligonucleotide template comprising at least one copy of a nucleotide
CC sequence complementary to the sequence of the desired RNA oligonucleotide
CC with at least 2 types of ribonucleotide triphosphate and a polymerase
CC enzyme to yield a single-stranded RNA oligonucleotide multimer
CC complementary to the circular oligonucleotide template, where the RNA
CC oligonucleotide multimer comprises multiple copies of the desired RNA
CC oligonucleotide. The methods can be used for producing RNA
CC oligonucleotides having a specific sequence and well defined ends. The
CC RNA oligonucleotides produced can be used as probes, standards and
CC diagnostic or therapeutic agents. They can be used for modifying the
CC structure or function of a target molecule. They can also be used to
CC cleave disease-associated RNA, DNA or protein
XX
XX Sequence 29 BP; 0 A; 0 C; 2 G; 27 T; 0 U; 0 Other;
SQ
Query Match
Best Local Similarity 88.0%; Score 20.2; DB 1; Length 29;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4464 TTTTATTTTATTTTATTTTATTTTATTTT 4488
DB 5 TTTTATTTTATTTTATTTTATTTTATTTT 29

RESULT 255
ADG65873
ID ADG65873 standard; DNA; 29 BP.
AC ADG65873;
XX
XX 18-DEC-2003 (first entry)
DT
XX DNA oligonucleotide #6.
XX
XX RNA oligonucleotide synthesis; ribonucleotide triphosphate; polymerase;
KM electroporation; calcium phosphate treatment; lipid-mediated delivery;
KM cation-mediated delivery; bacterial infection; viral infection;
KM drug resistant infection; double stranded DNA oligomer; ss.
XX
XX Synthetic.
XX
XX US2003087241-A1.
XX

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PD 08-MAY-2003.
XX
XX 30-NOV-2001; 2001US-0097931.
XX
XX 15-APR-1993; 93US-00047860.
XX 23-FEB-1995; 95US-00393439.
XX 26-FEB-1997; 97US-00805631.
XX 11-MAY-2000; 2000US-00569344.
XX
XX (UYRP ) UNIV ROCHESTER.
XX
XX Kool ET;
XX
XX WPI; 2003-755141/71.
XX
XX Synthesizing RNA oligonucleotide involves combining single-stranded
PT circular oligonucleotide, ribonucleotide triphosphate and polymerase
PT enzyme to yield desired RNA complementary to circular oligonucleotide
PT template.
XX
XX Example 2; SEQ ID NO 6; 78bp; English.
XX
XX The invention relates to a method for synthesizing an RNA
CC oligonucleotide, comprising combining a single-stranded circular
CC oligonucleotide template with at least two types of ribonucleotide
CC triphosphate and a polymerase enzyme to yield a single-stranded RNA
CC oligonucleotide multimer complementary to the circular oligonucleotide
CC template, where the RNA oligonucleotide multimer comprises multiple
CC copies of the desired RNA oligonucleotide. The method is useful for
CC synthesizing an RNA oligonucleotide with well-defined ends. The circular
CC oligonucleotide is introduced into the cell using direct injection,
CC electroporation, calcium phosphate treatment, lipid-mediated delivery, or
CC cation-mediated delivery. The method is useful for treating bacterial
CC and/or viral infections in mammals, particularly drug resistant
CC infections, and for producing double stranded DNA oligomers. The method
CC is performed in the absence of an oligonucleotide primer, or without the
CC addition of auxiliary proteins. This sequence represents an
CC oligonucleotide used in the method of the invention.
XX
XX Sequence 29 BP; 0 A; 0 C; 2 G; 27 T; 0 U; 0 Other;
SQ
Query Match 0.3%; Score 20.2; DB 1; Length 29;
Best Local Similarity 88.0%; Pred. No. 4.3e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4464 TTTTGTGTTTGTGCTT 4488
DB 5 TTTTGTGTTTGTGTTT 29

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XX
XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
XX Crow MK, Li Y;
XX
XX WPI; 2001-244776/25.
XX
XX New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.
XX
XX Example 1; Fig 3; 90bp; English.
XX
XX The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritic,
CC anti-rheumatic, immunosuppressive and anti-inflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX
XX Sequence 30 BP; 24 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.3%; Score 20.2; DB 1; Length 30;
Best Local Similarity 88.0%; Pred. No. 4.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4464 TTTTGTGTTTGTGCTT 4488
DB 25 TTTTGTGTTTGTGTTT 1

```

```

RESULT 256
AAF74908/C
ID AAF74908 standard; DNA; 30 BP.
XX
XX AAF74908;
XX
XX 23-MAY-2001 (first entry)
XX
XX CD40L poly-A tract sequence SEQ ID NO:5.
XX
XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
XX diagnosis; antiarthritic; anti-rheumatic; immunosuppressive;
XX anti-inflammatory; inflammatory disease; autoimmune disease; ds.
XX
XX Homo sapiens.
XX
XX WO200119844-A1.
XX
XX 22-MAR-2001.
XX
XX 13-SEP-2000; 2000WO-US024966.
XX
XX 13-SEP-1999; 99US-0153625P.

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RESULT 257
AAQ25565
ID AAQ25565 standard; DNA; 20 BP.
XX
XX AAQ25565;
XX
XX 25-MAR-2003 (revised)
XX 02-DEC-1992 (first entry)
XX
XX Dye-coupled 3'-amino modified oligonucleotide.
XX
XX DNA synthesis; RNA; antisense strands; detection; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 20 /*tag= a
FT /note= "3-amino modified"
XX
XX EP490281-A1.
XX
XX 17-JUN-1992.
XX
XX 06-DEC-1991; 91EP-00120935.
XX
XX 11-DEC-1990; 90DE-04039488.
XX
XX (FARH ) HOECHST AG.
XX
XX Engels J, Herrlein M, Konrad R, Mag M;
XX
XX WPI; 1992-201578/25.
XX
XX New dye-coupled modified nucleosides, nucleotides and oligonucleotides -
PT useful for synthesis of antisense DNA and RNA strands in presence of
PT template, also for in-vivo and in-vitro detection of genetic material.

```


DE	Alpha-anomeric oligonucleotide ligand 1803 for oestradiol hapten.
XX	
XX	Oligonucleotide ligand, steroid hormone; hapten; immobilisation;
KW	Immunodetection; estradiol; alpha-anomer; ss.
XX	
OS	Synthetic.
XX	
PH	Key
FT	misc_feature
FT	1..21
FT	/*tag= b
FT	/note= "the glycosidic bonds between nucleotides are all
FT	in the alpha-anomer form"
FT	20
FT	modified_base
FT	20
FT	/*tag= a
FT	/mod_base= OTHER
FT	/note= "carries a group derived ffrom aminopropanediol"
PN	
XX	WO9429723-A1.
PD	
XX	22-DEC-1994.
XX	
PF	10-JUN-1994; 94WO-FR000689.
XX	
PR	11-JUN-1993; 93FR-00007093.
XX	
PA	(CROS/) CROS P.
PA	(KURF/) KURFURST R.
PA	(BATT/) BATTAIL N.
PA	(PIGA/) PIGA N.
XX	
PI	Cros P, Kurfurst R, Battail N, Piga N;
DR	WPI; 1995-036665/05.
XX	
PT	Assay device for hapten or its specific antibodies - comprises support
PT	having competitive reagent immobilised via nucleic acid ligand to improve
PT	orientation and accessibility.
XX	
PS	Example 1; Page 10; 39pp; French.
XX	
CC	Oligonucleotides (AAQ94701-Q94705) were synthesised for use as ligands.
CC	The ligands are covalently linked to a hapten (esp. a steroid hormone) to
CC	form a conjugate which is then immobilised on a solid support for
CC	interaction with antibodies against the hapten. Nucleic acid ligands are
CC	less likely to be recognised by the antibodies than are peptide ligands
CC	and nucleic acids are also less likely to undergo intramolecular
CC	organisation which interferes with accessibility of the hapten to the
CC	antibodies. For immunodiagnosis of oestradiol, the active hapten
CC	oestradiol-6-carboxymethoxime-N-hydroxy succinimide ester was used.
CC	(Updated on 25-MAR-2003 to correct PN field.)
XX	
XX	Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
QY	
DB	Query Match 0.3%; Score 20; DB 1; Length 20;
	Best Local Similarity 100.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0
	Matches 20; Conservative 0; Mismatches 0;
	4464 TTTTTTTTTTTTTTTTTTTT 4483
	1 TTTTTTTTTTTTTTTTTTTT 20
RESULT 261	
AAQ75570	
ID	AAQ75570 standard; DNA; 20 BP.
XX	
XX	AAQ75570;
XX	
DT	04-AUG-1995 (first entry)
DE	Reverse transcription primer used in cDNA analysis technique.

KW	Analysts; gene expression; reverse transcription; primer; cDNA;
KV	aggregate; restriction enzyme; ss.
XX	Synthetic.
OS	JP0630397-A.
PN	
XX	
PD	01-NOV-1994.
XX	
PF	16-APR-1993; 93JP-00112515.
XX	
PR	16-APR-1993; 93JP-00112515.
PA	(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX	
DR	WPI; 1995-018287/03.
XX	
FT	Analysis of cDNA and gene expression - by amplification of mRNA followed
PT	by digestion with restriction enzymes.
XX	
PS	Disclosure; Page 5; 11pp; Japanese.
XX	
CC	A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC	double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC	labelled reverse transcription primers (GENBSEQ files AAQ75547-Q75798)
CC	and using the aggregate of mRNAs as the template for each reverse
CC	transcription primer; (b) digesting each of the prepared aggregates of
CC	the double-stranded cDNAs with restriction enzyme and; (c)
CC	electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC	method can be used to analyse gene expression rapidly and easily
XX	
SQ	Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match	0.3%; Score 20; DB 1; Length 20;
Best Local Similarity	100.0%; Pred. No. 2,7e+02;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	4467 TTTTTTTTTTTTTTTGTC 4486 1 TTTTTTTTTTTTTTTGTC 20
DB	
RESULT 262	
AAQ90405	
ID	AAQ90405 standard; DNA; 20 BP.
XX	
AC	AAQ90405;
XX	
DT	08-JAN-1996 (first entry)
XX	
T2	(synthetic DNA probe with 5' amino terminal #4).
DE	
KW	T2; HNA; dQa; self-addressable electronic device; SASE; hybridisation;
KV	ss.
XX	Synthetic.
OS	
XX	
FH	Key Location/Qualifiers
FT	misc_feature 1
FT	/tag= a
FT	/note= "3' aminolink2 Thymine; allows binding to any
FT	amine"
XX	
FN	WO9512808-AI.
XX	
PD	11-MAY-1995.
XX	
PF	26-OCT-1994; 94MO-US012270.
XX	
PR	01-NOV-1993; 93US-00146504.
XX	
PA	(NANO-) NANODEN INC.
XX	

```

PI Heller MJ, Tu E;
XX
XX
DR WPI, 1995-185870/24.
XX
XX New self-addressable electronic devices - used for multi-step and
PT multiplex reactions such as DNA hybridisation(s), clinical diagnostics
PT and bio-polymer synthesis.
XX
XX Example 1; Page 41; 86pp; English.
XX
XX The sequences represented by, AAQ90402-15 are synthetic DNA probes
CC containing 5' amino termini. The sequences shown in AAQ90390-401 are
CC synthetic DNA probes with 3' ribonucleoside termini. These sequences were
CC specific for the polymorphisms of H1A gene dga. The sequences were used
CC in the device of the invention. This is a self-addressable electronic
CC device (SAD) that can be used to carry out multi-step and multiplex
CC reactions, such as nucleic acid hybridisations. The advantages of this
CC method are that these reactions can be carried out with complete and
CC precise electronic control, and that the rate, specificity and
CC sensitivity of these reactions are greatly improved at micro-locations
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
SQ
SQ
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY 4464 TTTTTTTTTTTTTTTTTT 4483
Db 1 TTTTTTTTTTTTTTTTTT 20
RESULT 263
AA63649
ID AAT63649 standard; DNA; 20 BP.
AC AAT63649;
XX
XX 06-JUN-1997 (first entry)
DT
DE Anti-HTLV antisense reference oligonucleotide HT.
XX
XX antisense; complementary; tax gene; inhibit; HTLV-1;
KW human T-cell lymphotropic virus type 1; viral antigen expression; ss.
OS Synthetic.
XX
XX JP09052898-A.
XX
XX 25-FEB-1997.
XX
XX 09-AUG-1995; 95UP-00224606.
XX
XX 09-AUG-1995; 95UP-00224606.
XX
XX (SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.
XX
XX WPI, 1997-197252/18.
XX
XX Anti-HTLV-1 anti-sense oligo:nucleotide - is complementary to region of
PT tax gene from human T-cell lymphotropic virus type 1 and inhibits viral
PT antigen expression.
XX
XX Example 1; Page 8; 10pp; Japanese.
XX
XX Oligonucleotides having a partial sequence consisting of at least 15
CC bases of AAT63641 (an antisense oligo complementary to a region of the
CC tax gene which can inhibit human T-cell lymphotropic virus type 1 (HTLV-
CC 1) viral antigen expression) are claimed. In an example, six antisense
CC oligos were designed. T1-T6 (AAT63650-55) and were compared to six oligos
CC derived from other regions of HTLV-1, i.e. SUI (splice junction), PI
CC (p21), RI (rex), RRI (rex response element), EI (env) and GI (gag), four
CC reference oligonucleotides T1S (tax-sense), HC (dC20), HT (dT20)

```

```

CC      (AAAT6364/-49) and a random 20mer (RAN) in a HIV-1 virus antigen
CC      expression inhibiting test. Oligonucleotide T1 gave the best results
XX      1
SQ      Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match          0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      4464 TTTTTTTTTTTTTTTTTT 4483
        |||||
Db       1 TTTTTTTTTTTTTTTTTT 20

RESULT 264
AAY34591/C
ID      AAV34591 standard; DNA; 20 BP.
AC      AAV34591;
XX
XX      25-AUG-1998 (first entry)
DT
DE      M. vaccae antigenic sequence hybridising oligo AD12.
KW      Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;
KW      M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
KW      mycobacteria infection; vaccine; cancer; ss.
XX
OS      Synthetic.
OS      Mycobacterium vaccae.
XX
XX      WO9808542-A2.
PN
PD      05-MAR-1998.
XX
XX      28-AUG-1997; 97WO-NZ000105.
PF
PR      29-AUG-1996; 96US-00705347.
PR      12-JUN-1997; 97US-00873970.
XX
PA      (GENE-) GENESIS RES & DEV CORP.
XX
XX      Tan P, Hiyaama J, Visser E, Skinner MA, Scott LM, Prestidge RL,
PI
DR      WPI; 1998-216926/19.
XX
PT      Mycobacterium vaccae polypeptides - used to develop products for use in
PT      detection, therapy and prevention of mycobacteria infections or as immune
PT      response enhancers.
XX
PS      Example 8; Page 99; 153pp; English.
XX
XX      This oligonucleotide is used in the DNA cloning strategies of the
CC
CC      Mycobacterium vaccae antigens. The invention provides M. vaccae
CC      polypeptides that comprise an immunogenic portion of a soluble M. vaccae
CC      antigen, or a variant, where the antigen induces an immune response in
CC      patients previously exposed to a mycobacterium. Such M. vaccae
CC      polypeptides can be used in methods for enhancing non-specific immune
CC      response. The methods and products can be used for the detection,
CC      treatment and prevention of infectious diseases caused by mycobacteria
CC      such as M. vaccae, M. avium or M. tuberculosis. The products also have
CC      the ability to induce cell proliferation and cytokine production (e.g.,
CC      interferon-gamma and interleukin-12 production) in T cells, NK cells, B
CC      cells, or macrophages. They can be used for enhancing immune responses
CC      for use in vaccines or immunotherapy of infectious diseases and cancers
XX
SQ      Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match          0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      4464 TTTTTTTTTTTTTTTTTT 4483

```

Db 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 265

AAAT86606
ID AAT86606 standard; DNA; 20 BP.

AC AAT86606;

DT 04-JUN-1998 (first entry)

DE Oligonucleotide separated by capillary affinity gel electrophoresis.

KM Capillary affinity gel electrophoresis; separation; polymer-gel;

KW polyacrylamide; ss.

OS Synthetic.

PN WO9745721-A1.

PD 04-DEC-1997.

PF 23-MAY-1997; 97WO-EP002647.

PR 24-MAY-1996; 96CH-00001320.

PA (NOVS) NOVARTIS AG.

PI Muscate A, Paulus A, Natt F;

DR WPI; 1998-041763/04.

PT Separation of electrically charged target molecules - by capillary
affinity gel electrophoresis using polymer-gel to which receptors for
target molecules are bound.

PS Example D3; Page 25; 41pp; English.

CC A mixture of oligonucleotides (AAT86604-7) were separated by a new
CC process using capillary affinity gel electrophoresis. The invention
CC relates to selective separation of electrically charged target molecules
CC in an analytical mixture. It comprises capillary affinity gel
CC electrophoresis using a capillary tube which is at least partly filled
CC with a polymer gel. Receptors for target molecules are covalently bound
CC to the polymer. An electric field of at least 50 volts/cm is applied. The
CC capillary tube is charged with the analytical mixture. In a first
CC separation stage, the target molecules in the mixture are bound to the
CC receptors and the remaining components are eluted, optionally whilst
CC splitting open. In a second stage, the elution conditions are changed,
CC optionally in stages, so that the affinity of the target molecules for
CC the receptor is eliminated and the target molecules are eluted and
CC detected, optionally whilst splitting open. The process is useful for
CC selective separation and/or determination of charged organic compounds,
CC such as oligonucleotides, peptides or carbohydrates. It may be used, e.g.
CC for isolation of specific proteins and DNA molecules, purification of
CC antibodies. Analysis of antisense compounds or screening for enzyme
CC inhibitors. The process achieves higher resolution and selectivity than
CC prior art processes, especially in the case of complex biological
CC analytical mixtures. It has high sensitivity, even with small amounts of
CC samples. The derivatised polymers may be synthesised specifically using
CC standard methods

SO Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match

Best Local Similarity 0.3%; Score 20; DB 1; Length 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483

Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 266

AAAX27533
ID AAX27533 standard; RNA; 20 BP.

AC AAX27533;

DT 27-MAY-1999 (first entry)

DE Synthetic RNA sequence produced by the method of the invention.

KM Silyloxymethyl; phosphonate; silyloxymethyl halide; diagnosis; ss;

KW cyanoethyl phosphoramidate coupling; isomerisation; steric hindrance.

OS Synthetic.

PN WO9909044-A1.

PD 25-FEB-1999.

PF 17-AUG-1998; 98WO-EP005215.

PR 18-AUG-1997; 97CH-00001931.

PA (PITS/) PITSCH S.

PA (WEIS/) WEISS P A.

PA (JENN/) JENNY L.

PI Pitsch S, Weiss PA, Jenny L;

DR WPI; 1999-180963/15.

PT 2-Silyloxymethyl ribonucleosides and their phosphonate derivatives - have
PT high purity, use in machine synthesis of ribonucleic acids, enable longer
PT oligonucleotide chain construction, and larger amounts.

PS Example 6; Page 25; 38pp; English.

CC The invention relates to silyloxymethyl protected D- or L-ribonucleosides
CC and their phosphonates (I), and silyloxymethyl halides (II). (I) are
CC intermediates for synthesis of RNA-oligonucleotides with predetermined
CC nucleotide sequence, particularly by machine synthesis. The groups
CC specified above, apart from those on silyl, are those particularly for
CC the cyanoethyl phosphoramidate coupling. Uses of the oligoribonucleotide
CC products in diagnosis, therapy, and as research tools, are well known,
CC and are not dealt with in detail. (II) is an intermediate for (I). The
CC silyloxymethyl halide reagent is easy to prepare, and yields are high.
CC introduction of the silyloxymethyl group into the ribonucleoside is
CC simple and rapid, and the acetal bond formed does not migrate,
CC eliminating particularly the prior art problem of 2' to 3' isomerisation.
CC The methylenedioxy group spacer between the silyl group and nucleoside
CC ring results in less steric hindrance than bulky direct silyloxy
CC linkages, enabling first, a range of choices for the silyl substituents,
CC to provide, e.g., acid or base stability; and second, higher yields in
CC coupling. Purer products are therefore obtained than in prior art,
CC enabling larger quantities and longer chains of oligoribonucleotides to
CC be synthesised successfully, and in shorter times

SO Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 20 U; 0 Other;

Query Match

Best Local Similarity 0.0%; Score 20; DB 1; Length 20;

Matches 0; Conservative 20; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483

Db 1 UUUUUUUUUUUUUUUUUUUUU 20

RESULT 267

AAZ11326/C
ID AAZ11326 standard; DNA; 20 BP.

XX

AC AA21326;
 XX 25-OCT-1999 (first entry)
 DT
 XX Mycobacterium 16S rRNA specific oligo AD12.
 DE
 XX
 XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
 KM dendritic cell maturation; infectious disease; immune disorder; cancer;
 KM respiratory system; mycobacterial infection; allergy; tuberculosis;
 KM leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
 KM dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
 KM squamous cell carcinoma; melanoma; PCR primer; ss.
 XX
 OS Synthetic.
 OS Mycobacterium vaccae.
 PN WO932634-A2.
 XX
 PD 01-JUL-1999.
 XX
 PF 23-DEC-1998; 98MO-NZ000189.
 XX
 PR 23-DEC-1997; 97US-00996624.
 PR 23-DEC-1997; 97US-00997080.
 PR 23-DEC-1997; 97US-00997362.
 PR 11-JUN-1998; 98US-00095855.
 PR 17-SEP-1998; 98US-00156181.
 PR 04-DEC-1998; 98US-00205426.
 XX
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 XX
 PI Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;
 XX WPI; 1999-430163/36.
 DR
 XX
 PT Enhancing immune response to an antigen.
 XX
 PS Example 15; Page 177; 243pp; English.
 XX
 XX The invention provides heat-killed Mycobacterium vaccae, or recombinant
 CC M. vaccae proteins. The M. vaccae proteins may be employed to activate T
 CC cells and natural killer cells, to stimulate the production of cytokines,
 CC to enhance the expression of co-stimulatory molecules on dendritic cells
 CC and monocytes, and to enhance dendritic cell maturation and function. The
 CC proteins can be expressed by standard recombinant methodology.
 CC Pharmaceutical compositions comprising the proteins or nucleic acid
 CC sequences encoding the proteins can be used for the treatment,
 CC prevention, and detection of disorders including infectious diseases,
 CC immune disorders and cancer. In particular, the compounds and methods are
 CC used for treatment of diseases of the respiratory system, such as
 CC mycobacterial infections, asthma, allergies, tuberculosis, leprosy,
 CC sarcoidosis and lung cancers, and disorders of the skin such as
 CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
 CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
 CC carcinoma and melanoma
 CC
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 XX
 XX
 Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
 DB 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1
 XX
 RESULT 268
 AAA0449/c
 ID AAA0449 standard; DNA; 20 BP.
 XX
 AC AAA0449;
 XX

DT 13-NOV-2000 (first entry)
 XX
 DE Electrochemical detection method sample DNA target.
 XX
 KM Electrochemical detection; glucose; cholesterol; urea nitrogen;
 KM bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood;
 KM plasma; serum; urine; lymph diagnosis; ss.
 XX
 OS Synthetic.
 OS
 PN EP1018646-A2.
 XX
 PD 12-JUL-2000.
 XX
 PF 07-JAN-2000; 2000EP-00100126.
 XX
 PR 06-JAN-1999; 99JP-00001111.
 PR 24-MAY-1999; 99JP-00143599.
 XX
 PA (FUJIFILM) FUJIFILM CO LTD.
 XX
 PI Ogawa M, Takenaka S, Takagi M;
 XX WPI; 2000-444372/39.
 DR
 XX
 PT Quantitative analysis of a biochemical compound such as glucose, in body
 PT a body fluid such as blood, comprising detecting enhanced electron
 PT transfer between an oxidase and a DNA-immobilized electrode, useful for
 PT diagnosis of disease.
 XX
 PS Example 1; Page 8; 14pp; English.
 XX
 XX This invention describes a novel method for quantitatively analysing a
 CC biochemical compound (I) which comprises contacting (I) with double
 CC stranded DNA fixed to the surface of an electrode at their terminals in
 CC which electrochemically active threading intercalators are intercalated,
 CC in an aqueous medium under application of electric potential to the
 CC electrode in the presence of an oxidase which oxidizes the biochemical
 CC compound and becomes reduced, and detecting electric current flowing
 CC between the electrode and a second electrode in the aqueous medium. The
 CC method is useful for detection of biochemical compounds such as glucose,
 CC cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic
 CC acid in body fluids such as whole blood, plasma, serum, urine, and lymph
 CC for diagnosis of various diseases. The method allows detection of
 CC biochemical compounds quickly and easily with a high sensitivity using a
 CC sample apparatus. This sequence represents DNA fragment used as a target
 CC sample in the method of the invention
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 XX
 XX
 Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
 DB 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1
 XX
 RESULT 269
 AAA0448
 ID AAA0448 standard; DNA; 20 BP.
 XX
 AC AAA0448;
 XX
 DT 13-NOV-2000 (first entry)
 XX
 DE Electrochemical detection method fixed probe DNA.
 XX
 KM Electrochemical detection; glucose; cholesterol; urea nitrogen;
 KM bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood;
 KM plasma; serum; urine; lymph diagnosis; probe; ss.
 XX

PS Example 12; Page 34; 49pp; English.

XX The present sequence is that of a phosphodiester oligonucleotide
 CC containing 20 T nucleobases, 19 having a 2'-methoxyethoxy group on its 5'
 CC ribose sugar moiety. It is an example of an oligomeric compound produced
 CC according to the methods of the invention. The invention provides
 CC compounds and methods for the preparation of mixed backbone oligomeric,
 CC or chimeric, compounds having phosphodiester internucleoside linkages in
 CC addition to phosphorothioate and/or phosphoramidate internucleoside
 CC linkages. The methods also include incorporation of boranophosphate
 CC internucleoside linkages. The methods utilize H-phosphate intermediates
 CC that are coupled together forming contiguous regions of 1 or more H-
 CC phosphonate internucleoside linkages. Each contiguous region is
 CC subsequently oxidized to phosphodiester, phosphorothioate,
 CC phosphoramidate or boranophosphate internucleoside linkages prior to
 CC further elongation. Mixed backbone oligomeric compounds are prepared in
 CC this manner by oxidizing adjacent regions with different reagents.
 CC Oligomeric compounds of the invention are prepared using novel oxidation
 CC steps that oxidize a region of 1 or more H-phosphate internucleoside
 CC linkages without degrading existing linkages that have been previously
 CC oxidized. The oligonucleotides obtained are useful as primers in PCR,
 CC probes, linkers, gene fragments and for other diagnostic tests on e.g.
 CC biological tissue, fluid, cells etc., as research reagents, and as
 CC antiviral agents

XX
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4483
 Db 1 TTTTTTTTTTTTTTTTTT 20

RESULT 272
 AAC87238
 ID AAC87238 standard; DNA; 20 BP.

XX AAC87238;
 XX
 DT 09-MAR-2001 (first entry)

DE Phosphorothioate poly T oligonucleotide, SEQ ID NO:17.

XX
 XX Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
 KW immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;
 KW hnRNP A1; lupus Ia protein; functional modifier identification; agonist;
 KW antagonist; mimic; inhibitor; drug screening;
 KW cellular target identification; oligonucleotide optimisation;
 XX immunotherapy; ss.

XX
 OS Synthetic.

XX
 PN WO200067023-A1.

XX
 PD 09-NOV-2000.

XX
 PF 28-APR-2000; 2000WO-US011697.

XX
 PR 29-APR-1999; 99US-0131830P.

XX
 PR 03-MAR-2000; 2000US-0186845P.

XX
 PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
 PA (IOWA) UNIV IOWA RES FOUND.

XX
 PI N011 BO, Schetter C, Krieg AM;

XX
 DR WPI; 2001-016002/02.

PT Immunostimulatory DNA binding proteins to identify immunostimulatory DNA
 functional modifiers, immunostimulatory DNA binding competitors and to

PT optimize immunostimulatory oligodeoxynucleotides for stimulation.

XX
 PS Example 1; Page 45; 95pp; English.

XX The invention relates to the use of an immunostimulatory single-stranded
 CC DNA-binding protein in screening assays to identify compounds which bind
 CC to it and thereby act as functional modifiers of immunostimulatory
 CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity
 CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory
 CC DNA mimics, and immunostimulatory DNA agonists and antagonists.
 CC Immunostimulatory DNA-binding proteins can also be used in screening
 CC methods to identify immunostimulatory DNA binding competitors, and to
 CC optimize an immunostimulatory ODN for immune stimulation. Isolated
 CC complexes of an immunostimulatory DNA-binding protein bound to an
 CC immunostimulatory ODN can additionally be used to screen a panel of
 CC candidate target molecules to identify the cellular target molecules of
 CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins
 CC used in the methods of the invention are the RNA-binding proteins
 CC nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus Ia protein. The screening
 CC methods are useful for identifying a compound that inhibits interaction
 CC between immunostimulatory DNA and an immunostimulatory DNA-binding
 CC protein and for identifying agonists useful in immunotherapy. The complex
 CC is useful in screening for immunostimulatory DNA cellular target
 CC molecules. The candidate immunostimulatory ODN competitors allow the
 CC investigation of structure/activity relationships of immunostimulatory
 CC DNA-binding proteins and immunostimulatory ODNs. The present sequence
 CC represents an oligonucleotide used in an exemplification of the invention

XX
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4483
 Db 1 TTTTTTTTTTTTTTTTTT 20

RESULT 273
 AAC87230
 ID AAC87230 standard; DNA; 20 BP.

XX AAC87230;
 XX
 DT 09-MAR-2001 (first entry)

DE Digoxigenin-labelled poly T oligonucleotide, SEQ ID NO:9.

XX
 XX Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
 KW immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;
 KW hnRNP A1; lupus Ia protein; functional modifier identification; agonist;
 KW antagonist; mimic; inhibitor; drug screening;
 KW cellular target identification; oligonucleotide optimisation;
 KW immunotherapy; ss.

XX
 OS Synthetic.

XX
 PN WO200067023-A1.

XX
 PD 09-NOV-2000.

XX
 PF 28-APR-2000; 2000WO-US011697.

XX
 PR 29-APR-1999; 99US-0131830P.

XX
 PR 03-MAR-2000; 2000US-0186845P.

XX
 PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
 PA (IOWA) UNIV IOWA RES FOUND.

XX
 PI N011 BO, Schetter C, Krieg AM;

XX
 DR WPI; 2001-016002/02.

XX Immunostimulatory DNA binding proteins to identify immunostimulatory DNA
PT functional modifiers, immunostimulatory DNA binding competitors and to
XX optimize immunostimulatory oligodeoxynucleotides for stimulation.
XX

PS Example 1; Page 45; 95pp; English.

XX The invention relates to the use of an immunostimulatory single-stranded
CC DNA-binding protein in screening assays to identify compounds which bind
CC to it and thereby act as functional modifiers of immunostimulatory
CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity
CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory
CC DNA mimics, and immunostimulatory DNA agonists and antagonists.
CC Immunostimulatory DNA-binding proteins can also be used in screening
CC methods to identify immunostimulatory DNA binding competitors, and to
CC optimize an immunostimulatory ODN for immune stimulation. Isolated
CC complexes of an immunostimulatory DNA-binding protein bound to an
CC immunostimulatory ODN can additionally be used to screen a panel of
CC candidate target molecules to identify the cellular target molecules of
CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins
CC used in the methods of the invention are the RNA-binding proteins
CC nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening
CC methods are useful for identifying a compound that inhibits interaction
CC between immunostimulatory DNA and an immunostimulatory DNA-binding
CC protein and for identifying agonists useful in immunotherapy. The complex
CC is useful in screening for immunostimulatory DNA cellular target
CC molecules. The candidate immunostimulatory ODN competitors allow the
CC investigation of structure/activity relationships of immunostimulatory
CC DNA-binding proteins and immunostimulatory ODNs. The present sequence
CC represents an oligonucleotide used in an exemplification of the invention
SQ

Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
|||||
DB 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 274

AAC87241
ID AAC87241 standard; DNA; 20 BP.

AC AAC87241;

XX 09-MAR-2001 (first entry)

DE Poly T oligonucleotide, SEQ ID NO:20.

XX Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
XX immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;
XX hnRNP A1; lupus La protein; functional modifier identification; agonist;
XX antagonist; mimic; inhibitor; drug screening;
XX cellular target identification; oligonucleotide optimization;
XX immunotherapy; ss.

OS Synthetic.

PN WO200067023-A1.

PD 09-NOV-2000.

PF 28-APR-2000; 2000WO-US011697.

PR 29-APR-1999; 99US-0131830P.

XX 03-MAR-2000; 2000US-0186845P.

PA (CPG1-) CPG IMMUNOPHARMACEUTICALS GMBH.
PA (IOWA) UNIV IOWA RES FOUND.

PI Noll BO, Schetter C, Kries AM;
XX WPI; 2001-016002/02.

PT Immunostimulatory DNA binding proteins to identify immunostimulatory DNA
XX functional modifiers, immunostimulatory DNA binding competitors and to
XX optimize immunostimulatory oligodeoxynucleotides for stimulation.
XX

PS Example 1; Page 45; 95pp; English.

XX The invention relates to the use of an immunostimulatory single-stranded
CC DNA-binding protein in screening assays to identify compounds which bind
CC to it and thereby act as functional modifiers of immunostimulatory
CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity
CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory
CC DNA mimics, and immunostimulatory DNA agonists and antagonists.
CC Immunostimulatory DNA-binding proteins can also be used in screening
CC methods to identify immunostimulatory DNA binding competitors, and to
CC optimize an immunostimulatory ODN for immune stimulation. Isolated
CC complexes of an immunostimulatory ODN for immune stimulation. Isolated
CC immunostimulatory ODN can additionally be used to screen a panel of
CC candidate target molecules to identify the cellular target molecules of
CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins
CC used in the methods of the invention are the RNA-binding proteins
CC nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening
CC methods are useful for identifying a compound that inhibits interaction
CC between immunostimulatory DNA and an immunostimulatory DNA-binding
CC protein and for identifying agonists useful in immunotherapy. The complex
CC is useful in screening for immunostimulatory DNA cellular target
CC molecules. The candidate immunostimulatory ODN competitors allow the
CC investigation of structure/activity relationships of immunostimulatory
CC DNA-binding proteins and immunostimulatory ODNs. The present sequence
CC represents an oligonucleotide used in an exemplification of the invention
SQ

Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
|||||
DB 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 275

AAS10402
ID AAS10402 standard; DNA; 20 BP.

AC AAS10402;

XX 24-OCT-2001 (first entry)

DE DNA template for 3' end labeling of an RNA molecule, #14.

XX 3' RNA end labeling; DNA template; Okazaki fragment; 5' overhang; ss.

OS Synthetic.

PN US6238865-B1.

PD 29-MAY-2001.

PF 16-OCT-1998; 98US-00173936.

PR 17-OCT-1997; 97US-0063757P.

XX (CHEN/) CHEN G.

PA (HUAN/) HUANG Z.

XX (SZOS/) SZOSTAK J W.
XX Huang Z, Szostak JW,
XX

DR WPI; 2001-366470/38.
 XX
 PT Modifying a 3' terminus of a pre-selected DNA sequence, useful for
 PT labeling and modifying 3'-termini of other nucleic acids, comprises using
 PT a synthetic nucleotide template with a defined overhang nucleotide.
 XX
 PS Example 5; Col 13; 22pp; English.
 XX
 CC The sequence represents a synthetic DNA template molecule used to
 CC demonstrate the method of the invention. The invention relates to a
 CC method of modifying (e.g. 3' end labelling with 32P dATP) the 3' terminus
 CC of an RNA molecule by providing a DNA oligonucleotide, complementary to
 CC the 3' end of the RNA molecule, with an overhang at the 5' end which
 CC allows incorporation of the labeling nucleotide into the RNA molecule.
 CC The method, based on the synthesis of Okazaki fragments, is useful for
 CC labeling and modifying the 3'-termini of other nucleic acids such as DNA
 CC fragments. The method is a simple and efficient way of labeling or
 CC modifying RNA 3'-termini using DNA polymerase and a synthetic template
 CC with defined overhang nucleotides
 CC
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
 XX
 Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
 DB 1 TTTT TTTT TTTT TTTT TTTT TTTT 20
 XX
 RESULT 276
 AAD16997
 ID AAD16997 standard; DNA; 20 BP.
 XX
 AC AAD16997;
 XX
 DT 29-NOV-2001 (first entry)
 XX
 DE Capture probe CP5'.
 XX
 KM Scaffold protein; antibody mimic; fibronectin type III domain;
 KM randomised loop; randomised beta-sheet; diagnostic purpose;
 KM protein designing; probe; tenth module of human Fn3; 10Fn3;
 KM fibronectin module of type III; Fn3; ss.
 XX
 OS Unidentified.
 XX
 PN WO200164942-A1.
 XX
 PD 07-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US006414.
 XX
 PR 29-FEB-2000; 2000US-00515260.
 XX
 PA (PHYL-) PHYLLOS INC.
 XX
 PI Lipovsek D, Wagner RW, Kuimelis RG;
 XX
 DR WPI; 2001-557782/62.
 XX
 PT Fibronectin scaffold protein array for obtaining a protein/compound which
 PT binds to a compound/protein, comprises a fibronectin type III domain
 PT having a randomized loop, a randomized beta-sheet or their combination.
 XX
 PS Disclosure; Page 41; 67pp; English.
 XX
 CC The present invention relates to an array of proteins (antibody mimics)
 CC comprising a fibronectin type III domain having a randomised loop, a
 CC randomised beta-sheet, or their combination, and has the capacity to bind
 CC to a compound that is not bound by a corresponding naturally-occurring
 CC fibronectin, immobilised onto a solid support. The antibody mimics is

CC useful for detecting a compound preferably a protein, in a biological
 CC sample. It is also useful to detect one or more different analytes
 CC simultaneously in a sample. Hence is useful for diagnostic purposes. It
 CC is also useful for the purpose of designing proteins capable of binding
 CC to virtually any compound of interest. The present sequence is a capture
 CC probe used to self-assemble and anchor the tenth module of human
 CC fibronectin module of type III (Fn3) (10Fn3) which is used in an
 CC exemplification of the invention
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
 XX
 Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
 DB 1 TTTT TTTT TTTT TTTT TTTT TTTT 20
 XX
 RESULT 277
 AAF60896/c
 ID AAF60896 standard; DNA; 20 BP.
 XX
 AC AAF60896;
 XX
 DT 15-MAY-2001 (first entry)
 XX
 DE Conjugate forming oligonucleotide ON5 SEQ ID 5.
 XX
 KM Transport; membrane; cytosolic; virocidic; vasotropic; dermatological;
 KM antipsoriatic; antiaesthetic; gene therapy; tumor cell; antisense;
 KM tumor therapy; drug; phosphodiester linkage; ss.
 XX
 OS Unidentified.
 XX
 PN DE19935302-A1.
 XX
 PD 08-FEB-2001.
 XX
 PF 28-JUL-1999; 99DE-01035302.
 XX
 PR 28-JUL-1999; 99DE-01035302.
 XX
 PA (AVENTIS PHARMA DEUT GMBH.
 XX
 PI Uhlmann E, Greiner B, Unger E, Gothe G, Schwerdel M;
 XX
 DR WPI; 2001-203679/21.
 XX
 PT New substituted aryl conjugates of parent molecules, especially
 PT oligonucleotides, having improved transmembrane and intracellular
 PT transport properties, useful as medicaments or diagnostic agents.
 XX
 PS Disclosure; Page 9; 28pp; German.
 XX
 CC This invention describes a novel conjugate (I) which consists of (A) a
 CC molecule to be transported and (B) at least one aryl residue of formula -
 CC Ar-(X-C(Y)-R1)n (II). Ar = group containing at least one aromatic ring;
 CC X = O or N (Sic); Y = O, S or NH-R2 (Sic); R1 = optionally substituted
 CC 1-23C alkyl (optionally containing double and/or triple bonds); R2 =
 CC optionally substituted 1-18C alkyl (optionally containing double and/or
 CC triple bonds); n = integer of 1 or more. (A) is bonded to (B) directly or
 CC via a chemical group, provided that the chemical group is other than CH2
 CC -S if the bond is via a phosphodiester linkage of (A). The invention also
 CC describes (i) the preparation of a conjugate (I') of (A') a molecule to
 CC be transported and (B') at least one aryl residue (not restricted to
 CC (II)), by preparing (A') containing a reactive function at the position
 CC at which (B') is to be bonded, preparing (B') and reacting (A') and (B');
 CC and (ii) the use of aryl groups (II) (optionally bonded via a chemical
 CC group) for transporting (A) across biological membranes. The products of
 CC the invention have cytostatic, virocidic, vasotropic, dermatological,
 CC antipsoriatic and antiaesthetic activity and can be used for gene

XX The present sequence is an oligonucleotide used in a method for detecting
CC a nucleic acid having at least 2 portions. The method comprises
CC hybridizing the nucleic acid with oligonucleotides, such as the present
CC sequence, attached to a substrate and/or particle and detecting a change
CC in colour, conductivity or optical density. The method is useful for the
CC diagnosis and/or monitoring of diseases, in forensics, in DNA sequencing,
CC for paternity testing, for cell line authentication and for monitoring
CC gene therapy. Detecting nucleic acids based upon observing a colour
CC change is cheap, fast, simple, and does not require specialised or
CC expensive equipment. The nanoparticle oligonucleotide conjugates remain
CC stable for at least 6 months. A single base mismatch and as little as 20
CC femtomoles (fm) of target can be detected using the conjugates
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
Db 20 TTTT TTTT TTTT TTTT TTTT 1
RESULT 280
AAS10371/c
ID AAS10371 standard; DNA; 20 BP.
XX
AC AAS10371;
XX
DT 24-OCT-2001 (first entry)
XX
DE Oligonucleotide-cyclic disulphide linker, d.
XX
KM Nanoparticle; cyclic disulphide-oligonucleotide; DNA detection;
KM DNA isolation; genetic disease; bacterial disease; viral disease;
KM forensic science; paternity testing; gene therapy; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1
FT /note= "A is covalently linked to a cyclic-disulphide
FT moiety"
XX
XX PN WO200151665-A2.
XX
XX PD 19-JUL-2001.
XX
XX PF 12-JAN-2001; 2001WO-US001190.
XX
XX PR 13-JAN-2000; 2000US-0176409P.
XX PR 26-APR-2000; 2000US-0200161P.
XX PR 26-JUN-2000; 2000US-00603830.
XX PR 12-JAN-2001; 2001US-00760500.
XX
XX PA (NANO-) NANOSPHERE INC.
XX
XX PI Mirkin CA, Letsinger RL, Nucleic RC, Storchhoff JJ, Elghanian R;
XX PI Taton TA, Li Z;
XX DR WPI; 2001-451868/48.
XX
XX PT Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or
XX PT viral diseases, by contacting the nucleic acid with oligonucleotides
XX PT attached to nanoparticles and having sequences complementary a portion of
XX PT the nucleic acid.
XX
XX PS Example 24; Fig 44; 323pp; English.
XX
XX CC The sequence represents a cyclic disulphide linked oligonucleotide which

CC may be coupled with colloidal gold particles (nanoparticles) and used to
CC demonstrate the method of the invention. The invention relates to
CC isolating or detecting a nucleic acid of interest, in a mixture of
CC nucleic acids, by binding it to 2 or more complementary nucleotides which
CC have a nanoparticle attached to their 5' ends. The nanoparticles (e.g.
CC colloidal gold) are used to both isolate and detect (e.g. by linking the
CC particle to a fluorescent probe) the resultant complex. The methods are
CC useful for detecting nucleic acids, natural or synthetic, and modified or
CC unmodified. The methods may also be applied in the diagnosis of genetic,
CC bacterial and viral diseases, in forensics, in DNA sequencing, for
CC paternity testing, for cell line authentication, and for monitoring gene
CC therapy. The methods are further useful in research and analytical
CC laboratories in DNA sequencing, in the field to detect the presence of
CC specific pathogens, for quick identification of an infection to assist in
CC drug prescription, and in homes and health centres for inexpensive first-
CC line screening. The methods, which are based on observing colour change
CC with the naked eye, are cheap, fast, simple, robust (reagents are
CC stable), do not require specialised or expensive equipment, and little or
CC no instrumentation is required
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
Db 20 TTTT TTTT TTTT TTTT TTTT 1
RESULT 281
AAF99427
ID AAF99427 standard; DNA; 20 BP.
XX
XX AAF99427;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #543.
XX
XX KM Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
XX KM immunostimulatory; tumour; viral infection; cancer; bacterial infection;
XX KM fungal infection; parasitic infection; cancer; asthma;
XX KM infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
XX OS Synthetic.
XX
XX PN WO200122972-A2.
XX
XX PD 05-APR-2001.
XX
XX PF 25-SEP-2000; 2000WO-US026383.
XX
XX PR 25-SEP-1999; 99US-0156113P.
XX PR 27-SEP-1999; 99US-0156135P.
XX PR 23-AUG-2000; 2000US-0227436P.
XX
XX PA (IOWA) UNIV IOWA RES FOUND.
XX PA (COLE-) COLEY PHARM GMBH.
XX
XX PI Krieg AM, Schetter C, Vollmer J;
XX PI
XX DR WPI; 2001-273485/28.
XX
XX PT Vaccinating against tumors, infectious diseases, allergies and asthma
XX PT using immunostimulatory Py-rich and TG nucleic acids.
XX
XX PS Claim 101; Page 49; 338pp; English.
XX
XX CC The present invention relates to a method for stimulating an immune
XX CC response. The method comprises administering an immunostimulatory nucleic
XX CC acid to a non-rodent subject in sufficient quantity to stimulate an

KW Influenza; herpes; infection; ss.
 XX Unidentified.
 OS
 XX
 PN US6169176-B1.
 XX
 PD 02-JAN-2001.
 XX
 PF 28-SEP-1999; 99US-00407675.
 XX
 PR 02-JUL-1998; 98US-0091481P.
 XX 11-DEC-1998; 98US-0111800P.
 PR 02-JUL-1999; 99US-00347443.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Dev AP, Bruce TC;
 XX
 DR WPI; 2001-122276/13.
 XX
 XX Preparing novel deoxynucleic alkyl thiourea oligonucleotide for use in
 PT antisense therapy, by synthesizing oligonucleotides comprising backbone
 PT of alkyl or alkoxy thiourea linkages in solution or on solid phase.
 XX
 PS Example 7; Fig 16; 48pp; English.
 XX
 CC The present sequence was used to demonstrate the ability of deoxynucleic
 CC S-methylthiourea (DMT) compounds to form triplets with DNA oligomers. An
 CC increase in the C content of the oligo resulted in a large decrease in
 CC binding. This experiment was performed as an example of a method for
 CC preparing oligonucleotides comprising a backbone of alkyl or alkoxy
 CC thiourea linkages. The method is useful for preparing oligonucleotides
 CC for use in antisense or antisense therapy, to inhibit production of
 CC proteins associated with genetic diseases, cardiovascular, inflammatory
 CC and neurocellular diseases, and for antiviral therapy, e.g. to treat
 CC human immunodeficiency virus, human cytomegalovirus, influenza and herpes
 CC infections. The compounds are also useful as diagnostic reagents to
 CC detect the presence or absence of the target DNA or RNA sequences to
 CC which they specifically bind and by antagonising the normal biological
 CC activity of a target protein, they can be used in the manipulation of
 CC tissue e.g. tissue differentiation, both in vivo and in ex vivo tissue
 CC cultures. The method provides an efficient and rapid solid-phase method
 CC for the synthesis of thiourea and S-methylthiourea
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 XX
 Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 4464 TTTT TTTT TTTT TTTT TTTT 4483
 Db 20 TTTT TTTT TTTT TTTT TTTT 1
 XX
 RESULT 287
 ID ABS77742
 ID ABS77742 standard; DNA; 20 BP.
 XX
 AC ABS77742;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Angiogenesis inhibitory oligonucleotide #226.
 XX
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubecosis; Osler-Webber Syndrome; myocardial angiodysplasia;
 KW plaque neovascularisation; telangiectasia; haemophilic joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.

XX
 OS Synthetic.
 XX
 PN WO200253141-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 14-DEC-2001; 2001WO-US048458.
 XX
 PR 14-DEC-2000; 2000US-0255534P.
 XX
 PA (COLE-) COLEY PHARM GROUP INC.
 XX
 PI Bratzler RL;
 XX
 DR WPI; 2002-566690/60.
 XX
 PT Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.
 XX
 PS Claim 2; Page 23; 276pp; English.
 XX
 CC The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubecosis, Osler-Webber Syndrome, myocardial angiodysplasia, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
 XX
 Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 4464 TTTT TTTT TTTT TTTT TTTT 4483
 Db 1 TTTT TTTT TTTT TTTT TTTT 20
 XX
 RESULT 288
 ID ABS78072
 ID ABS78072 standard; DNA; 20 BP.
 XX
 AC ABS78072;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Angiogenesis inhibitory oligonucleotide #556.
 XX
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubecosis; Osler-Webber Syndrome; myocardial angiodysplasia;
 KW plaque neovascularisation; telangiectasia; haemophilic joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.
 XX
 OS Synthetic.
 XX
 PN WO200253141-A2.
 XX
 PD 11-JUL-2002.

PF 14-DEC-2001; 2001WO-US048458.
 XX
 XX 14-DEC-2000; 2000US-0255534P.
 XX
 PA (COLB-) COLEY PHARM GROUP INC.
 XX
 XX Bratzler RL;
 PI
 DR WPI; 2002-566690/60.
 XX
 XX Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.
 XX
 PS Claim 2; Page 29; 276pp; English.
 XX
 CC The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubecosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiodiroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 SO Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
 Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
 Db 1 TTTT TTTT TTTT TTTT TTTT 20
 RESULT 289
 ABS78076/c
 ID ABS78076 standard; DNA; 20 BP.
 XX
 AC ABS78076;
 XX
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Angiogenesis inhibitory oligonucleotide #560.
 XX
 KM Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KM tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KM diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KM corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KM rubecosis; Osler-Webber Syndrome; myocardial angiogenesis;
 KM plaque neovascularisation; telangiectasia; haemophilic joint;
 KM angiodiroma; wound granulation; intestinal adhesions; atherosclerosis;
 KM scleroderma; hypertrophic scar.
 XX
 OS Synthetic.
 XX
 PN WO200253141-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 14-DEC-2001; 2001WO-US048458.
 XX
 PR 14-DEC-2000; 2000US-0255534P.
 XX
 PA (COLB-) COLEY PHARM GROUP INC.
 XX
 PI Bratzler RL;

XX
 DR WPI; 2002-566690/60.
 XX
 XX Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.
 XX
 XX Claim 2; Page 29; 276pp; English.
 XX
 CC The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubecosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiodiroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 SO Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
 Db 20 TTTT TTTT TTTT TTTT TTTT 1
 RESULT 290
 ABL39402
 ID ABL39402 standard; DNA; 20 BP.
 XX
 AC ABL39402;
 XX
 XX
 DT 16-APR-2002 (first entry)
 XX
 DE Immunostimulatory nucleic acid SEQ ID NO: 838.
 XX
 KM Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
 KM angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone"
 PN WO200197843-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 22-JUN-2001; 2001WO-US020154.
 XX
 PR 22-JUN-2000; 2000US-0213346P.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Weiner G, Hartmann G;
 XX
 XX WPI; 2002-154611/20.
 XX
 XX Treating or preventing cancer, such as basal cell carcinoma, comprises
 PT administering immunostimulatory nucleic acids that induce expression of
 PT cell surface antigens and antibodies to a subject having or at risk of
 PT developing cancer.

XX Disclosure; Page 309; 312pp; English.
PS
XX The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
DB 1 TTTT TTTT TTTT TTTT TTTT 20
RESULT 291
ABL38648/C
ID ABL38648 standard; DNA; 20 BP.
XX
AC ABL38648;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 2.
XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
XX angio genesis; metastasis; cytostatic; ss.
XX
OS Synthetic.
XX
PN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020154.
XX
PR 22-JUN-2000; 2000US-0213346P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
PS Disclosure; Page 95; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-

CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
DB 20 TTTT TTTT TTTT TTTT TTTT 1
RESULT 292
ABL39403
ID ABL39403 standard; DNA; 20 BP.
XX
AC ABL39403;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 839.
XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
XX angio genesis; metastasis; cytostatic; ss.
XX
OS Synthetic.
XX
PN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020154.
XX
PR 22-JUN-2000; 2000US-0213346P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
PS Disclosure; Page 309; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 293

ABLS4775
 ID ABL54775 standard; DNA; 20 BP.

AC ABL54775;

DT 10-JUN-2002 (first entry)

DE CD14 receptor PCR primer SEQ ID NO 9.

XX Angiotensin-I converting enzyme; ACE; CD14; receptor; SNP;

KM single-nucleotide polymorphism; PCR; primer; ss.

OS Synthetic.

PN JP2002034599-A.

PD 05-FEB-2002.

PF 26-JUL-2000; 2000JP-00225354.

PR 26-JUL-2000; 2000JP-00225354.

PA (TOYM) TOYOBO KK.

DR WPI; 2002-275727/32.

PT Detecting 1 base polymorphism on a sequence of a chromosome or its fragment.

PS Example 2; Page 10; 10pp; Japanese.

XX The invention relates to a method for detecting 1 base polymorphism on the sequence of a chromosome or its fragment in which a sample nucleic acid is reacted with a reaction liquor containing a nucleic acid primer having a base adjacent to the polymorphic base at its 3'-end, one dideoxynucleotide corresponding to a polymorphic base having a composition distinguishable feature or its mixture, DNA polymerase and a composition required for its activity expression to detect the presence of taking dideoxynucleotide in the nucleic acid primer and to detect the type of the base to be specified. The method is used for detecting 1 base polymorphism on the sequence of a chromosome or its fragment. The present sequence is that of a PCR primer, useful in examples of the invention

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 294

ABK65035/c
 ID ABK65035 standard; DNA; 20 BP.

AC ABK65035;

DT 02-JUL-2002 (first entry)

DE Nanoparticle-oligonucleotide #55.

XX Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;

KM ss.

XX Synthetic.

OS WO200218643-A2.

PN 07-MAR-2002.

PD 10-AUG-2001; 2001WO-US025237.

PF 11-AUG-2000; 2000US-0224631P.

PR 08-DEC-2000; 2000US-0254392P.

PR 11-DEC-2000; 2000US-0255235P.

PR 12-JAN-2001; 2001US-00760500.

PR 28-MAR-2001; 2001US-00820279.

XX (NANO-) NANOSPHERE INC.

PI Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JF, Elghanian R;

PI Taton TA, Garimella V, Li Z, Park S;

DR WPI; 2002-258024/30.

XX Detecting nucleic acid, useful for diagnosis of genetic, viral or bacterial disease, comprises hybridizing nanoparticles with attached oligonucleotides to nucleic acid and detecting change brought about by hybridization.

XX Example 18; Page 410; 412pp; English.

XX The invention relates to a method of detecting a nucleic acid (NA) having at least 2 portions comprising: (a) providing nanoparticles (NP) with attached oligonucleotides (OGN), where OGN has a sequence complementary to the sequence of NA; (b) contacting NA and NP under conditions effective to allow hybridisation of OGN with NA; and (c) observing a detectable change brought about by hybridisation of OGN with NA. The method is useful for detecting a nucleic acid, separating a selected nucleic acid from others and methods of nanofabrication. Detecting analytes such as nucleic acids and proteins are useful for the diagnosis of genetic, bacterial and viral diseases. The OGN-NP conjugates that use cyclic disulphide linkers improve the sensitivity of diagnostic assays. In particular assays using OGN-NP conjugates prepared using linkers comprising a steroid residue attached to a cyclic disulphide have been found to be approximately 10 times more sensitive than assays employing conjugates prepared using alkanethiols or acyclic disulphides as the linker. The OGN-NP conjugates are stable allowing them to be used directly in PCR solutions. Therefore conjugates added as probes to a DNA target to be PCR amplified can be carried through the 30 or 40 heating cooling cycles of the PCR and are still able to detect the amplicons without opening the tubes and causing contamination. ABK64981-ABK65055 represent nanoparticle-oligonucleotides of the invention

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 DB 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 295

ABK65050/c
 ID ABK65050 standard; DNA; 20 BP.

AC ABK65050;

DT 02-JUL-2002 (first entry)

DE Nanoparticle-oligonucleotide #70.

XX

CC They are also useful in antisense therapy. The present sequence is an
CC antisense oligonucleotide targeted to human MEK4 DNA. This sequence is
CC used in the exemplification of the invention
XX
SQ Sequence 20 BP; 6 A; 7 C; 7 G; 0 T; 0 U; 0 Other;
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7415 GCAGCAGCAGCAGCAGCAGC 7434
DB 1 GCAGCAGCAGCAGCAGCAGC 20
RESULT 297
ID AAL45122 standard; DNA; 20 BP.
XX AAL45122;
AC AAL45122;
XX 24-MAY-2002 (first entry)
XX
XX Oligonucleotide synthesis method related DNA #1.
DE Oligonucleotide synthesis; polynucleotide array; protecting group;
KM oxidation; ss.
XX
XX Synthetic.
XX EP1176151-A1.
XX 30-JAN-2002.
XX 27-JUL-2001; 2001BP-00118360.
XX 28-JUL-2000; 2000US-00627249.
XX
XX (AGIL-) AGILENT TECHNOLOGIES INC.
XX Dellinger DJ, Perdest MCM, Betley JR, Caruthers M;
PI WPI; 2002-156732/21.
XX
XX Synthesis of polynucleotide useful during fabrication of an array
PT involves coupling nucleoside phosphoramidite and a solid-supported
PT nucleoside and treating the product with an oxidation/deprotection
PT composition.
XX
XX Example 1; Page 15; 36pp; English.
XX
XX The present invention relates to a method for the synthesis of a
CC polynucleotide which involves coupling a second nucleoside to a first
CC nucleoside through a phosphite linkage, where the second nucleoside has a
CC non-carbonate protecting group protecting a hydroxyl, and exposing the
CC product to a composition which concurrently oxidizes the phosphite formed
CC to a phosphate and deprotects the protected hydroxyl of the second
CC nucleoside. The method is useful for synthesizing the polynucleotides,
CC for carrying out either 3' to 5' or 5' to 3' synthesis and for
CC fabricating an addressable array of polynucleotides on a substrate. The
CC present sequence is an oligonucleotide produced to demonstrate the method
CC of the invention
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTTTTTTTTTTTTTTTT 4483
DB 1 TTTTTTTTTTTTTTTTTT 20

RESULT 298
ID ABL36232/C
XX ABL36232 standard; DNA; 20 BP.
XX ABL36232;
AC ABL36232;
XX
XX 08-APR-2002 (first entry)
XX
XX M tuberculosis rRNA probe SEQ ID NO: 83.
DE
XX
XX Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
KM alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
KM antipsoriatic; dermatological; antiinflammatory; antiallergic;
KM Th2 immune response; immunomodulatory; probe; ss.
XX
XX Mycobacterium tuberculosis.
OS
XX US6328978-B1.
XX
XX 11-DEC-2001.
XX
XX 02-JUN-1999; 99US-00324542.
XX
XX 23-DEC-1997; 97US-00997080.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Watson JD, Tan PLJ, Prestidge R;
PI WPI; 2002-138361/18.
XX
XX Inhibiting skin inflammation associated with skin disorder e.g.
PT psoriasis, by administering composition comprising delipidated and
PT delipidated Mycobacterium vaccae cells or Mycobacterium vaccae
PT culture filtrate.
XX
XX Example 5; Col 99-100; 116pp; English.
XX
XX The present invention relates to a method of inhibiting skin inflammation
CC associated with a skin disorder selected from psoriasis, atopic
CC dermatitis and allergic contact dermatitis, which involves administering
CC a composition containing delipidated and delipidated Mycobacterium
CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
CC treated may also include alopecia areata, and skin cancers such as basal
CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
CC acts by inhibiting the Th2 immune response. The present sequence is a
CC probe described in the exemplification of the invention
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTTTTTTTTTTTTTTTT 4483
DB 20 TTTTTTTTTTTTTTTTTT 1
RESULT 299
ID ABS64673/C
XX ABS64673 standard; DNA; 20 BP.
XX ABS64673;
AC ABS64673;
XX
XX 15-NOV-2002 (first entry)
XX
XX Nucleic acid detection method associated polynucleotide #55.
DE
XX Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KM nanoparticle; viral RNA detection; bacterial DNA detection;
KM fungal DNA detection; nanoprobe conjugate; ss.

```

XX Synthetic.
XX
XX WO200246472-A2.
XX
XX 13-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046418.
XX
XX 08-DEC-2000; 2000US-0254392P.
XX
XX 08-DEC-2000; 2000US-0254418P.
XX
XX 11-DEC-2000; 2000US-0255235P.
XX
XX 11-DEC-2000; 2000US-0255236P.
XX
XX 12-JAN-2001; 2001US-00760500.
XX
XX 28-MAR-2001; 2001US-00880279.
XX
XX 09-APR-2001; 2001US-0282640P.
XX
XX 10-AUG-2001; 2001US-00927777.
XX
XX (NANO-) NANOSPHERE INC.
XX
XX Mitkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;
XX Pi Taton TA, Gattimella V, Li Z, Park S;
XX WPI; 2002-608256/65.
XX
XX Detecting nucleic acid having two portions, by providing nanoparticles
XX PT having oligonucleotides attached to it, contacting nucleic acid and
XX PR nanoparticles to allow hybridization, and observing detectable change.
XX
XX Example 18; Page 437; 442pp; English.
XX
XX The invention describes a method of detecting (M1) a nucleic acid having
XX CC two portions, involving providing nanoparticles having oligonucleotides
XX CC attached to it, which has a sequence complementary to sequence of two
XX CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to
XX CC allow hybridisation of oligonucleotides with two or more portions of
XX CC nucleic acid, and observing a detectable change brought about by
XX CC hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
XX CC conjugates (II) and the aggregate probe are useful for detecting two or
XX CC more nucleic acids (from a biological source) having at least two
XX CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated
XX CC with a disease, synthetic, or structurally-modified natural or synthetic
XX CC RNA or DNA, or a product of a polymerase chain reaction amplification.
XX CC (II) is useful for preparing a nanoprobe conjugate for detecting an
XX CC analyte, and for detecting a nucleic acid bound to an electrode surface.
XX CC (I) and (II) are useful for fabrication, and for separating a selected
XX CC nucleic acid having two portions from other nucleic acids. (I), (II) and
XX CC the aggregate probe are useful for detecting an analyte (especially a
XX CC polyvalent analyte) in a sample. This sequence represents a
XX CC polynucleotide used to demonstrate the method of the invention
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred.No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
XX Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 1
XX
XX RESULT 300
XX ABS64688/C
XX ID ABS64688 standard; DNA; 20 BP.
XX
XX ABS64688;
XX AC
XX DT 15-NOV-2002 (first entry)
XX DE Nucleic acid detection method associated polynucleotide #70.
XX NW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;

```

KW		nanoParticle; viral RNA detection; bacterial DNA detection;
KW		fungal DNA detection; nanoprobe conjugate; ss.
XX	OS	Synthetic.
XX	PV	WO200246472-A2.
PD		13-JUN-2002.
PP		07-DEC-2001; 2001MO-US046418.
XX		08-DEC-2000; 2000US-0254392P.
PR		08-DEC-2000; 2000US-0254418P.
PR		11-DEC-2000; 2000US-0255235P.
PR		11-DEC-2000; 2000US-0255236P.
PR		12-JAN-2001; 2001US-00760500.
PR		28-MAR-2001; 2001US-00820279.
PR		09-APR-2001; 2001US-0282640P.
PR		10-AUG-2001; 2001US-00927777.
PA		(NANO-) NANOSPHERE INC.
PI		Mickin CA, Letsinger RL, Mucic RC, Storchoff JT, Elghanian R; Pi Tacon TA, Garimella V, Li Z, Park S; WP1; 2002-608256/65.
DR		Detecting nucleic acid having two portions, by providing nanoparticles PT having oligonucleotides attached to it, contacting nucleic acid and PT nanoparticles to allow hybridization, and observing detectable change. XX Example 24; Fig 44; 442pp; English.
PS		The invention describes a method of detecting (M1) a nucleic acid having XX two portions, involving providing nanoparticles having oligonucleotides CC attached to it, which has a sequence complementary to sequence of two CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to CC allow hybridisation of oligonucleotides with two or more portions of CC nucleic acid, and observing a detectable change brought about by CC hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide CC conjugates (II) and the aggregate probe are useful for detecting two or CC more nucleic acids (from a biological source) having at least two CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated CC with a disease, synthetic, or structurally-modified natural or synthetic CC RNA or DNA, or a product of a polymerase chain reaction amplification. CC (II) is useful for preparing a nanoprobe conjugate for detecting an CC analyte, and for detecting a nucleic acid bound to an electrode surface. CC (I) and (II) are useful for fabrication, and for separating a selected CC nucleic acid having two portions from other nucleic acids. (I), (II) and CC the aggregate probe are useful for detecting an analyte (especially a CC polyvalent analyte) in a sample. This sequence represents a CC polynucleotide used to demonstrate the method of the invention SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
QY		Query Match 0.3%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
DB		4464 TTTTTTTTTTTTTTTTTT 4483 20 TTTTTTTTTTTTTTTTTTTT 1
RESULT 301		
ID	ABN87103	standard; DNA; 20 BP.
AC	ABN87103;	
DT	30-JUL-2002	(first entry)
Capture probe CP5' SEQ ID NO:23.		

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR MPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3807; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
DB 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 304
AB288619/C
ID AB288619 standard; DNA; 20 BP.
XX
XX AB288619;
AC
XX
XX 17-OCT-2003 (first entry)
DT
XX
XX Human oligonucleotide sequence.
DE
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR MPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3861; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
DB 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 305
AB289705/C
ID AB289705 standard; DNA; 20 BP.
XX
XX AB289705;
AC
XX
XX 17-OCT-2003 (first entry)
DT
XX
XX Human oligonucleotide sequence.
DE
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;

KW		antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KX		antihistaminic; hypotensive; immunosuppressive; cytoskeletal; gene therapy;
KV		antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW		adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KX		lung inflammation; respiratory disease; ds.
XX		
OS	Homo sapiens.	
XX		
FN	WO200285308-A2.	
XX		
PD	31-OCT-2002.	
XX		
PE	23-APR-2002; 2002WO-US013135.	
XX		
PR	24-APR-2001; 2001US-0286137P.	
XX		
PA	(EP1G-) EPIGENESIS PHARM INC.	
XX		
P1	Nyce JW, Li Y, Sandraeagra A, Katz E, Pabalan J, Aguilar D,	
XX	Miller S, Tang L, Shahabuddin S;	
DR	WPI; 2003-229219/22.	
XX		
PT	Pharmaceutical composition for treating ailments associated with impaired	
XX	respiration, has oligo(s) antisense to specific gene(s) or its	
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or	
XX	ubiquinone.	
PS	Disclosure; SEQ ID NO 4947; 872pp; English.	
XX		
CC	The invention relates to a novel pharmaceutical composition, which has a	
CC	first active agent comprising an oligonucleotide antisense to the	
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,	
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of	
CC	junctions of genes encoding a polypeptide associated with lung and/or	
CC	nasal airway dysfunction and a second active agent comprising an	
CC	antiinflammatory steroid and ubiquinone. A composition of the invention	
CC	has antiinflammatory, antiallergic, antiasthmatic, hypotensive,	
CC	immunosuppressive, and cytostatic activity. The composition may have a	
CC	use in antisense gene therapy. The composition is useful for treating or	
CC	preventing a respiratory, lung or malignant disease or condition, also	
CC	for enhancing the prophylactic or therapeutic respiratory effect of an	
CC	antiinflammatory steroid in a subject, for reducing or depleting levels	
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine	
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or	
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,	
CC	lung inflammation, lung allergies, or a respiratory disease or condition.	
CC	Note: The sequence data for this patent is not represented in the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences	
XX		
SQ	Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;	
	Query Match 0.3%; Score 20; DB 1; Length 20;	
	Best Local Similarity 100.0%; Pred. No. 2.7e+02;	
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	4464 TTTT TTTTTTTTTTTTTTTTTT 4483	
DB	20 TTTT TTTTTTTTTTTTTTTTTT 1	
	RESULT 306	
	ABZ88816/C	
ID	ABZ88816 standard; DNA; 20 BP.	
XX		
AC	ABZ88816;	
XX		
DT	17-OCT-2003 (first entry)	
XX		
DE	Human oligonucleotide sequence.	
XX		
KW	Human; antisense; lung dysfunction; nasal airway dysfunction;	

KW		antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KX		antiaesthetic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KY		antisense gene therapy; respiratory; lung; adenosine sensitivity;
KZ		adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
LW		lung inflammation; respiratory disease; ds.
XX		
OS	Homo sapiens.	
XX		
PN	WO200285308-A2.	
PD	31-OCT-2002.	
XX		
PE	23-APR-2002; 2002WO-US013135.	
XX		
PR	24-APR-2001; 2001US-0286137P.	
XX		
PA	(EPIG-) EPIGENESIS PHARM INC.	
PI	Nyee JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;	
PL	Miller S, Tang L, Shanabuddin S;	
DR	WI; 2003-229219/22.	
XX		
PT	Pharmaceutical composition for treating ailments associated with impaired	
PT	respiration, has oligo(s) antisense to specific gene(s) or its	
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or	
XX	ubiquinone.	
PS	Disclosure; SEQ ID NO 4058; 872pp; English.	
XX		
CC	The invention relates to a novel pharmaceutical composition, which has a	
CC	first active agent comprising an oligonucleotide antisense to the	
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,	
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of	
CC	junctions of genes encoding a polypeptide associated with lung and/or	
CC	nasal airway dysfunction and a second active agent comprising an	
CC	antiinflammatory steroid and ubiquinone. A composition of the invention	
CC	has antiinflammatory, antiallergic, antiaesthetic, hypotensive,	
CC	immunosuppressive, and cytostatic activity. The composition may have a	
CC	use in antisense gene therapy. The composition is useful for treating or	
CC	preventing a respiratory, lung or malignant disease or condition, also	
CC	for enhancing the prophylactic or therapeutic respiratory effect of an	
CC	antiinflammatory steroid in a subject, for reducing or depleting levels	
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine	
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or	
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,	
CC	lung inflammation, lung allergies, or a respiratory disease or condition.	
CC	Note: The sequence data for this patent are not represented in the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences	
XX		
SQ	Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;	
	Query Match	0.3%; Score 20; DB 1; Length 20;
	Best Local Similarity	100.0%; Pred. No. 2.7e+02;
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	4464 TTTTTTTTTTTTTTTTTT 4483	
Db	20 TTTTYYYYYYYYTTTTTT 1	
	RESULT 307	
ID	AB288881/C	
XX	AB288881 standard; DNA; 20 BP.	
AC	AB288881;	
XX		
DT	17-OCT-2003 (first entry)	
XX		
DE	Human oligonucleotide sequence.	
XX		
KW	Human; antisense; lung dysfunction; nasal airway dysfunction;	

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antileukemic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN MO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIDERMIS PHARM INC.
XX
PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR MPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4123; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antileukemic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
DB 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 308
AB289706/c
ID AB289706 standard; DNA; 20 BP.
XX
XX AB289706;
AC
XX
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antileukemic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN MO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIDERMIS PHARM INC.
XX
PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR MPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4948; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antileukemic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
DB 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 309
AB288620/c
ID AB288620 standard; DNA; 20 BP.
XX
XX AB288620;
AC
XX
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW		antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XV		antihypertensive; immunosuppressive; cyclostatic; gene therapy;
KM		antisense gene therapy; respiratory; lung; adenosine sensitivity;
KN		adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KX		lung inflammation; respiratory disease; ds.
OS		Homo sapiens.
XX		WO200285308-A2.
PY		31-OCT-2002.
PD		23-APR-2002; 2002MO-USO13135.
PE		24-APR-2001; 2001US-0286137P.
PR		(EPIG-) EPIGENESIS PHARM INC.
PA		Nyge JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D,
PL		Miller S, Tang L, Shahabbudin S;
DR		WIPO; 2003-229219/22.
DZ		Pharmaceutical composition for treating ailments associated with impaired
PT		respiration, has oligo(s) antisense to specific gene(s) or its
PF		corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT		ubiquinolone.
PS		Disclosure; SEQ ID NO 3862; 872pp; English.
XX		The invention relates to a novel pharmaceutical composition, which has a
CC		first active agent comprising an oligonucleotide antisense to the
CC		initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC		5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC		junctions of genes encoding a polypeptide associated with lung and/or
CC		nasal airway dysfunction and a second active agent comprising an
CC		antiinflammatory steroid and ubiqunone. A composition of the invention
CC		has antiinflammatory, cytostatic activity. The composition may have a
CC		immunopressive, and anticarcinogenic activity. The composition may have a
CC		use in antisense gene therapy. The composition is useful for treating or
CC		preventing a respiratory, lung or malignant disease or condition, also
CC		for enhancing the prophylactic or therapeutic respiratory effect of an
CC		antiinflammatory steroid in a subject, for reducing or depleting levels
CC		of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC		receptor, producing bronchodilation, increasing levels of ubiquinone or
CC		lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC		lung inflammation, lung allergies, or a respiratory disease or condition.
CC		Note: The sequence data for this patent is not represented in the printed
CC		specification, but was obtained in electronic format directly from WIPO
CC		at ftp.wipo.int/pub/published_pct_sequences
SQ		Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other:
OY		Query Match 0.3%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ID	AB288814/C	
AC	AB288814 standard DNA, 20 BP.	
DT	17-OCT-2003 (first entry)	
DE	Human oligonucleotide sequence.	
XX	Human; antisense; lung dysfunction; nasal airway dysfunction;	
KV		

KW		antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM		antihistaminic; hypotensive; immunosuppressive; cytosolic; gene therapy;
KV		antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW		adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KX		lung inflammation; respiratory disease; ds.
OS		Homo sapiens.
NN		WO200285308-A2.
NN		31-OCT-2002.
PD		23-APR-2002; 2002WO-US013135.
PF		24-APR-2001; 2001US-0286137P.
XX		(EPIG-) EPIGENESIS PHARM INC.
PA		Nyge JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI		Miller S, Tang L, Shahabuddin S,
DR		WPI; 2003-229219/22.
PT		Pharmaceutical composition for treating ailments associated with impaired
PT		respiration, has oligo(s) antisense to specific gene(s) or its
PT		corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX		ubiquinone.
PS		Disclosure; SEQ ID NO 4056; 872pp; English.
XX		The invention relates to a novel pharmaceutical composition, which has a
CC		first active agent comprising an oligonucleotide antisense to the
CC		initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC		5' and 3', intron-exon junctions, or regions within 2-10 nucleotides of
CC		junctions of genes encoding a polypeptide associated with lung and/or
CC		nasal airway dysfunction and a second active agent comprising an
CC		antiinflammatory steroid and ubiquinone. A composition of the invention
CC		has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC		immunosuppressive, and cytostatic activity. The composition may have a
CC		use in antisense gene therapy. The composition is useful for treating or
CC		preventing a respiratory, lung or malignant disease or condition, also
CC		for enhancing the prophylactic or therapeutic respiratory effect of an
CC		antiinflammatory steroid in a subject, for reducing or depleting levels
CC		of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC		receptor, producing bronchodilation, increasing levels of ubiquinone or
CC		lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC		lung inflammation, lung allergies, or a respiratory disease or condition.
CC		Note: The sequence data for this patent is not represented in the printed
CC		specification, but was obtained in electronic format directly from WIPO
CC		at ftp.wipo.int/pub/published_pct_sequences
XX		
SQ		Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
		Query Match 0.3%; Score 20; DB 1; Length 20;
		Best local Similarity 100.0%; Prid. No. 2.7e+02;
		Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY		4464 TTTTTTTTTTTTTTTTTTTT 4463
DB		
		20 TTTTTTTTTTTTTTTTTTTT 1
		RESULT 111
ID		ABZ89241/c
XX		ABZ89241 standard; DNA; 20 BP.
AC		ABZ89241;
XX		
DT		17-OCT-2003 (first entry)
DE		Human oligonucleotide sequence.
XX		
KW		Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Myce JW, Li Y, Sandraasgra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4483; 872bp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiallergic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
DB 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 312
AB290650/c
ID AB290650 standard; DNA; 20 BP.
XX
AC AB290650;
XX
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Myce JW, Li Y, Sandraasgra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 5892; 872bp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiallergic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
DB 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 313
AB288618/c
ID AB288618 standard; DNA; 20 BP.
XX
AC AB288618;
XX
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antiasthma gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;
XX
XX MPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Claim 15; SEQ ID NO 553; 872bp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT TTTT 4483
XX Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 316
AB285435
ID AB285435 standard; DNA; 20 BP.
XX
XX AB285435;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antiasthma gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;
XX
XX MPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Claim 15; SEQ ID NO 677; 872bp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT TTTT 4483
XX Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 317
AB288817/c
ID AB288817 standard; DNA; 20 BP.
XX
XX AB288817;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;

KW		antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM		antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX		antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM		adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX		lung inflammation; respiratory disease; ds.
OS		Homo sapiens.
PN		WO200285308-A2.
XX		
PD		31-OCT-2002.
XX		
PP		23-APR-2002; 2002WO-US013135.
PR		24-APR-2001; 2001US-0286137P.
PA		(EPIC-) EPIGENESIS PHARM INC.
P1		Nyee JM, Li Y, Sandraasgra A, Katz E, Pabalan J, Aguilar D;
P1		Miller S, Tang L, Shanabuddin S;
DR		WPI, 2003-229219/22.
XX		
PT		Pharmaceutical composition for treating ailments associated with impaired
PT		respiration, has oligo(s) antisense to specific gene(s) or its
PT		corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX		ubiquinone.
PS		Disclosure; SEQ ID NO 4059; 87zpp; English.
XX		
CC		The invention relates to a novel pharmaceutical composition, which has a
CC		first active agent comprising an oligonucleotide antisense to the
CC		initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC		5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC		junctions of genes encoding a polypeptide associated with lung and/or
CC		nasal airway dysfunction and a second active agent comprising an
CC		antiinflammatory steroid and ubiquinone. A composition of the invention
CC		has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC		immunosuppressive, and cytostatic activity. The composition may have a
CC		use in antisense gene therapy. The composition is useful for treating or
CC		preventing a respiratory, lung or malignant disease or condition, also
CC		for enhancing the prophylactic or therapeutic respiratory effect of an
CC		antiinflammatory steroid in a subject, for reducing or depleting levels
CC		of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC		receptor, producing bronchodilation, increasing levels of ubiquinone or
CC		lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC		lung inflammation, lung allergies, or a respiratory disease or condition.
CC		Note: The sequence data for this patent is not represented in the printed
CC		specification, but was obtained in electronic format directly from WINDO
CC		at ftp.wipo.int/pub/published_pct_sequences
XX		
SQ		Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
		Query Match 0.3%; Score 20; DB 1; Length 20;
		Best Local Similarity 100.0%; Pred.No. 2.7e+02;
		Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY		4464 TTTT TTTTTTTTTTTTTTTTTT 4483
Dd		
		20 TTTT TTTTTTTTTTTTTTTTTT 1
RESULT 318		
ID		ABZ88939/C
ID		ABZ88939 standard; DNA, 20 BP.
XX		
AC		ABZ88939;
XX		
DT		17-OCT-2003 (first entry)
XX		
DE		Human oligonucleotide sequence.
XX		
KW		Human; antisense; lung dysfunction; nasal airway dysfunction;

KM		antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM		antiashmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KX		[antisense gene therapy]; respiratory; lung; adenosine sensitivity;
KW		adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KV		lung inflammation; respiratory disease; ds-
XX		
OS	Homo sapiens.	
PN	WO200285308-A2.	
PD	31-OCT-2002.	
PD		
PF	23-APR-2002; 2002MO-USO13135.	
PR	24-APR-2001; 2001US-0286137P.	
PA	(EPIC-) EPIGENESIS PHARM INC.	
PI	Nyee JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;	
PI	Miller S, Tang L, Shahabuddin S,	
DR	WPI; 2003-229219/22.	
PT		
PT	Pharmaceutical composition for treating ailments associated with impaired	
PT	respiration, has oligo(s) antisense to specific gene(s) or its	
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or	
PT	ubiquinone.	
PS	Disclosure; SEQ ID NO 4181; 872pp; English.	
XX		
CC	The invention relates to a novel pharmaceutical composition, which has a	
CC	first active agent comprising an oligonucleotide antisense to the	
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,	
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of	
CC	junctions of genes encoding a polypeptide associated with lung and/or	
CC	nasal airway dysfunction and a second active agent comprising an	
CC	antiinflammatory steroid and ubiquinone. A composition of the invention	
CC	has antiinflammatory, antiallergic, antiashmatic, hypotensive,	
CC	immunosuppressive, and cytostatic activity. The composition may have a	
CC	use in antisense gene therapy. The composition is useful for treating or	
CC	preventing a respiratory, lung or malignant disease or condition, also	
CC	for enhancing the prophylactic or therapeutic respiratory effect of an	
CC	antiinflammatory steroid in a subject, for reducing or depleting levels	
CC	of, or reducing sensitivity to adenose, reducing levels of adenosine	
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or	
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,	
CC	lung inflammation, lung allergies, or a respiratory disease or condition.	
CC	Note: The sequence data for this patent is not represented in the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences	
XX		
SQ	Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;	
	Query Match	0.3%; Score 20; DB 1; Length 20;
	Best Local Similarity	100.0%; Freq. No. 2.7e+02;
	Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	4464 TTTT[T]TTTTTTT[TTTTTTT]	4463
DB	20 TTTT[T]TTTTTTT[TTTTTTT]	1
RESULT 319		
ID	ABZ89302/C	
XX	ABZ89302 standard; DNA; 20 BP.	
AC	ABZ89302;	
XX		
DT	17-OCT-2003 (first entry)	
DE	Human oligonucleotide sequence.	
XX		
XX	Human; antisense; lung dysfunction; nasal airway dysfunction;	

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytoskeletal; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN MO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4544; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC fire active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytoskeletal activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
DB 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 320
AB288566/c
ID AB288566 standard; DNA; 20 BP.
XX
AC AB288566;
XX
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytoskeletal; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN MO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3808; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC fire active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytoskeletal activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
DB 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 321
AB289086/c
ID AB289086 standard; DNA; 20 BP.
XX
AC AB289086;
XX
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW adenosine gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4328; 872bp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 322
AB285533/c
ID AB285533 standard; DNA; 20 BP.
XX
AC AB285533;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW adenosine gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 775; 872bp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 323
AB285595/c
ID AB285595 standard; DNA; 20 BP.
XX
AC AB285595;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antialstematic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; db.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 837; 872bp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antialstematic, hypotensive,
CC immunosuppressive, and cytosstatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 5 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7419 CAGCAGCAGCAGCAGCA 7438
DB 20 CAGCAGCAGCAGCAGCA 1

RESULT 324
AB289015/c
ID AB289015 standard; DNA; 20 BP.
XX
XX AB289015;
AC
XX
XX 17-OCT-2003 (first entry)
DT
XX
XX Human oligonucleotide sequence.
DE
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antialstematic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; db.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4257; 872bp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antialstematic, hypotensive,
CC immunosuppressive, and cytosstatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTTTT 4483
DB 20 TTTTTTTTTTTTTTTTTT 1

RESULT 325
AB289441/c
ID AB289441 standard; DNA; 20 BP.
XX
XX AB289441;
AC
XX
XX 17-OCT-2003 (first entry)
DT
XX
XX Human oligonucleotide sequence.
DE
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW adenine gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Myce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4362; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2,7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
DB 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 328
AB289704/c
ID AB289704 standard; DNA; 20 BP.
XX
AC AB289704;
XX
XX 17-OCT-2003 (first entry)
DT
XX Human oligonucleotide sequence.
DE
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW adenine gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Myce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4946; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2,7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
DB 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 329
ACD27320/c
ID ACD27320 standard; DNA; 20 BP.
XX
AC ACD27320;
XX
XX 15-OCT-2003 (first entry)
DT
XX Nanotechnology nucleic acid detection method associated #54.
DE
XX Nanotechnology; ss; nucleic acid detection; nanoparticle;
KW


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FH Key Location/Qualifiers
PT modified_base 1..20
PT /+tag= a
PT /mod_base= OTHER
PT /note= "phosphorothioate linkages"
XX
XX WO2002102815-A2.
XX
XX 27-DEC-2002.
XX
XX 13-JUN-2002; 2002WO-US018581.
XX
XX 14-JUN-2001; 2001US-00881535.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ravikumar VT;
XX
XX WPI; 2003-157021/15.
XX
XX Preparing internucleotide phosphorothioate linkage enhanced in Sp/Rp
PT enantiomer by coupling a synthon with 2'-substituted nucleoside in
PT presence of coupling agent having a pKa that enhances linkage in Sp/Rp
PT enantiomer.
XX
XX Example 1; Page 31; 65pp; English.
XX
XX The present invention describes a method (M1) for preparing an
XX internucleotide phosphorothioate linkage enriched in the Sp or Rp
XX enantiomer between a synthon having a hydroxyl moiety at the 5' position
XX and a 2'-substituted nucleoside having an activated phosphate moiety at
XX the 3'-position, comprising coupling a synthon with a 2'-substituted
XX nucleoside in the presence of coupling agent that is selected to enhance
XX either the Rp or Sp enantiomer according to its pKa. This method is
XX useful for preparing an oligonucleotide having at least one region of
XX internucleotide linkages that is enhanced in the Sp or Rp enantiomer,
XX which involves providing a nucleoside having a hydroxyl moiety at the 5'-
XX position or a growing oligonucleotide chain having a hydroxyl moiety at
XX the 5'-position, coupling the nucleoside or growing oligonucleotide chain
XX to a 2'-substituted nucleoside having an activated phosphate moiety at
XX the 3' position in the presence of the coupling agent, and repeating the
XX coupling step until the desired number of linkages is established. The
XX oligonucleotide having a region of internucleotide linkages that is
XX enhanced in the Sp enantiomer is further processed to include another
XX region of internucleotide linkages that is enhanced in the Sp and/or Rp
XX enantiomer. Oligonucleotides prepared by the method lead to improved
XX drugs, diagnostics and research reagents. The present sequence represents
XX an oligonucleotide used in the exemplification of the present invention
XX
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
XX |||||
XX 1 TTTT TTTT TTTT TTTT TTTT 20
XX
XX Db
XX
XX RESULT 332
XX AAL61645/c
XX ID AAL61645 standard; DNA; 20 BP.
XX
XX AC AAL61645;
XX
XX 22-SEP-2003 (first entry)
XX
XX Thiol-modified oligo #4 used in the nucleic acid detection method.
XX
XX Nucleic acid detection; fabrication; ss.
XX
XX OS Unidentified.

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XX
XX WO2003035829-A2.
XX
XX 01-MAY-2003.
XX
XX 08-OCT-2002; 2002WO-US032088.
XX
XX 09-OCT-2001; 2001US-0327864P.
XX
XX 07-DEC-2001; 2001US-00008978.
XX
XX (NANO-) NANOSPHERE INC.
XX
XX Park S, Taton TA, Mirkin CA;
XX
XX WPI; 2003-430409/40.
XX
XX Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change.
XX
XX Example 18; Page 179; 467pp; English.
XX
XX The invention relates to a method of detecting a nucleic acid having two
XX portions. The method involves providing nanoparticles having
XX oligonucleotides attached to it which has a sequence complementary to
XX sequence of two portions of nucleic acid, contacting nucleic acid and
XX nanoparticles to allow hybridization of oligonucleotides with two or more
XX portions of nucleic acid and observing a detectable change brought about
XX by hybridization. The method and aggregate probes are useful for
XX detecting two or more nucleic acids (from a biological source) having at
XX least two portions such as viral RNA, bacterial or fungal DNA, a gene
XX associated with a disease, synthetic or structurally modified natural or
XX synthetic RNA or DNA, or a product of a polymerase chain reaction
XX amplification. The invention is useful for preparing a nanoprobe
XX configured for detecting an analyte and for detecting a nucleic acid bound
XX to an electrode surface. It is also useful for fabrication and for
XX separating a selected nucleic acid having two portions from other nucleic
XX acids. The present sequence is an oligo used to illustrate the method of
XX the invention
XX
XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
XX |||||
XX 20 TTTT TTTT TTTT TTTT TTTT 1
XX
XX Db
XX
XX RESULT 333
XX ABZ59815
XX ID ABZ59815 standard; RNA; 20 BP.
XX
XX AC ABZ59815;
XX
XX 01-APR-2003 (first entry)
XX
XX Potato gene PCR primer dT20.
XX
XX Potato; plant; mitochondrial carrier protein; elongation factor EF-2;
XX transferin binding protein; receptor-like protein kinase; halicase;
XX non-long terminal repeat retroelement reverse transcriptase;
XX overwatering; transgenic; reverse transcriptase; PCR; primer; ss.
XX
XX OS Synthetic.
XX
XX DE10114063-A1.
XX
XX 10-OCT-2002.
XX
XX 22-MAR-2001; 2001DE-01014063.
XX
XX PF

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XX 22-MAR-2001; 2001IDE-01014063.
PR
XX
XX (MPBC-) MPB COLOGNE GMBH MOLECULAR PLANT & PROTE.
PA
XX
XX Buelow L, Tscharncke M, Hausuehl K;
PI
XX WPI; 2003-041808/04.
DR
XX
XX New DNA sequences from potato, useful for producing plants with altered
PT properties, e.g. tolerance of flooding, also related proteins, antibodies
PT and inhibitory sequences.
XX
XX Example 1; Page 8; 26pp; German.
PS
XX
XX The invention relates to DNA sequences (I) that encode six specific plant
CC proteins: (i) a protein (ABP60425) with mitochondrial carrier protein
CC activity (Iia); (ii) a protein (ABP60426) with transferrin binding
CC protein activity (Iib); (iii) a protein (ABP60427) with receptor-like
CC protein kinase activity (Iic); (iv) a protein (ABP60428) with elongation
CC factor EF-2 activity (Iid); (v) a protein (ABP60429) with non-long
CC terminal repeat retroelement reverse transcriptase activity (Iie); or
CC (vi) a protein (ABP60430) with helicase activity (Iif). (I), also related
CC sequences, derived ribozymes and antisense sequences, expression vectors,
CC encoded proteins and antibodies against the proteins, are used to produce
CC plants with altered properties, including the tolerance of overwatering. The
CC antibodies are also used for isolation of the proteins and in
CC immunassays. Also (I) or their primer or probe fragments are used to
CC screen for terminators and constitutively, aerobically or anaerobically
CC inducible plant promoters, specifically for use in potatoes and the
CC sequence that encodes (Iid) is used to alter the translation profile in
CC plants. Since (I) are derived from potato, their promoters and
CC terminators provide high level transgene expression in potato, with
CC improved tissue specificity and inducibility, and can also be used to
CC control endogenous genes. The present sequence is that of a PCR primer
CC used in the first strand synthesis of cDNAs derived from potato
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 20
RESULT 334
ABX79181/c
ID ABX79181 standard; DNA; 20 BP.
XX
XX
XX ABX79181;
AC
XX
XX 15-APR-2003 (first entry)
DT
XX
XX Thio-modified 20da oligonucleotide.
DE
XX
XX Nanoparticle; ss; nucleic acid detection; viral disease; probe;
KM human immunodeficiency virus infection; hepatitis virus infection;
KM herpes virus infection; cytomegalovirus infection; forensic science;
KM Epstein-Barr virus infection; bacterial disease; gene therapy;
KM sexually transmitted disease; inherited disorder; DNA sequencing;
KM paternity testing; cell line authentication.
XX
XX Synthetic.
OS
XX
XX US2002155462-A1.
PN
XX
XX 24-OCT-2002.
PD
XX
XX 12-OCT-2001; 2001US-00976577.
PF
XX

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PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WC-US012783.
PR 23-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
XX (NANO-) NANOSPHERE INC.
PA
XX
XX Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;
PI Taton TA;
PI WPI; 2003-198491/19.
DR
XX
XX Detecting nucleic acids having at least 2 portions comprises use of
PT nanoparticles which have oligonucleotides attached to them that are
PT complementary to portions of the nucleic acid sequence.
XX
XX Example 18; Page 44; 130pp; English.
PS
XX
XX The invention relates to detecting a nucleic acid (NA) having at least 2
CC portions, comprising providing a type of nanoparticles (NP) having
CC attached to oligonucleotides (O) ((O) on each NP has a sequence
CC complementary to sequence of at least 2 portions of NA), contacting NA
CC and NP to allow hybridisation of (O) on NP with 2 or more portions of NA,
CC and observing a detectable change brought about by hybridisation of (O)
CC on NP with NA. The nanoparticle is useful for separating a selected
CC nucleic acid having at least 2 portions, from other nucleic acids, and
CC for detecting nucleic acids having at least 2 portions. The method of
CC using NP is useful for detecting any type of nucleic acids which may be
CC used for diagnosis of disease and in sequencing of nucleic acids.
CC Preferably, the method is useful for detecting nucleic acids for
CC diagnosis and/or monitoring of viral diseases (human immunodeficiency
CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
CC virus), bacterial diseases, sexually transmitted diseases, inherited
CC disorders, in forensics, in DNA sequencing, for paternity testing, for
CC cell line authentication and for monitoring gene therapy. The method is
CC useful in research and analytical laboratories in DNA sequencing and in
CC the field to detect the presence of specific pathogens. Detecting nucleic
CC acids based on observing a colour change with the naked eye is cheap,
CC fast, simple and robust, and do not require specialised expensive
CC equipment. The present sequence is a nanoparticle (e.g. gold particles)
CC labelled probe used to demonstrate the method of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 1
RESULT 335
ABX92177/c
ID ABX92177 standard; DNA; 20 BP.
XX
XX
XX ABX92177;
AC
XX
XX 12-MAY-2003 (first entry)
DT
XX
XX Nanoparticle-associated oligonucleotide SEQ ID 55.
DE
XX
XX Nanoparticle; nucleic acid detection; hybridisation; diagnosis;
KM sequencing; viral infection; human immunodeficiency virus; HIV;
KM hepatitis virus; herpes virus; cytomegalovirus; Epstein-Barr virus;
KM bacterial infection; sexually transmitted disease; inherited disorder;
KM forensic; paternity testing; cell line authentication; gene therapy; ss.
XX
XX Synthetic.
OS
XX

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PN US2002155458-A1.
XX
XX 24-OCT-2002.
XX
XX 28-SEP-2001; 2001US-00967409.
XX
XX 29-JUL-1996; 96US-0031809P.
XX 21-JUL-1997; 97WO-US012783.
XX 29-JAN-1999; 99US-00240755.
XX 25-JUN-1999; 99US-00344667.
XX 26-APR-2000; 2000US-0200161P.
XX 26-JUN-2000; 2000US-00603830.
XX
XX (NANO-) NANOSPHERE INC.
XX
XX Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;
XX Taton TA;
XX
XX WPI; 2003-182627/18.
XX
XX Detecting nucleic acids having at least two portions involves use of
XX nanoparticles which have oligonucleotides attached to them that are
XX complementary to portions of the nucleic acid sequence.
XX
XX Disclosure; Page 59; 130pp; English.
XX
XX This invention describes a novel method of detecting nucleic acid having
XX at least two portions. The method involves providing nanoparticles
XX attached to oligonucleotides, where the oligonucleotide on each
XX nanoparticle have a sequence complementary to a sequence of at least two
XX portions of nucleic acid, contacting nucleic acid and nanoparticle to
XX allow hybridisation of the oligonucleotide on the nanoparticle with two
XX or more portions of nucleic acid and observing a detectable change
XX brought about by hybridisation of the oligonucleotide nanoparticle with
XX nucleic acid. The method is useful for separating a selected nucleic acid
XX having at least two portions, from other nucleic acids and for detecting
XX nucleic acids having at least two portions. The method is useful for
XX detecting any type of nucleic acids which may be used for diagnosis of
XX disease and in sequencing of nucleic acids. Preferably, the method is
XX useful for detecting nucleic acids for diagnosis and/or monitoring of
XX viral infections (human immunodeficiency virus (HIV), hepatitis virus,
XX herpes virus, cytomegalovirus and Epstein-Barr virus), bacterial
XX diseases, sexually transmitted diseases, inherited disorders, in
XX forensics, in DNA sequencing, for paternity testing, for cell line
XX authentication, and for monitoring gene therapy. The method is useful in
XX research and analytical laboratories in DNA sequencing, in the field to
XX detect the presence of specific pathogens, detecting nucleic acids based
XX on observing a colour change with the naked eye is cheap, fast, simple
XX and robust and does not require specialised expensive equipment. ABX92123
XX -ABX92186 and ABQ77356 represent oligonucleotides used to illustrate the
XX method of the invention
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
XX 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1
XX
XX RESULT 336
XX ACD27255/c
XX ID ACD27255 standard; DNA; 20 BP.
XX
XX ACD27255;
XX
XX 15-OCT-2003 (first entry)
XX
XX Nanotechnology nucleic acid detection method associated #54.
XX

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KW Nanotechnology; ss; nucleic acid detection; nanoparticle;
KW virus detection; human immunodeficiency virus; HIV; hepatitis; herpes;
KW cytomegalovirus; Epstein-Barr virus; bacterial diseases; DNA sequencing;
KW sexually transmitted disease; inherited disorder; forensics;
KW paternity testing; cell line authentication.
XX
XX Synthetic.
XX
XX Key 1 Location/Qualifiers
XX modified_base 1
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= Thiol modified"
XX
XX PN US2002155459-A1.
XX
XX 24-OCT-2002.
XX
XX 11-OCT-2001; 2001US-00975062.
XX
XX 29-JUL-1996; 96US-0031809P.
XX 21-JUL-1997; 97WO-US012783.
XX 29-JAN-1999; 99US-00240755.
XX 25-JUN-1999; 99US-00344667.
XX 26-APR-2000; 2000US-0200161P.
XX 26-JUN-2000; 2000US-00603830.
XX
XX (NANO-) NANOSPHERE INC.
XX
XX Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;
XX Taton TA;
XX
XX WPI; 2003-228114/22.
XX
XX Detecting nucleic acids having 2 portions e.g. for detecting disease,
XX comprises use of nanoparticles which have oligonucleotides attached to
XX them that are complementary to portions of the nucleic acid sequence.
XX
XX Example 18; Page 43; 129pp; English.
XX
XX This invention relates to a novel method for detecting a nucleic acid
XX having 2 portions. The method comprises providing nanoparticles having
XX oligonucleotides attached, where the oligonucleotide on each nanoparticle
XX has a sequence complementary to a sequence of 2 portions of nucleic acid.
XX The nucleic acid and nanoparticle are contacted to allow hybridisation of
XX the oligonucleotide on the nanoparticle with two or more portions of
XX nucleic acid and observing a detectable change brought about by the
XX hybridisation. The method of the invention is useful for separating a
XX selected nucleic acid having 2 portions, from other nucleic acids, and
XX for detecting nucleic acids having 2 portions. The method of the
XX invention is useful for detecting any type of nucleic acids which may be
XX used for diagnosis of disease and in sequencing of nucleic acids.
XX Preferably, the method is useful for detecting nucleic acids for
XX diagnosis and/or monitoring of viral diseases (human immunodeficiency
XX virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
XX virus), bacterial diseases, sexually transmitted diseases, inherited
XX disorders, in forensics, in DNA sequencing, for paternity testing, for
XX cell line authentication, for monitoring gene therapy, etc. This method
XX involves detecting nucleic acids based on observing a colour change with
XX the naked eye so is cheap, fast, simple and robust, and does not require
XX specialised expensive equipment. The present sequence represents a Thiol
XX modified oligonucleotide sequence used to demonstrate the method of the
XX invention
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
XX 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1
XX

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RESULT 337
ACD27125/C
ID ACD27125 standard; DNA; 20 BP.
XX
XX AC ACD27125;
XX DT 15-OCT-2003 (first entry)
XX DE Nanotechnology nucleic acid detection method oligonucleotide #54.
XX KW Nanotechnology; nucleic acid detection; nanoparticle; ss; forensic;
XX KM DNA sequencing; paternity testing; cell line authentication.
XX OS Synthetic.
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT . /note= "OTHER= Thiol modified" "
XX US002164605-A1.
PN
PD 07-NOV-2002.
XX
XX 28-SEP-2001; 2001US-00966312.
PF
XX 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97MO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
XX 26-JUN-2000; 2000US-00603830.
PA (NANO-) NANOSPHERE INC.
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JI, Elghanian R,
PT Taton TA;
XX WPI; 2003-247253/24.
XX
PT Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change,
PT useful in forensics.
PS Example 18; Page 44; 130pp; English.

This invention relates to a novel method for detecting nucleic acid sequences having two portions. The method involves providing nanoparticles having oligonucleotides attached to them, which has a sequence complementary to sequence of two portions of nucleic acid, contacting nucleic acid and nanoparticles, to allow hybridisation of oligonucleotides with two or more portions of nucleic acid, and observing a detectable change brought about by hybridisation. The method of the invention and the aggregate probes are useful for detecting two or more nucleic acids (from a biological source) having at least two portions, such as viral RNA or DNA, bacterial or fungal DNA, a gene associated with a disease, synthetic, or structurally-modified natural or synthetic RNA or DNA, or a product of a polymerase chain reaction amplification. Nanoparticles and nanoparticle-oligonucleotide conjugates of the invention are useful for nanofabrication, and for separating a selected nucleic acid having two portions from other nucleic acids. The method of the invention is useful in forensics, DNA sequencing, for paternity testing, call line authentication, and monitoring gene therapy. Diagnostic assays employing the nanoparticle-oligonucleotide conjugates of the invention improve the sensitivity of the nucleic acid detection assay. The present sequence represents a thiol modified oligonucleotide sequence used to demonstrate the method of the invention

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

```

Query Match      0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2..7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4464 TTTTXXXXXXXXXXXXTTTT 4483
          ||| ||||| ||||| ||||| |||||
DB       20 TTTTXXXXXXXXXXXXTTTT 1

RESULT 338
ACD27385/C
ID ACD27385 standard; DNA; 20 BP.
XX
AC ACD27385;
XX
DT 15-OCT-2003 (first entry)
XX
DE Nanotechnology nucleic acid detection method associated #54.
XX
KW Nanoparticle; ss; nucleic acid detection; DNA sequencing;
KM pathogen detection.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "Thiol modified" "
FT FT
XX
PN US2002182611-A1.
XX
PD 05-DEC-2002.
XX
PF 28-SEP-2001; 2001US-00966491.
XX
PR 29-JUN-1996; 96WO-0031809P.
PR 21-JUL-1997; 97MO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
XX WPI; 2003-596264/56.
DR
PT Detection of nucleic acid for, e.g., research and analytical laboratories
PT in deoxyribonucleic acid sequencing, involves contacting nucleic acid
PT with nanoparticles having oligonucleotides.
XX
PS Example 18; Page 43; 109pp; English.
XX
XX This invention relates to a novel method for detecting a nucleic acid by
CC contracting a nucleic acid with at least two types of nanoparticles having
CC oligonucleotides attached, allowing hybridisation of the oligonucleotides
CC on the nanoparticle, and observing a detectable change. The
CC oligonucleotides on each nanoparticle have a sequence complementary to
CC its respective portion of the sequence of the nucleic acid to be
CC detected. The method of the invention may be used for the detection of a
CC nucleic acid used in, e.g., research and analytical laboratories in DNA
CC sequencing, in the field to detect the presence of specific pathogens, in
CC the doctor's office for quick identification of an infection to assist in
CC prescribing a drug for treatment, and in homes and health centres for
CC inexpensive first-line screening. The method of the invention detects
CC nucleic acids based on observing a colour change with the naked eye. This
CC method is cheap, fast, simple, robust and does not require specialised or
CC expensive equipment. The present sequence represents a thiol modified
CC oligonucleotide sequence used to demonstrate the method of the invention

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XX		Sequence	20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
QY		Query Match	0.3%; Score 20; DB 1; Length 20;
		Best Local Similarity	100.0%; Pred. No. 2.7e+02;
Matches	20;	Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	464	TTTTTTT	TTTTTTT
D8	20	TTTTTTTTTTTTTTTTTT	T
			1
			4483
RESULT 339			
ACD27190/c			
ID	ACD27190	standard; DNA; 20 BP.	
XX AC	ACD27190;		
XX DT	15-OCT-2003	(first entry)	
DE	Nanotechnology nucleic acid detection method associated #54.		
XX XX	Nanoparticle; ss; nucleic acid detection; DNA sequencing.		
OS	Synthetic.		
XX Key	Location/Qualifiers		
FH modified_base	1	*tag= a	
FT /mod_base= OTHER	/note= "OTHER= Thiol modified"	" "	
FN US2002182613-A1.			
PB PD	05-DEC-2002.		
PF PF	12-OCT-2001; 2001US-0097697L.		
PR PR	29-JUL-1996; 96US-0031809P.		
PR PR	21-JUL-1997; 97WO-US012783.		
PR PR	29-JAN-1999; 99US-00240755.		
PR PR	25-JUN-1999; 99US-00344667.		
PR PR	26-APR-2000; 2000US-0200161P.		
PA PA	26-JUN-2000; 2000US-00603830.		
	(NANO-) NANOSPHERE INC.		
XI Mirkin CA,	Ietsinger RL,	Mucic RC,	Storhoff JU,
PI Tatou TA;			Elgantian R;
DR WPI; 2003-596265/56.			
PT Detection of nucleic acid for, e.g., research and analytical laboratories			
PT in deoxyribonucleic acid sequencing, involves contacting nucleic acid			
XT with nanoparticles having oligonucleotides.			
PS Example 18; Page 43; 107pp; English.			
CC This invention relates to a novel method for detecting a nucleic acid by			
CC contacting nucleic acid with at least two types of nanoparticles having			
CC oligonucleotides, allowing hybridization of the oligonucleotides on the			
CC nanoparticles, and observing a detectable change. The oligonucleotides			
CC each nanoparticle have a sequence complementary to its respective portion			
CC of the sequence of the nucleic acid. The method of the invention may be			
CC used for the detection of a nucleic acid used in, e.g., research and			
CC analytical laboratories in DNA sequencing, in the field to detect the			
CC presence of specific pathogens, in the doctor's office for quick			
CC identification of an infection to assist in prescribing a drug for			
CC treatment, and in homes and health centres for inexpensive first-line			
CC screening. The inventive method of detecting nucleic acids based on			
CC observing a colour change with the naked eye are cheap, fast, simple,			
CC robust (the reagents are stable), do not require specialised or expensive			
CC equipment, and little or no instrumentation is required. The present			

```
CC sequence represents a thiol modified oligonucleotide sequence used to
CC demonstrate the method of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2,7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 4464 TTTTNTTTTTTTTTTTTTTTT 4483
DB 20 TTTTNTTTTTTTTTTTTTTTT 1
RESULT 340
ACD27060/c
ID ACD27060 standard; DNA; 20 BP.
XX
AC ACD27060;
DX 15-OCT-2003 (first entry)
XX
DE Nanotechnology nucleic acid detection method oligonucleotide #54.
XX
KM Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
XX /note= "OTHER= Thiol modified" "
XX PN US2003044805-A1.
PD
XX 06-MAR-2003.
PF
XX 15-OCT-2001; 2001US-00981344.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 25-JAN-1999; 98US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
PI Mirkin CA, Letsinger RU, Mucic RC, Scorhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-521746/49.
PS Example 18; Page 44; 130pp; English.
XX
CC This invention relates to a novel method for detecting nucleic acids. The
CC method comprises providing nanoparticles with oligonucleotides attached
CC to them, which have a sequence complementary to a sequence of two
CC portions of nucleic acid; contacting the nucleic acid and nanoparticles
CC to allow hybridization of the oligonucleotides with two or more portions
CC of the nucleic acid; and observing a detectable change brought about by
CC the hybridisation. The nucleic acid to be detected must have at least two
CC portions and the distances between these are chosen so that when the
CC nanoparticle-oligonucleotide conjugate binds the target sequence a
CC detectable change occurs. The method of the invention is useful for
CC detecting two or more nucleic acids (from a biological source) having at
CC least two portions, such as viral RNA, bacterial or fungal DNA, a gene
CC associated with a disease, synthetic, or structurally- modified natural
```

CC	or synthetic RNA or DNA, or a product of a polymerase chain reaction
CC	amplification. Nanoparticle-oligonucleotide conjugates of the invention
CC	are useful for preparing a nanoprobe conjugate for detecting an analyte,
CC	and for detecting a nucleic acid bound to an electrode surface.
CC	Nanoparticles and nanoparticle conjugates of the invention are useful for
CC	nano fabrication and for separating a selected nucleic acid having two
CC	portions from other nucleic acids. Diagnostic assays employing
CC	nano particle-oligonucleotide conjugates improve the sensitivity of
CC	nucleic acid detection methods and can be used to detect nucleic acids
CC	that are present in only small amounts in a sample. The invention also
CC	provides highly desirable nanoparticle-oligonucleotide conjugates. These
CC	conjugates are stable with tailored hybridisation abilities. The present
CC	sequence represents a thiol modified oligonucleotide sequence used to
CC	demonstrate the method of the invention
XX	
SQ	Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match	0.3%; Score 20; DB 1; Length 20;
Best Local Similarity	100.0%; Pred.No. 2.7e+02;
Matches 20; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	4464 TTTTTTTTTTTTTTTTTT 4483
Db	20 TTTTTTTTTTTTTTTTTT 1
RESULT 341	
ACH00064/C	
ID	ACH00064 standard; DNA; 20 BP.
AC	ACH00064;
XX	
DT	15-OCT-2003 (first entry)
XX	
DE	Nanotechnology nucleic acid detection method oligonucleotide #54.
XX	
KW	Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	modified_base 1 /tag= a
FT	/mod_base= OTHER
FT	/note= "OTHER= Thiol modified" "
PX	US2003049631-A1.
PD	
PD	13-MAR-2003.
PF	10-OCT-2001; 2001US-00974500.
PR	29-JUL-1996; 96US-0031809P.
PR	21-JUL-1997; 97WO-0S012783.
PR	29-JAN-1999; 99US-00240755.
PR	25-JUN-1999; 99US-00344667.
PR	26-APR-2000; 2000US-0200161P.
PR	26-JUN-2000; 2000US-00603830.
PA	(NANO-) NANOSPHERE INC.
PI	Mitkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Bighanian R;
PI	Taton TA;
XX	
DR	WPI; 2003-634854/60.
PT	Detection of nucleic acid having at least two portions, by contacting
PT	nucleic acid and nanoparticles under conditions, which allows
PT	hybridization of oligonucleotides on nanoparticles with at least two
PT	portions of nucleic acid.
PS	Example 18; Page 44; 108pp; English.
XX	

CC	This invention relates to a novel method for detecting nucleic acids. The
CC	method comprises providing nanoparticles with oligonucleotides attached
CC	to them, which have a sequence complementary to a sequence of two
CC	portions of nucleic acid, contacting the nucleic acid and nanoparticles
CC	to allow hybridisation of the oligonucleotides with two or more portions
CC	of the nucleic acid, and observing a detectable change brought about by
CC	the hybridisation. The nucleic acid to be detected must have at least two
CC	portions and the distances between these are chosen so that when the
CC	nanoarticle-oligonucleotide conjugate binds the target sequence a
CC	detectable change occurs. The method of the invention is useful for
CC	detecting two or more nucleic acids (from a biological source) having at
CC	least two portions, such as viral RNA, bacterial or fungal DNA, a gene
CC	associated with a disease, synthetic, or structurally-modified natural
CC	or synthetic RNA or DNA, or a product of a polymerase chain reaction
CC	amplification. Nanoparticle-oligonucleotide conjugates of the invention
CC	are useful for preparing a nanoprobe conjugate for detecting an analyte,
CC	and for detecting a nucleic acid bound to an electrode surface.
CC	Nanoparticles and nanoparticle conjugates of the invention are useful for
CC	nanofabrication and for separating a selected nucleic acid having two
CC	portions from other nucleic acids. Diagnostic assays employing
CC	nanoarticle-oligonucleotide conjugates improve the sensitivity of
CC	nucleic acid detection methods and can be used to detect nucleic acids
CC	that are present in only small amounts in a sample. The invention also
CC	provides highly desirable nanoparticle-oligonucleotide conjugates. These
CC	conjugates are stable with tailored hybridisation abilities. The present
CC	sequence represents a thiol modified oligonucleotide sequence used to
CC	demonstrate the method of the invention
SO	
XX	Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Qy	
Db	
Query Match	0.3%; Score 20; DB 1; Length 20;
Best Local Similarity	100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
4464 TTTTTTTTTTTTTTTTTTTT 4483	
20 TTTTTTTTTTTTTTTTTTTT 1	
RESULT 342	
ACD99861/c	
ID ACD99861 standard; DNA; 20 BP.	
XX ACD99861;	
XX	
DT 25-SEP-2003 (first entry)	
DE Immunostimulatory nucleic acid #337.	
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;	
KW anticancer; gene therapy; vaccine; non-allergic inflammatory disease;	
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;	
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.	
XX Synthetic.	
OS	
XX US2003050268-A1.	
PN	
PD 13-MAR-2003.	
XX	
PF 29-MAR-2002; 2002US-00112653.	
XX	
PR 29-MAR-2001; 2001US-0279642P.	
XX	
PA (KRIE/) KRIEG A M.	
XX (BERG/) BERG D J.	
PI Krieg AM, Berg DJ;	
XX WPI; 2003-521815/49.	
XX	
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,	
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel	

DT		06-NOV-2003	(first entry)
DE		Hairpin target sequence, #2, used in an example of the invention.	
XX			
XX		Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;	
KW		quencha ble fluorescing agent; microarray; semiconductor; nanocrystal;	
KM		rhodamine B-labelled dye; detection; gold support; ss.	
XX			
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	misc_binding	1..20	
FT		/tag= a	
FT		/bound_moiety= "Hairpin oligonucleotide #2"	
FT		/note= "Forms a double-stranded region with the hairpin	
FT		oligonucleotide shown in examples 3, 4 and 5"	
XX			
PN	US2003013109-A1.		
XX			
PD	16-JAN-2003.		
XX			
PJ	21-JUN-2002; 2002US-00176055.		
XX			
PR	21-JUN-2001; 2001US-0299460P.		
XX			
PA	(BALL/) BALLINGER C T.		
PA	(LOCA/) LOCASCIO M.		
PA	(LAND/) LANDRY D P.		
PL	Ballinger CT, Locascio M, Landry DP;		
DR	WPI; 2003-596312/56.		
XX			
PT	Hairpin sensor useful for detecting a target nucleotide sequence in a		
PT	sample, comprises a hairpin loop assembly including a complementary probe		
PT	and a quencha ble fluorescing agent.		
XX			
PS	Example 3; Page 11; 16pp; English.		
CC	The invention discloses a hairpin sensor comprising a hairpin loop		
CC	assembly including a complementary probe positioned between a first		
CC	inverse repeat arm and a second inverse repeat arm, and a quencha ble		
CC	fluorescing agent joined, directly or indirectly, to the end of the		
CC	second inverse repeat arm of the hairpin loop assembly opposite the		
CC	complementary probe. Also claimed is a microarray comprising the hairpin		
CC	sensor, where the end of the first inverse repeat arm opposite the		
CC	complementary probe is bound, directly or indirectly, to a support, a kit		
CC	for detecting a target nucleotide sequence in a sample comprising the		
CC	hairpin sensor, and a support, and a hairpin sensor system, in which the		
CC	particle is conductive or semi-conductive, including at least one of the		
CC	above hairpin sensor assemblies. The hairpin sensor further comprises a		
CC	functional group joined to the end of the first inverse repeat arm		
CC	opposite the complementary probe, or first spacer opposite the first		
CC	inverse repeat arm, the functional group selected from amino, carboxyl,		
CC	thiol and hydroxyl. Further, the sensor comprises a ligand positioned		
CC	between the second inverse repeat arm and the quencha ble fluorescing		
CC	agent, where the ligand is selected from mercapto, hydroxyl, amino,		
CC	nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The		
CC	second spacer is positioned between the second inverse repeat arm and the		
CC	quencha ble fluorescing agent which comprises a semiconductor nanocrystal		
CC	or rhodamine B-labelled dye. Within the microarray the support is capable		
CC	of accepting a charge. At least one hairpin sensor comprises two or more		
CC	hairpin sensors. The two or more hairpin sensors include complementary		
CC	probes that are the same or different and respective quencha ble		
CC	fluorescing agents that are the same or different. The two or more		
CC	hairpin sensors are arranged in a spatially-defined pattern. The sensor		
CC	and system are useful for detecting a target nucleotide sequence in a		
CC	sample. Further, the method involves identifying the target nucleotide		
CC	sequence by the location of the complementary probe to which the target		
CC	nucleotide sequence binds. The two or more hairpin sensors include		
CC	complementary probes or quencha ble fluorescing agents, that are		
CC	different. The sequence presented is the hairpin oligonucleotide target		
CC	sequence, #2, used in an example of the invention.		

```

SQ      Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match      0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db      20 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 346
ADA06159/c
ID      ADA06159 standard; DNA; 20 BP.
XX
XX      ADA06159;
AC
DE      06-NOV-2003 (first entry)
XX
XX      Nanoparticle labelled oligonucleotides, spacer DNA #2.
DE
XX      ss; nanoparticle; colloidal gold; semiconductor; nanomaterial;
XX      nanostructure; viral disease; human immunodeficiency virus infection;
XX      hepatitis virus infection; herpes virus infection;
XX      cytomegalovirus virus infection; Epstein-Barr virus; bacterial disease;
XX      sexually transmitted disease; inherited disorders; paternity testing;
XX      cell line authentication; gene therapy.
OS      Synthetic.
PN      US2003068622-A1.
PD      10-APR-2003.
PF      12-OCT-2001; 2001US-00976863.
XX
XX      29-JUL-1996; 96US-0031809P.
XX      21-JUL-1997; 97WC-US012783.
XX      29-JAN-1999; 99US-00240755.
XX      25-JUN-1999; 99US-00344667.
XX      26-APR-2000; 2000US-0200161P.
XX      26-JUN-2000; 2000US-00603830.
XX
XX      (NANO-) NANOSPHERE INC.
XX
XX      Mirtin CA, Letsinger RL, Mucic RC, Stornhoff JT, Elghanian R;
XX      Taton TA;
XX
XX      WPI; 2003-576420/54.
XX
XX      Detecting nucleic acids having at least 2 portions comprises use of
XX      PT      complementary to portions of the target nucleic acid sequence.
XX      PT
XX
XX      Example 18; Page 44; 130pp; English.
XX
XX      The invention relates to detecting a nucleic acid (NA) having at least 2
XX      CC      portions comprising providing a type of nanoparticles (NP, e.g. colloidal
XX      CC      gold) having oligonucleotides (O) attached (where (O) on each NP has a
XX      CC      sequence complementary to sequence of at least two portions of NA),
XX      CC      contacting NA and NP to allow hybridisation of (O) on NP with 2 or more
XX      CC      portions of NA, and observing a detectable change brought about by
XX      CC      hybridization of (O) on NP with NA. Also included are aggregate probes,
XX      CC      core probes, substrate having NP attached to it, a metallic or
XX      CC      semiconductor NP having (O) attached to it, nanomaterials/nanostructures
XX      CC      comprising nanoparticles and methods of nanofabrication utilizing
XX      CC      nanoparticles and satellite probes. The methods, probes nucleic acids,
XX      CC      nanoparticles and oligonucleotides are useful for separating a selected
XX      CC      nucleic acid having at least two portions, from other nucleic acids, and
XX      CC      for detecting nucleic acids having at least two portions, for detecting
XX      CC      NA having at least two portions. The method is useful for detecting any
XX      CC      type of nucleic acids which may be used for diagnosis of disease and in

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CC sequencing of nucleic acids. Preferably, the method is useful for
 CC detecting nucleic acids for diagnosis and/or monitoring of viral diseases
 CC (human immunodeficiency virus, hepatitis virus, herpes virus,
 CC cytomegalovirus and Epstein-Barr virus), bacterial diseases, sexually
 CC transmitted diseases, inherited disorders, in forensics, in DNA
 CC sequencing, for paternity testing, for cell line authentication, for
 CC monitoring gene therapy, etc. The method is useful in research and
 CC analytical laboratories in DNA sequencing, in the field to detect the
 CC presence of specific pathogens, etc. Detecting nucleic acids based on
 CC observing a colour change with the naked eye is cheap, fast, simple and
 CC robust, and do not require specialised expensive equipment. The present
 CC sequence is a spacer oligonucleotide used to illustrate the method of the
 CC invention.

CC Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

CC SQ

CC Query Match 0.3%; Score 20; DB 1; Length 20;
 CC Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
 CC 20 TTTT TTTT TTTT TTTT TTTT 1

CC Db

CC RESULT 347
 CC ACD26995/C
 CC ID ACD26995 standard; DNA; 20 BP.
 CC AC ACD26995;
 CC DT 15-OCT-2003 (first entry)
 CC XX
 CC DE Nanotechnology nucleic acid detection method oligonucleotide #54.
 CC KW Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.
 CC OS Synthetic.
 CC FH Key Location/Qualifiers
 CC FT modified_base 1 /*tag= a
 CC FT /mod_base= OTHER
 CC FT /note= "OTHER= Thiol modified" "

CC PN US2003049630-A1.
 CC XX
 CC PD 13-MAR-2003.
 CC XX
 CC PF 20-SEP-2001; 2001US-00957318.
 CC XX
 CC PR 29-JUL-1996; 96US-0031809P.
 CC PR 21-JUL-1997; 97MO-US012783.
 CC PR 29-JAN-1999; 99US-00240755.
 CC PR 25-JUN-1999; 99US-00344667.
 CC PR 26-APR-2000; 2000US-0200161P.
 CC PR 26-JUN-2000; 2000US-00603830.
 CC XX
 CC PA (NANO-) NANOSPHERE INC.
 CC XX
 CC PI Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;
 CC PI Taton TA;
 CC XX
 CC DR WPI; 2003-615795/58.
 CC XX
 CC PT Detecting nucleic acid having two portions, by providing nanoparticles
 CC PT having oligonucleotides attached to it, contacting nucleic acid and
 CC PT nanoparticles to allow hybridization, and observing detectable change.
 CC XX
 CC PS Example 18; Page 43; 12pp; English.
 CC XX
 CC CC This invention relates to a novel method for detecting nucleic acids. The
 CC method comprises providing nanoparticles with oligonucleotides attached

CC to them, which have a sequence complementary to a sequence of two
 CC portions of nucleic acid, contacting the nucleic acid and nanoparticles
 CC to allow hybridisation of the oligonucleotides with two or more portions
 CC of the nucleic acid, and observing a detectable change brought about by
 CC the hybridisation. The nucleic acid to be detected must have at least two
 CC portions and the distances between these are chosen so that when the
 CC nanoparticle-oligonucleotide conjugate binds the target sequence a
 CC detectable change occurs. The method of the invention is useful for
 CC detecting two or more nucleic acids (from a biological source) having at
 CC least two portions, such as viral RNA, bacterial or fungal DNA, a gene
 CC associated with a disease, synthetic, or structurally- modified natural
 CC or synthetic RNA or DNA, or a product of a polymerase chain reaction
 CC amplification. Nanoparticle-oligonucleotide conjugates of the invention
 CC are useful for preparing a nanoprobe conjugate for detecting an analyte,
 CC and for detecting a nucleic acid bound to an electrode surface.
 CC Nanoparticles and nanoparticle conjugates of the invention are useful for
 CC nanofabrication and for separating a selected nucleic acid having two
 CC portions from other nucleic acids. Diagnostic assays employing
 CC nanoparticle-oligonucleotide conjugates improve the sensitivity of
 CC nucleic acid detection methods and can be used to detect nucleic acids
 CC that are present in only small amounts in a sample. The present sequence
 CC represents a thiol modified oligonucleotide sequence used to demonstrate
 CC the method of the invention

CC SQ

CC Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

CC Query Match 0.3%; Score 20; DB 1; Length 20;
 CC Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
 CC 20 TTTT TTTT TTTT TTTT TTTT 1

CC Db

CC RESULT 348
 CC ADB36933/C
 CC ID ADB36933 standard; DNA; 20 BP.
 CC AC ADB36933;
 CC DT 04-DEC-2003 (first entry)
 CC XX
 CC DE Immunostimulatory nucleic acid #547.
 CC KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
 CC KW hypo-responsive subject; immunostimulatory.
 CC OS Synthetic.
 CC FH Key Location/Qualifiers
 CC FT modified_base 1 /*tag= a
 CC FT /mod_base= OTHER
 CC FT /note= "OTHER= Thiol modified" "

CC PN US2003087848-A1.
 CC XX
 CC PD 08-MAY-2003.
 CC XX
 CC PF 02-FEB-2001; 2001US-00776479.
 CC PR 03-FEB-2000; 2000US-0179991P.
 CC XX
 CC PA (BRAT/) BRATZLER R L.
 CC PA (PETE/) PETERSEN D M.
 CC PA (FOUR/) FOURON Y.
 CC XX
 CC PI Bratzler RL, Petersen DM, Fouron Y;
 CC PI Taton TA;
 CC XX
 CC DR WPI; 2003-657977/62.
 CC XX
 CC PT Treating and/or preventing allergy or asthma using an immunostimulatory
 CC PT nucleic acid alone or in combination with an asthma/allergy medicament.
 CC XX
 CC PS Disclosure; Page 13; 22pp; English.
 CC XX
 CC CC The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid


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FT FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX XX
XX WO2003040321-A2.
XX PD 15-MAY-2003.
XX PF 04-NOV-2002; 2002WO-US035324.
XX PR 08-NOV-2001; 2001US-00007078.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ward DT, Watt AT;
XX WPI; 2003-449448/42.
XX DR
XX PT New compound, having a sequence targeted to a nucleic acid encoding human
XX PT collapsin response mediator protein 2, useful for preparing a composition
XX PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX PT cancer.
XX PS Claim 3; Page 76; 120pp; English.
XX CC This invention relates to novel antisense oligonucleotides that modulate
XX CC the expression of human eukaryotic translation initiation factor 2C 1
XX CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
XX CC Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
XX CC intracellular membrane associated protein thought to be involved in
XX CC cellular differentiation, such that altered expression of EIF2C1 can
XX CC affect cell growth, morphology and tumorigenicity. Accordingly,
XX CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
XX CC or tissues can be used in gene therapy to treat various conditions
XX CC including hyperproliferative disorders, familial hypercholesterolemia
XX CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX CC progeroid syndrome. As such, the oligos of the present invention can be
XX CC described as having cytosstatic and antipapemic activities. This
XX CC oligonucleotide sequence is an antisense oligo used to inhibit expression
XX CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX CC of the invention.
XX SQ Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 414 AGTCACCGGAGAGTGAG 433
XX DB 20 AGTCACCGGAGAGTGAG 1
XX
XX RESULT 352
XX ADB81500/C
XX ID ADB81500 standard; DNA; 20 BP.
XX AC ADB81500;
XX DT 04-DEC-2003 (first entry)
XX DE Antisense oligo (SeqID 17) used to inhibit human EIF2C1 DNA.
XX XX
XX XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99;
XX KW gene therapy; hyperproliferative disorder;
XX KW familial hypercholesterolemia; cancer; polycystic kidney disease;
XX KW cystic fibrosis; progeroid syndrome; cytosstatic; antipapemic.
XX OS Homo sapiens.
XX XX
XX XX Key Location/Qualifiers
XX FH modified_base 1..20
XX FT

```

```

FT FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX XX
XX WO2003040321-A2.
XX PD 15-MAY-2003.
XX PF 04-NOV-2002; 2002WO-US035324.
XX PR 08-NOV-2001; 2001US-00007078.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ward DT, Watt AT;
XX WPI; 2003-449448/42.
XX DR
XX PT New compound, having a sequence targeted to a nucleic acid encoding human
XX PT collapsin response mediator protein 2, useful for preparing a composition
XX PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX PT cancer.
XX PS Claim 3; Page 76; 120pp; English.
XX CC This invention relates to novel antisense oligonucleotides that modulate
XX CC the expression of human eukaryotic translation initiation factor 2C 1
XX CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
XX CC Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
XX CC intracellular membrane associated protein thought to be involved in
XX CC cellular differentiation, such that altered expression of EIF2C1 can
XX CC affect cell growth, morphology and tumorigenicity. Accordingly,
XX CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
XX CC or tissues can be used in gene therapy to treat various conditions
XX CC including hyperproliferative disorders, familial hypercholesterolemia
XX CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX CC progeroid syndrome. As such, the oligos of the present invention can be
XX CC described as having cytosstatic and antipapemic activities. This
XX CC oligonucleotide sequence is an antisense oligo used to inhibit expression
XX CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX CC of the invention.
XX SQ Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 555 GGTCACATCCCTGGGAG 574
XX DB 20 GGTCACATCCCTGGGAG 1
XX
XX RESULT 353
XX ADB81513/C
XX ID ADB81513 standard; DNA; 20 BP.
XX AC ADB81513;
XX DT 04-DEC-2003 (first entry)
XX DE Antisense oligo (SeqID 30) used to inhibit human EIF2C1 DNA.
XX XX
XX XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99;
XX KW gene therapy; hyperproliferative disorder;
XX KW familial hypercholesterolemia; cancer; polycystic kidney disease;
XX KW cystic fibrosis; progeroid syndrome; cytosstatic; antipapemic.
XX OS Homo sapiens.
XX XX
XX XX Key Location/Qualifiers
XX FH modified_base 1..20
XX FT

```

```

FH Key Location/Qualifiers
FT modified_base 1..20
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT FT 5-methylcytidines"
PN WO2003040321-A2.
XX
XX 15-MAY-2003.
XX
XX 04-NOV-2002; 2002WO-US035324.
XX
XX 08-NOV-2001; 2001US-00007078.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ward DT, Watt AT;
XX
XX WPI; 2003-449448/42.
XX
XX New compound, having a sequence targeted to a nucleic acid encoding human
XX PT collapsin response mediator protein 2, useful for preparing a composition
XX PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX PT cancer.
XX
XX Claim 3; Page 76; 120pp; English.
XX
XX This invention relates to novel antisense oligonucleotides that modulate
XX CC the expression of human eukaryotic translation initiation factor 2C 1
XX CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
XX CC Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
XX CC intracellular membrane associated protein thought to be involved in
XX CC cellular differentiation, such that altered expression of EIF2C1 can
XX CC affect cell growth, morphology and tumorigenicity. Accordingly,
XX CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
XX CC or tissues can be used in gene therapy to treat various conditions
XX CC including hyperproliferative disorders, familial hypercholesterolemia
XX CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX CC progeroid syndrome. As such, the oligos of the present invention can be
XX CC described as having cytotatic and antiproliferative activities. This
XX CC oligonucleotide sequence is an antisense oligo used to inhibit expression
XX CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX
XX Sequence 20 BP; 3 A; 2 C; 9 G; 6 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1484 CCATTGCCACACCCCAATCAG 1503
DB 20 CCATTGCCACACCCCAATCAG 1

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```

OS Homo sapiens.
FH Key Location/Qualifiers
FT modified_base 1..20
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT FT 5-methylcytidines"
PN WO2003040321-A2.
XX
XX 15-MAY-2003.
XX
XX 04-NOV-2002; 2002WO-US035324.
XX
XX 08-NOV-2001; 2001US-00007078.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ward DT, Watt AT;
XX
XX WPI; 2003-449448/42.
XX
XX New compound, having a sequence targeted to a nucleic acid encoding human
XX PT collapsin response mediator protein 2, useful for preparing a composition
XX PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX PT cancer.
XX
XX Claim 3; Page 76; 120pp; English.
XX
XX This invention relates to novel antisense oligonucleotides that modulate
XX CC the expression of human eukaryotic translation initiation factor 2C 1
XX CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
XX CC Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
XX CC intracellular membrane associated protein thought to be involved in
XX CC cellular differentiation, such that altered expression of EIF2C1 can
XX CC affect cell growth, morphology and tumorigenicity. Accordingly,
XX CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
XX CC or tissues can be used in gene therapy to treat various conditions
XX CC including hyperproliferative disorders, familial hypercholesterolemia
XX CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX CC progeroid syndrome. As such, the oligos of the present invention can be
XX CC described as having cytotatic and antiproliferative activities. This
XX CC oligonucleotide sequence is an antisense oligo used to inhibit expression
XX CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX
XX Sequence 20 BP; 3 A; 8 C; 1 G; 8 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2368 AATGACCGAATTGGGAAGAG 2387
DB 20 AATGACCGAATTGGGAAGAG 1

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RESULT 354
ADBB81519/c
ID ADB81519 standard; DNA; 20 BP.
XX
XX ADB81519;
XX
XX 04-DEC-2003 (first entry)
XX
XX Antisense oligo (SeqID 36) used to inhibit human EIF2C1 DNA.
XX
XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX KW EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
XX KW gene therapy; hyperproliferative disorder;
XX KW familial hypercholesterolemia; cancer; polycystic kidney disease;
XX KW cystic fibrosis; progeroid syndrome; cytotatic; antiproliferative.
XX

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```

RESULT 355
ADBB81541/c
ID ADB81541 standard; DNA; 20 BP.
XX
XX ADB81541;
XX
XX 04-DEC-2003 (first entry)
XX
XX Antisense oligo (SeqID 58) used to inhibit human EIF2C1 DNA.
XX
XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX KW EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
XX KW gene therapy; hyperproliferative disorder;
XX KW familial hypercholesterolemia; cancer; polycystic kidney disease;
XX

```

KW	cystic fibrosis; progeroid syndrome; cytotostatic; antihypertensive.
XX	
OS	Homo sapiens.
FH	
FT	Key
FT	Location/Qualifiers
FT	modified_base
FT	1..20
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "OTHER= phosphorothioate backbone, where 1-5 and 16-20 are 2'-methoxyethyl nucleotides. All cytidines are 5-methylcytidines"
FT	
XX	
PN	WO2003040321-A2.
PD	
XD	15-MAY-2003.
XX	
PF	04-NOV-2002; 2002WO-US035324.
XX	
PR	08-NOV-2001; 2001US-00007078.
XX	
PA	(ISIS-) ISIS PHARM INC.
PI	
XX	
DR	Ward DF, Watt AT;
XX	
PT	WPI; 2003-449448/42.
PT	
PT	New compound, having a sequence targeted to a nucleic acid encoding human
PT	collapsin response mediator protein 2, useful for preparing a composition
PT	for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT	cancer.
PS	
XX	Claim 3; Page 76; 120pp; English.
XX	
CC	This invention relates to novel antisense oligonucleotides that modulate
CC	the expression of human eukaryotic translation initiation factor 2C 1
CC	(EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC	Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC	intracellular membrane associated protein thought to be involved in
CC	cellular differentiation, such that altered expression of EIF2C1 can
CC	affect cell growth, morphology and tumorigenicity. Accordingly,
CC	antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC	or tissues can be used in gene therapy to treat various conditions
CC	including hyperproliferative disorders, familial hypercholesterolaemia
CC	and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC	progeroid syndrome. As such, the oligos of the present invention can be
CC	described as having cytostatic and anti-neoplastic activities. This
CC	oligonucleotide sequence is an antisense oligo used to inhibit expression
CC	of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC	of the invention.
CC	
SQ	Sequence 20 BP; 7 A; 3 C; 5 G; 5 T; 0 U; 0 Other;
XX	
Query Match	0.3%; Score 20; DB 1; Length 20;
Best Local Similarity	100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	5185 ATGTTCTCCACCTGGATACA 5204
DB	 20 ATGTTCTCCACTTGGATACA 1
RESULT 356	
ADB81501/C	
ID	ADB81501 standard; DNA; 20 BP.
XX	
AC	ADB81501;
XX	
DT	04-DEC-2003 (first entry)
XX	
DE	Antisense oligo (Seqid 18) used to inhibit human EIF2C1 DNA.
XX	
KW	antisense; ss; human; eukaryotic translation initiation factor 2C 1;
KW	EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;

KM	gene therapy; hyperproliferative disorder;
KM	familial hypercholesterolaemia; cancer; polycystic kidney disease;
KW	cyclic fibrosis; progeria syndrome; cytostatic; antilipemic.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	modified_base
FT	Location/Qualifiers
FT	1..20
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "OTHER= phosphorochloate backbone, where 1-5 and
FT	16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT	5-methylcytidines"
XX	
PN	WO2003040321-A2.
PD	
PD	15-MAY-2003.
XX	
PF	04-NOV-2002; 2002MO-US035324.
XX	
PR	08-NOV-2001; 2001US-00007078.
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
PI	Ward DT, Watt AT;
XX	
XX	WPI, 2003-449448/42.
XX	
PT	New compound, having a sequence targeted to a nucleic acid encoding human
PT	collapsin response mediator protein 2, useful for preparing a composition
PT	for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT	cancer.
PS	
PS	Claim 3; Page 76; 120pp; English.
CC	This invention relates to novel antisense oligonucleotides that modulate
CC	the expression of human eukaryotic translation initiation factor 2C 1
CC	(EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC	Co-eIFC, eIFC, Golgi ER protein 95kDa, GERP5 and Q99. It is an
CC	intracellular membrane associated protein thought to be involved in
CC	cellular differentiation, such that altered expression of EIF2C1 can
CC	affect cell growth, morphology and tumorigenicity. Accordingly,
CC	antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC	or tissues can be used in gene therapy to treat various conditions
CC	including hyperproliferative disorders, familial hypercholesterolemia
CC	and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC	progeria syndrome. As such, the oligos of the present invention can be
CC	described as having cytostatic and antilipemic activities. This
CC	oligonucleotide sequence is an antisense oligo used to inhibit expression
CC	of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC	of the invention.
XX	
SQ	Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
QY	
QY	Query Match 0.3%; Score 20; DB 1; Length 20;
QY	Best Local Similarity 100.0%; Pred. No. 2.7e+02;
QY	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
DB	
DB	680 CTGTGCAAGCCCTGGATGTG 699
DB	
DB	20 CTGTGCAAGCCCTGGATGTG 1
RESULT 357	
ADB81517/c	
ID	ADB81517 standard; DNA; 20 BP.
XX	
AC	ADB81517;
XX	
DT	04-DEC-2003 (first entry)
XX	
DE	Antisense oligo (SeqID 34) used to inhibit human EIF2C1 DNA.
XX	

KM antisense; ss; human; eukaryotic translation initiation factor 2C 1;
 KM EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
 KM gene therapy; hyperproliferative disorder;
 KM familial hypercholesterolaemia; cancer; polycystic kidney disease;
 KM cystic fibrosis; progeroid syndrome; cytosstatic; antilipaeamic.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 FT 5-methylcytidines"
 XX
 XX WC02003040321-A2.
 XX
 XX PD 15-MAY-2003.
 XX PF 04-NOV-2002; 2002MO-US035324.
 XX PR 08-NOV-2001; 2001US-00007078.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Ward DT, Walt AT;
 XX WP1; 2003-449448/42.
 XX
 PT New compound, having a sequence targeted to a nucleic acid encoding human
 PT collapsin response mediator protein 2, useful for preparing a composition
 PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
 PT cancer.
 PS Claim 3; Page 76; 120pp; English.
 XX
 CC This invention relates to novel antisense oligonucleotides that modulate
 CC the expression of human eukaryotic translation initiation factor 2C 1
 CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
 CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
 CC intracellular membrane associated protein thought to be involved in
 CC cellular differentiation, such that altered expression of EIF2C1 can
 CC affect cell growth, morphology and tumorigenicity. Accordingly,
 CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
 CC or tissues can be used in gene therapy to treat various conditions
 CC including hyperproliferative disorders, familial hypercholesterolemia
 CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
 CC progeroid syndrome. As such, the oligos of the present invention can be
 CC described as having cytosstatic and antilipaeamic activities. This
 CC oligonucleotide sequence is an antisense oligo used to inhibit expression
 CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
 CC of the invention.
 SO Sequence 20 BP; 5 A; 9 C; 3 G; 3 T; 0 U; 0 Other;
 XX
 XX
 Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1785 GCCGCTATGCTGAGGTGA 1804
 DB 20 GCCGCTATGCTGAGGTGA 1
 XX
 RESULT 358
 ADB81527/c
 ID ADB81527 standard; DNA; 20 BP.
 XX
 XX ADB81527;
 XX
 DT 04-DEC-2003 (first entry)
 XX

DE Antisense oligo (SeqID 44) used to inhibit human EIF2C1 DNA.
 KM "antisense; ss; human; eukaryotic translation initiation factor 2C 1;
 KM EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
 KM gene therapy; hyperproliferative disorder;
 KM familial hypercholesterolaemia; cancer; polycystic kidney disease;
 KM cystic fibrosis; progeroid syndrome; cytosstatic; antilipaeamic.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 FT 5-methylcytidines"
 XX
 XX WC02003040321-A2.
 XX
 XX PD 15-MAY-2003.
 XX PF 04-NOV-2002; 2002MO-US035324.
 XX PR 08-NOV-2001; 2001US-00007078.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Ward DT, Walt AT;
 XX WP1; 2003-449448/42.
 XX
 PT New compound, having a sequence targeted to a nucleic acid encoding human
 PT collapsin response mediator protein 2, useful for preparing a composition
 PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
 PT cancer.
 PS Claim 3; Page 76; 120pp; English.
 XX
 CC This invention relates to novel antisense oligonucleotides that modulate
 CC the expression of human eukaryotic translation initiation factor 2C 1
 CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
 CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
 CC intracellular membrane associated protein thought to be involved in
 CC cellular differentiation, such that altered expression of EIF2C1 can
 CC affect cell growth, morphology and tumorigenicity. Accordingly,
 CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
 CC or tissues can be used in gene therapy to treat various conditions
 CC including hyperproliferative disorders, familial hypercholesterolemia
 CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
 CC progeroid syndrome. As such, the oligos of the present invention can be
 CC described as having cytosstatic and antilipaeamic activities. This
 CC oligonucleotide sequence is an antisense oligo used to inhibit expression
 CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
 CC of the invention.
 SO Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
 XX
 XX
 Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3112 ACTCATGCTTGACAGCTTG 3131
 DB 20 ACTCATGCTTGACAGCTTG 1
 XX
 RESULT 359
 ADB81546/c
 ID ADB81546 standard; DNA; 20 BP.
 XX
 XX ADB81546;
 XX
 AC ADB81546;
 XX

```

DT 04-DEC-2003 (first entry)
XX Antisense oligo (SeqID 63) used to inhibit human E1F2C1 DNA.
DE Antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX E1F2C1; Co-e1F2C; e1F2C; Golgi ER protein 95kDa; GERp95; Q99;
XX gene therapy; hyperproliferative disorder;
XX familial hypercholesterolaemia; cancer; polycystic kidney disease;
XX cystic fibrosis; progeria syndrome; cytostatic; antilipemic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= a
XX /mod_base= OTHER
XX /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX 5-methylcytidines"
XX
XX MO2003040321-A2.
XX
XX 15-MAY-2003.
XX
XX 04-NOV-2002; 2002WO-US035324.
XX
XX 08-NOV-2001; 2001US-00007078.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ward DT, Watt AT;
XX
XX MPI; 2003-449448/42.
XX
XX New compound, having a sequence targeted to a nucleic acid encoding human
XX collapsin response mediator protein 2, useful for preparing a composition
XX for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX cancer.
XX
XX Claim 3; Page 77; 120pp; English.
XX
XX This invention relates to novel antisense oligonucleotides that modulate
XX the expression of human eukaryotic translation initiation factor 2C 1
XX (E1F2C1). E1F2C1 is located on chromosome 1p34-35, and is also known as
XX Co-e1F2C, e1F2C, Golgi ER protein 95kDa, GERp95 and Q99. It is an
XX intracellular membrane associated protein thought to be involved in
XX cellular differentiation, such that altered expression of E1F2C1 can
XX affect cell growth, morphology and tumorigenicity. Accordingly,
XX antisense oligonucleotides that inhibit the expression of E1F2C1 in cells
XX or tissues can be used in gene therapy to treat various conditions
XX including hyperproliferative disorders, familial hypercholesterolaemia
XX and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX progeria syndrome. As such, the oligos of the present invention can be
XX described as having cytostatic and antilipemic activities. This
XX oligonucleotide sequence is an antisense oligo used to inhibit expression
XX of the human eukaryotic translation initiation factor 2C 1 (E1F2C1) DNA
XX of the invention.
XX
XX Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other:
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6028 CCTGTCACTCTCTTGAGCT 6047
XX |||||
XX 20 CCTGTCACTCTCTTGAGCT 1
XX
XX RESULT 360
XX ADB81550/c
XX ID ADB81550 standard; DNA; 20 BP.
XX

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AC ADB81550;
XX
XX 04-DEC-2003 (first entry)
XX
XX Antisense oligo (SeqID 67) used to inhibit human E1F2C1 DNA.
DE Antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX E1F2C1; Co-e1F2C; e1F2C; Golgi ER protein 95kDa; GERp95; Q99;
XX gene therapy; hyperproliferative disorder;
XX familial hypercholesterolaemia; cancer; polycystic kidney disease;
XX cystic fibrosis; progeria syndrome; cytostatic; antilipemic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= a
XX /mod_base= OTHER
XX /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX 5-methylcytidines"
XX
XX MO2003040321-A2.
XX
XX 15-MAY-2003.
XX
XX 04-NOV-2002; 2002WO-US035324.
XX
XX 08-NOV-2001; 2001US-00007078.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ward DT, Watt AT;
XX
XX MPI; 2003-449448/42.
XX
XX New compound, having a sequence targeted to a nucleic acid encoding human
XX collapsin response mediator protein 2, useful for preparing a composition
XX for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX cancer.
XX
XX Claim 3; Page 77; 120pp; English.
XX
XX This invention relates to novel antisense oligonucleotides that modulate
XX the expression of human eukaryotic translation initiation factor 2C 1
XX (E1F2C1). E1F2C1 is located on chromosome 1p34-35, and is also known as
XX Co-e1F2C, e1F2C, Golgi ER protein 95kDa, GERp95 and Q99. It is an
XX intracellular membrane associated protein thought to be involved in
XX cellular differentiation, such that altered expression of E1F2C1 can
XX affect cell growth, morphology and tumorigenicity. Accordingly,
XX antisense oligonucleotides that inhibit the expression of E1F2C1 in cells
XX or tissues can be used in gene therapy to treat various conditions
XX including hyperproliferative disorders, familial hypercholesterolaemia
XX and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX progeria syndrome. As such, the oligos of the present invention can be
XX described as having cytostatic and antilipemic activities. This
XX oligonucleotide sequence is an antisense oligo used to inhibit expression
XX of the human eukaryotic translation initiation factor 2C 1 (E1F2C1) DNA
XX of the invention.
XX
XX Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6533 TGGCCCATAGATATCTGTA 6552
XX |||||
XX 20 TGGCCCATAGATATCTGTA 1
XX
XX RESULT 361
XX ADB81553/c
XX

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```
ID ADB81553 standard; DNA; 20 BP.
XX
XX ADB81553;
XX
XX 04-DEC-2003 (first entry)
XX
DE Antisense oligo (SeqID 70) used to inhibit human EIF2C1 DNA.
XX
XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99;
XX gene therapy; hyperproliferative disorder;
XX familial hypercholesterolemia; cancer; polycystic kidney disease;
XX cystic fibrosis; progeria syndrome; cytosolic; antipapillary.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX 5-methylcytidines"
XX
XX MO2003040321-A2.
XX
XX 15-MAY-2003.
XX
XX 04-NOV-2002; 2002MO-US035324.
XX
XX 08-NOV-2001; 2001US-00007078.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ward DT, Watt AT;
XX
XX WPI; 2003-449448/42.
XX
XX New compound, having a sequence targeted to a nucleic acid encoding human
XX protein response mediator protein 2, useful for preparing a composition
XX for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX cancer.
XX
XX Claim 3; Page 77; 120pp; English.
XX
XX This invention relates to novel antisense oligonucleotides that modulate
XX the expression of human eukaryotic translation initiation factor 2C 1
XX (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
XX Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
XX intracellular membrane associated protein thought to be involved in
XX cellular differentiation, such that altered expression of EIF2C1 can
XX affect cell growth, morphology and tumorigenicity. Accordingly,
XX antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
XX or tissues can be used in gene therapy to treat various conditions
XX including hyperproliferative disorders, familial hypercholesterolemia
XX and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX progeria syndrome. As such, the oligos of the present invention can be
XX described as having cytosolic and antipapillary activities. This
XX oligonucleotide sequence is an antisense oligo used to inhibit expression
XX of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX
XX Sequence 20 BP; 7 A; 8 C; 1 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 362
ADB81503/C
ID ADB81503 standard; DNA; 20 BP.
XX
XX ADB81503;
XX
XX 04-DEC-2003 (first entry)
XX
DE Antisense oligo (SeqID 20) used to inhibit human EIF2C1 DNA.
XX
XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99;
XX gene therapy; hyperproliferative disorder;
XX familial hypercholesterolemia; cancer; polycystic kidney disease;
XX cystic fibrosis; progeria syndrome; cytosolic; antipapillary.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX 5-methylcytidines"
XX
XX MO2003040321-A2.
XX
XX 15-MAY-2003.
XX
XX 04-NOV-2002; 2002MO-US035324.
XX
XX 08-NOV-2001; 2001US-00007078.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ward DT, Watt AT;
XX
XX WPI; 2003-449448/42.
XX
XX New compound, having a sequence targeted to a nucleic acid encoding human
XX protein response mediator protein 2, useful for preparing a composition
XX for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX cancer.
XX
XX Claim 3; Page 76; 120pp; English.
XX
XX This invention relates to novel antisense oligonucleotides that modulate
XX the expression of human eukaryotic translation initiation factor 2C 1
XX (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
XX Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
XX intracellular membrane associated protein thought to be involved in
XX cellular differentiation, such that altered expression of EIF2C1 can
XX affect cell growth, morphology and tumorigenicity. Accordingly,
XX antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
XX or tissues can be used in gene therapy to treat various conditions
XX including hyperproliferative disorders, familial hypercholesterolemia
XX and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX progeria syndrome. As such, the oligos of the present invention can be
XX described as having cytosolic and antipapillary activities. This
XX oligonucleotide sequence is an antisense oligo used to inhibit expression
XX of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX
XX Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 363
ADB81510/c
ID ADB81510 standard; DNA; 20 BP.
XX
AC ADB81510;
XX
DT 04-DEC-2003 (first entry)
XX
DE Antisense oligo (SeqID 27) used to inhibit human EIF2C1 DNA.
XX
KM antisense; ss; human; eukaryotic translation initiation factor 2C 1;
KM EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
KM gene therapy; hyperproliferative disorder;
KM familial hypercholesterolaemia; cancer; polycystic kidney disease;
KM cystic fibrosis; progeria syndrome; cytoskeletal; antileukemic.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
PN WO2003040321-A2.
XX
PD 15-MAY-2003.
XX
PF 04-NOV-2002; 2002WO-US035324.
XX
PR 08-NOV-2001; 2001US-00007078.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ward DT, Watt AT;
XX
PI WPI; 2003-449448/42.
XX
DR New compound, having a sequence targeted to a nucleic acid encoding human
PT collapsin response mediator protein 2, useful for preparing a composition
PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT cancer.
XX
XX Claim 3; Page 76; 120pp; English.
XX
PS This invention relates to novel antisense oligonucleotides that modulate
CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
CC affect cell growth, morphology and tumorigenicity. Accordingly,
CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC or tissues can be used in gene therapy to treat various conditions
CC including hyperproliferative disorders, familial hypercholesterolaemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC progeria syndrome. As such, the oligos of the present invention can be
CC described as having cytoskeletal and antileukemic activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC of the invention.
XX
SQ Sequence 20 BP; 1 A; 7 C; 4 G; 8 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db
20 CAGACAGACAGAGAGATC 1
|||||
RESULT 364
ADB81511/c
ID ADB81511 standard; DNA; 20 BP.
XX
AC ADB81511;
XX
DT 04-DEC-2003 (first entry)
XX
DE Antisense oligo (SeqID 28) used to inhibit human EIF2C1 DNA.
XX
KM antisense; ss; human; eukaryotic translation initiation factor 2C 1;
KM EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
KM gene therapy; hyperproliferative disorder;
KM familial hypercholesterolaemia; cancer; polycystic kidney disease;
KM cystic fibrosis; progeria syndrome; cytoskeletal; antileukemic.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
PN WO2003040321-A2.
XX
PD 15-MAY-2003.
XX
PF 04-NOV-2002; 2002WO-US035324.
XX
PR 08-NOV-2001; 2001US-00007078.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ward DT, Watt AT;
XX
PI WPI; 2003-449448/42.
XX
DR New compound, having a sequence targeted to a nucleic acid encoding human
PT collapsin response mediator protein 2, useful for preparing a composition
PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT cancer.
XX
XX Claim 3; Page 76; 120pp; English.
XX
PS This invention relates to novel antisense oligonucleotides that modulate
CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
CC affect cell growth, morphology and tumorigenicity. Accordingly,
CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC or tissues can be used in gene therapy to treat various conditions
CC including hyperproliferative disorders, familial hypercholesterolaemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC progeria syndrome. As such, the oligos of the present invention can be
CC described as having cytoskeletal and antileukemic activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC of the invention.
XX
SQ Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


OY	1345	AGTCGCTGATGAAGAATGC	1364
Db	20	AGTCGCTGATGAAGAATGC	1

RESULT 365
ADB81549/c
ID ADB81549 standard; DNA; 20 BP

DE Antisense oligo (SeqID 66) used to inhibit human EIF2C1 DNA.

KM anti_sense: ss; human; eukaryotic translation initiation factor 2C 1
KM EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP5; Q99;
KM gene therapy; hyperproliferative disorder;
KM familial hypercholesterolaemia; cancer; polycystic kidney disease;
KM cystic fibrosis; progeria syndrome; cytostatic; antilipaeamic.
XX
XX
XX Homo sapiens.
OS

FT	Key	Location/Qualifiers
FT	modified_base	1..20
FT		/*cag= a
FT		/mod_base= OTHER
FT		/note= "OTHER= phosphorothioate backbone, where 1-5 and
FT		16-20 are 2', methoxyethyl nucleotides. All cytidines are
FT		5-methylcytidines"

PN WO2003040321-A2

PD 15-MAY-2003

PF 04-NOV-2002; 2002WO-US035324.

PR 08-NOV-2001; 2001US-00007078.

PA (ISIS-) ISIS PHARM INC.

PI Ward DT, Watt AT;

DR WPI; 2003-449448/42.

PT New compound, having a sequence targeted to a nucleic acid encoding human
PT collapsin response mediator protein 2, useful for preparing a composition
PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT cancer.

PS Claim 3; Page 77; 120pp; English.

CC This invention relates to novel antisense oligonucleotides that modulate
CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-EIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
CC affect cell growth, morphology and tumorigenicity. Accordingly,
CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC or tissues can be used in gene therapy to treat various conditions
CC including hyperproliferative disorders, familial hypercholesterolemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC progeria syndrome. As such, the oligos of the present invention can be
CC described as having cytostatic and antiproliferative activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC of the invention.

SQ Sequence 20 BP; 9 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;

	Best Local Similarity	100.0%	Pred. No. 2.7e+02	Matches 20	Conservative 0	Mismatches 0	Indels 0	Gaps 0
qy	6447	AGCAGTGTTCGATACTT	6466					
db	20	AGCAGTGTTCGATACTT	1					

RESULT 366
ADB81512/c
ID ADB81512 standard; DNA; 20 BP.

DT 04-DEC-2003 (first entry)

DE Antisense oligo (SeqID 29) used to inhibit human EIF2C1 DNA.

KM antiensis; ss; human; eukaryotic translation initiation factor 2C 1
KM ERF2C1; Co-eIF2C; eIF2C3; Golgi ER protein 95kDa; GERP95; Q99;
KM gene therapy; hyperproliferative disorder;
KM lamellar hypercholesterolaemia; cancer; polycystic kidney disease;
KM cystic fibrosis; progeroid syndrome; cytosclastic; antiliphaemic.
XX
OS Homo sapiens.

Key	Location/Qualifiers
FT modified_base	1..20
FT	/*tag= a
FT	/mod_base= OTHER
FT	/note= "OTHER= phosphate backbone, where 1-5 and 16-20 are 2' methoxyethyl nucleotides. All cytidines are 5-methylcytidines"
FT	
FT	
FT	

PN WO2003040321-A2.

PD 15-MAY-2003

PF 04-NOV-2002; 2002WO-US035324.

PR 08-NOV-2001; 2001US-00007078.

PA (ISIS-) ISIS PHARM INC.

PI Ward DT, Watt AT;

DR WPI; 2003-449448/42.

PT New compound, having a sequence targeted to a nucleic acid encoding human
PT collapsin response mediator protein 2, useful for preparing a composition
PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT cancer.

PS Claim 3; Page 76; 120pp; English

This invention relates to novel antisense oligonucleotides that modulate the expression of human eukaryotic translation initiation factor 2C 1 (EIF2C1). EIF2C1 is located on chromosome 13q4-35, and is also known as Co-eIFPC, eIFPC, Golgi ER protein 95kDa, GERP95 and Q99. It is an intracellular membrane associated protein thought to be involved in cellular differentiation, such that altered expression of EIF2C1 can affect cell growth, morphology and tumorigenicity. Accordingly, antisense oligonucleotides that inhibit the expression of EIF2C1 in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disorders, familial hypercholesterolaemia and cancer, as well as polycystic kidney disease, cystic fibrosis and progeroid syndrome. As such, the oligos of the present invention can be described as having cytostatic and antiproliferative activities. This oligonucleotide sequence is an antisense oligo used to inhibit expression of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA of the invention.

Sequence 20 BP; 3 A; 8 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 TGAAGATGACATGACGAG 1428
|||
DB 20 TGAAGATGACATGACGAG 1

RESULT 367
ADB81524/c
ID ADB81524 standard; DNA; 20 BP.
XX
AC ADB81524;
XX
DT 04-DEC-2003 (first entry)
XX
DE Antisense oligo (SeqID 41) used to inhibit human EIF2C1 DNA.
XX
KM antisense; ss; human; eukaryotic translation initiation factor 2C 1;
KM EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
KM gene therapy; hyperproliferative disorder;
KM familial hypercholesterolaemia; cancer; polycystic kidney disease;
KM cystic fibrosis; progeria syndrome; cytostatic; antilipemic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"

WO2003040321-A2.
XX
PN 15-MAY-2003.
XX
PD 04-NOV-2002; 2002WO-US035324.
XX
PF 08-NOV-2001; 2001US-00007078.
XX
PR (ISIS-) ISIS PHARM INC.
XX
PA Ward DT, Watt AT;
XX
PI WPI; 2003-449448/42.
XX
DR New compound, having a sequence targeted to a nucleic acid encoding human
XX PT collapsin response mediator protein 2, useful for preparing a composition
XX PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX PT cancer.
XX
PS Claim 3; Page 76; 120bp; English.
XX
CC This invention relates to novel antisense oligonucleotides that modulate
CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
CC affect cell growth, morphology and tumorigenicity. Accordingly,
CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC or tissues can be used in gene therapy to treat various conditions
CC including hyperproliferative disorders, familial hypercholesterolaemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC progeria syndrome. As such, the oligos of the present invention can be
CC described as having cytostatic and antilipemic activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA

XX
SQ Sequence 20 BP; 3 A; 4 C; 8 G; 5 T; 0 U; 0 Other;
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2841 GCTGTGCCACCCCAATCCAG 2860
|||
DB 20 GCTGTGCCACCCCAATCCAG 1

RESULT 368
ADB81526/c
ID ADB81526 standard; DNA; 20 BP.
XX
AC ADB81526;
XX
DT 04-DEC-2003 (first entry)
XX
DE Antisense oligo (SeqID 43) used to inhibit human EIF2C1 DNA.
XX
KM antisense; ss; human; eukaryotic translation initiation factor 2C 1;
KM EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
KM gene therapy; hyperproliferative disorder;
KM familial hypercholesterolaemia; cancer; polycystic kidney disease;
KM cystic fibrosis; progeria syndrome; cytostatic; antilipemic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"

WO2003040321-A2.
XX
PN 15-MAY-2003.
XX
PD 04-NOV-2002; 2002WO-US035324.
XX
PF 08-NOV-2001; 2001US-00007078.
XX
PR (ISIS-) ISIS PHARM INC.
XX
PA Ward DT, Watt AT;
XX
PI WPI; 2003-449448/42.
XX
DR New compound, having a sequence targeted to a nucleic acid encoding human
XX PT collapsin response mediator protein 2, useful for preparing a composition
XX PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX PT cancer.
XX
PS Claim 3; Page 76; 120bp; English.
XX
CC This invention relates to novel antisense oligonucleotides that modulate
CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
CC affect cell growth, morphology and tumorigenicity. Accordingly,
CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC or tissues can be used in gene therapy to treat various conditions
CC including hyperproliferative disorders, familial hypercholesterolaemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC progeria syndrome. As such, the oligos of the present invention can be
CC described as having cytostatic and antilipemic activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression

CC affect cell growth, morphology and tumorigenicity. Accordingly,
CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC or tissues can be used in gene therapy to treat various conditions
CC including hyperproliferative disorders, familial hypercholesterolaemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC progeroid syndrome. As such, the oligos of the present invention can be
CC described as having cytostatic and antiproliferative activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC of the invention.

XX SQ Sequence 20 BP; 9 A; 3 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7009 ATTTCTTCTTACAGAGA 7028
|||
Db 20 ATTTCTTCTTACAGAGA 1

RESULT 373
ADB81497/c
ID ADB81497 standard; DNA; 20 BP.

AC ADB81497;
XX
XX 04-DEC-2003 (first entry)

DE Antisense oligo (SeqID 14) used to inhibit human EIF2C1 DNA.

XX KM antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99;
XX gene therapy; hyperproliferative disorder;
XX familial hypercholesterolaemia; cancer; polycystic kidney disease;
XX cystic fibrosis; progeroid syndrome; cytostatic; antiproliferative.
XX Homo sapiens.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX FT 5-methylcytidines"

XX PN WC0003040321-A2.

XX PD 15-MAY-2003.

XX PF 04-NOV-2002; 2002MO-US035324.

XX PR 08-NOV-2001; 2001US-00007078.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Ward DT, Watt AT;
XX WPI; 2003-449448/42.

XX DR WPI; 2003-449448/42.

XX PT New compound, having a sequence targeted to a nucleic acid encoding human
XX PT collapse response mediator protein 2, useful for preparing a composition
XX PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX PT cancer.

XX PS Claim 3; Page 76; 120pp; English.

XX CC This invention relates to novel antisense oligonucleotides that modulate
XX CC the expression of human eukaryotic translation initiation factor 2C 1
XX CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
XX CC Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an

CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
CC affect cell growth, morphology and tumorigenicity. Accordingly,
CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC or tissues can be used in gene therapy to treat various conditions
CC including hyperproliferative disorders, familial hypercholesterolaemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC progeroid syndrome. As such, the oligos of the present invention can be
CC described as having cytostatic and antiproliferative activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC of the invention.

XX SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 382 GTGGACATCAAGCGGATAA 401
|||
Db 20 GTGGACATCAAGCGGATAA 1

RESULT 374
ADB81509/c
ID ADB81509 standard; DNA; 20 BP.

AC ADB81509;
XX
XX 04-DEC-2003 (first entry)

DE Antisense oligo (SeqID 26) used to inhibit human EIF2C1 DNA.

XX KM antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99;
XX gene therapy; hyperproliferative disorder;
XX familial hypercholesterolaemia; cancer; polycystic kidney disease;
XX cystic fibrosis; progeroid syndrome; cytostatic; antiproliferative.
XX Homo sapiens.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX FT 5-methylcytidines"

XX PN WC0003040321-A2.

XX PD 15-MAY-2003.

XX PF 04-NOV-2002; 2002MO-US035324.

XX PR 08-NOV-2001; 2001US-00007078.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Ward DT, Watt AT;
XX WPI; 2003-449448/42.

XX DR WPI; 2003-449448/42.

XX PT New compound, having a sequence targeted to a nucleic acid encoding human
XX PT collapse response mediator protein 2, useful for preparing a composition
XX PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX PT cancer.

XX PS Claim 3; Page 76; 120pp; English.

XX CC This invention relates to novel antisense oligonucleotides that modulate
XX CC the expression of human eukaryotic translation initiation factor 2C 1

CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
 CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
 CC intracellular membrane associated protein thought to be involved in
 CC cellular differentiation, such that altered expression of EIF2C1 can
 CC affect cell growth, morphology and tumorigenicity. Accordingly,
 CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
 CC or tissues can be used in gene therapy to treat various conditions
 CC including hyperproliferative disorders, familial hypercholesterolaemia
 CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
 CC progeroid syndrome. As such the oligos of the present invention can be
 CC described as having cytosolic and antiproliferative activities. This
 CC oligonucleotide sequence is an antisense oligo used to inhibit expression
 CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
 CC of the invention.

SQ Sequence 20 BP; 1 A; 5 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1268 AGAAGCTGACCGCAACGAG 1287
 DB 20 AGAAGCTGACCGCAACGAG 1

RESULT 375

ADB81532/C
 ID ADB81532 standard; DNA; 20 BP.

AC ADB81532;

DT 04-DEC-2003 (first entry)

XX Antisense oligo (SeqID 49) used to inhibit human EIF2C1 DNA.

XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;

KW EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;

KW gene therapy; hyperproliferative disorder;

KW familial hypercholesterolaemia; cancer; polycystic kidney disease;

KW cystic fibrosis; progeroid syndrome; cytosolic; antiproliferative.

XX Homo sapiens.

OS Homo sapiens.

XX Key

FT modified_base 1..20

FT /tag= a

FT /mod_base= OTHER

FT /note= "OTHER= phosphorothioate backbone, where 1-5 and

FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are

FT 5-methylcytidines"

XX WO2003040321-A2.

XX 15-MAY-2003.

XX 04-NOV-2002; 2002MO-US035324.

XX 08-NOV-2001; 2001US-00007078.

XX (ISIS-) ISIS PHARM INC.

XX Ward DT, Watt AT;

XX WPI; 2003-449448/42.

XX New compound, having a sequence targeted to a nucleic acid encoding human

XX PT collapsin response mediator protein 2, useful for preparing a composition

XX PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,

XX cancer.

XX Claim 3; Page 76; 120pp; English.

CC This invention relates to novel antisense oligonucleotides that modulate
 CC the expression of human eukaryotic translation initiation factor 2C 1
 CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
 CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
 CC intracellular membrane associated protein thought to be involved in
 CC cellular differentiation, such that altered expression of EIF2C1 can
 CC affect cell growth, morphology and tumorigenicity. Accordingly,
 CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
 CC or tissues can be used in gene therapy to treat various conditions
 CC including hyperproliferative disorders, familial hypercholesterolaemia
 CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
 CC progeroid syndrome. As such the oligos of the present invention can be
 CC described as having cytosolic and antiproliferative activities. This
 CC oligonucleotide sequence is an antisense oligo used to inhibit expression
 CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
 CC of the invention.

SQ Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4135 AATGAACGTGTGACTGATT 4154
 DB 20 AATGAACGTGTGACTGATT 1

RESULT 376

ADB81545/C
 ID ADB81545 standard; DNA; 20 BP.

AC ADB81545;

DT 04-DEC-2003 (first entry)

XX Antisense oligo (SeqID 62) used to inhibit human EIF2C1 DNA.

XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;

KW EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;

KW gene therapy; hyperproliferative disorder;

KW familial hypercholesterolaemia; cancer; polycystic kidney disease;

KW cystic fibrosis; progeroid syndrome; cytosolic; antiproliferative.

XX Homo sapiens.

OS Homo sapiens.

XX Key

FT modified_base 1..20

FT /tag= a

FT /mod_base= OTHER

FT /note= "OTHER= phosphorothioate backbone, where 1-5 and

FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are

FT 5-methylcytidines"

XX WO2003040321-A2.

XX 15-MAY-2003.

XX 04-NOV-2002; 2002MO-US035324.

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XX (ISIS-) ISIS PHARM INC.

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PT cancer.
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PS Claim 3; Page 77, 120pp; English.
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CC This invention relates to novel antisense oligonucleotides that modulate
CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
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CC including hyperproliferative disorders, familial hypercholesterolemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC progeria syndrome. As such, the oligos of the present invention can be
CC described as having cytostatic and antiproliferative activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC of the invention.
XX
SQ Sequence 20 BP; 8 A; 4 C; 4 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0;
Matches 20; Conservative 0; Indels 0; Gaps 0;
XX
QY 6769 TGCAGGCGCACTTTTACTAT 6788
DB 20 TGCAGGCGCACTTTTACTAT 1
XX
RESULT 379
ADB81496/C
XX ADB81496 standard; DNA; 20 BP.
XX
AC ADB81496;
XX
DT 04-DEC-2003 (first entry)
XX
DE Antisense oligo (SeqID 13) used to inhibit human EIF2C1 DNA.
XX
KW antisense; ss; human; eukaryotic translation initiation factor 2C 1;
KW EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99;
KW gene therapy; hyperproliferative disorder;
KW familial hypercholesterolemia; cancer; polycystic kidney disease;
KW cystic fibrosis; progeria syndrome; cytostatic; antiproliferative.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
PN WO2003040321-A2.
XX
PD 15-MAY-2003.
XX
PF 04-NOV-2002; 2002WO-US035324.
XX
PR 08-NOV-2001; 2001US-00007078.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ward DT, Wact AT;
XX
DR WPI; 2003-449448/42.

XX
PT New compound, having a sequence targeted to a nucleic acid encoding human
PT collapsin response mediator protein 2, useful for preparing a composition
PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT cancer.
XX
PS Claim 3; Page 76, 120pp; English.
XX
CC This invention relates to novel antisense oligonucleotides that modulate
CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
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CC described as having cytostatic and antiproliferative activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC of the invention.
XX
SQ Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0;
Matches 20; Conservative 0; Indels 0; Gaps 0;
XX
QY 326 TCCTGGCCCAATTACTTTGAG 345
DB 20 TCCTGGCCCAATTACTTTGAG 1
XX
RESULT 380
ADB81504/C
XX ADB81504 standard; DNA; 20 BP.
XX
AC ADB81504;
XX
DT 04-DEC-2003 (first entry)
XX
DE Antisense oligo (SeqID 21) used to inhibit human EIF2C1 DNA.
XX
KW antisense; ss; human; eukaryotic translation initiation factor 2C 1;
KW EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99;
KW gene therapy; hyperproliferative disorder;
KW familial hypercholesterolemia; cancer; polycystic kidney disease;
KW cystic fibrosis; progeria syndrome; cytostatic; antiproliferative.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
PN WO2003040321-A2.
XX
PD 15-MAY-2003.
XX
PF 04-NOV-2002; 2002WO-US035324.
XX
PR 08-NOV-2001; 2001US-00007078.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ward DT, Wact AT;
XX


```
XX DR WPI; 2003-449448/42.
XX
PT New compound, having a sequence targeted to a nucleic acid encoding human
PT collapsin response mediator protein 2, useful for preparing a composition
PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT cancer.
XX
PS Claim 3; Page 76; 120pp; English.
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CC This invention relates to novel antisense oligonucleotides that modulate
CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERp95 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
CC affect cell growth, morphology and tumorigenicity. Accordingly,
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CC or tissues can be used in gene therapy to treat various conditions
CC including hyperproliferative disorders, familial hypercholesterolemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC progeroid syndrome. As such, the oligos of the present invention can be
CC described as having cytosstatic and antiproliferative activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC
XX
SQ Sequence 20 BP; 8 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 863 TCTCAGCCACTGCCTTTAT 882
DB 20 TCTCAGCCACTGCCTTTAT 1
RESULT 381
ADB81539/c
ID ADB81539 standard; DNA; 20 BP.
XX
AC ADB81539;
XX
DT 04-DEC-2003 (first entry)
XX
DE Antisense oligo (SeqID 56) used to inhibit human EIF2C1 DNA.
XX
KW antisense; ss; human; eukaryotic translation initiation factor 2C 1;
KW EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERp95; Q99;
KW gene therapy; hyperproliferative disorder;
KW familial hypercholesterolemia; cancer; polycystic kidney disease;
KW cystic fibrosis; progeroid syndrome; cytosstatic; antiproliferative.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines."
XX
XX MO2003040321-A2.
XX
XX PD 15-MAY-2003.
XX
XX PF 04-NOV-2002; 2002MO-US035324.
XX
XX PR 08-NOV-2001; 2001US-00007078.
XX
XX PA (ISIS-) ISIS PHARM INC.
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XX PI Ward DT, Watt AT;
XX
XX DR WPI; 2003-449448/42.
XX
PT New compound, having a sequence targeted to a nucleic acid encoding human
PT collapsin response mediator protein 2, useful for preparing a composition
PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT cancer.
XX
PS Claim 3; Page 76; 120pp; English.
XX
CC This invention relates to novel antisense oligonucleotides that modulate
CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERp95 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
CC affect cell growth, morphology and tumorigenicity. Accordingly,
CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC or tissues can be used in gene therapy to treat various conditions
CC including hyperproliferative disorders, familial hypercholesterolemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC progeroid syndrome. As such, the oligos of the present invention can be
CC described as having cytosstatic and antiproliferative activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC
XX
SQ Sequence 20 BP; 1 A; 6 C; 6 G; 7 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4987 GGCACAAGCCCGACGTGAAG 5006
DB 20 GGCACAAGCCCGACGTGAAG 1
RESULT 382
ADB81521/c
ID ADB81521 standard; DNA; 20 BP.
XX
AC ADB81521;
XX
DT 04-DEC-2003 (first entry)
XX
DE Antisense oligo (SeqID 38) used to inhibit human EIF2C1 DNA.
XX
KW antisense; ss; human; eukaryotic translation initiation factor 2C 1;
KW EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERp95; Q99;
KW gene therapy; hyperproliferative disorder;
KW familial hypercholesterolemia; cancer; polycystic kidney disease;
KW cystic fibrosis; progeroid syndrome; cytosstatic; antiproliferative.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines."
XX
XX MO2003040321-A2.
XX
XX PD 15-MAY-2003.
XX
XX PF 04-NOV-2002; 2002MO-US035324.
XX
XX PR 08-NOV-2001; 2001US-00007078.
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```
XX (ISIS-) ISIS PHARM INC.
XX Ward DT, Walt AT;
XX WPI; 2003-449448/42.
XX
XX New compound, having a sequence targeted to a nucleic acid encoding human
XX collapsin response mediator protein 2, useful for preparing a composition
XX for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX cancer.
XX
XX Claim 3; Page 76; 120pp; English.
XX
XX This invention relates to novel antisense oligonucleotides that modulate
XX the expression of human eukaryotic translation initiation factor 2C 1
XX (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
XX Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
XX intracellular membrane associated protein thought to be involved in
XX cellular differentiation, such that altered expression of EIF2C1 can
XX affect cell growth, morphology and tumorigenicity. Accordingly,
XX antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
XX or tissues can be used in gene therapy to treat various conditions
XX including hyperproliferative disorders, familial hypercholesterolemia
XX and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX progeroid syndrome. As such, the oligos of the present invention can be
XX described as having cytosstatic and antipapemic activities. This
XX oligonucleotide sequence is an antisense oligo used to inhibit expression
XX of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX
XX Sequence 20 BP; 1 A; 5 C; 9 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2472 CATCCAGGACACGACCGAC 2491
XX |||||||||||||||||||
XX Db 20 CATCCAGGACACGACCGAC 1
XX
XX RESULT 383
XX ADB81536/c
XX ID ADB81536 standard; DNA; 20 BP.
XX
XX ADB81536;
XX
XX 04-DEC-2003 (first entry)
XX
XX Antisense oligo (SeqID 53) used to inhibit human EIF2C1 DNA.
XX
XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
XX gene therapy; hyperproliferative disorder;
XX familial hypercholesterolemia; cancer; polycystic kidney disease;
XX cystic fibrosis; progeroid syndrome; cytosstatic; antipapemic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= a
XX /mod_base= OTHER
XX /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX 5-methylcytidines"
XX
XX WO2003040321-A2.
XX
XX 15-MAY-2003.
XX
XX 04-NOV-2002; 2002WO-US035324.
XX
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XX 08-NOV-2001; 2001US-00007078.
XX
XX (ISIS-) ISIS PHARM INC.
XX Ward DT, Walt AT;
XX WPI; 2003-449448/42.
XX
XX New compound, having a sequence targeted to a nucleic acid encoding human
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XX for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
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XX
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XX the expression of human eukaryotic translation initiation factor 2C 1
XX (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
XX Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
XX intracellular membrane associated protein thought to be involved in
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XX affect cell growth, morphology and tumorigenicity. Accordingly,
XX antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
XX or tissues can be used in gene therapy to treat various conditions
XX including hyperproliferative disorders, familial hypercholesterolemia
XX and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX progeroid syndrome. As such, the oligos of the present invention can be
XX described as having cytosstatic and antipapemic activities. This
XX oligonucleotide sequence is an antisense oligo used to inhibit expression
XX of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX
XX Sequence 20 BP; 9 A; 5 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4853 CTGTTCTGTTGGCTACATT 4872
XX |||||||||||||||||||
XX Db 20 CTGTTCTGTTGGCTACATT 1
XX
XX RESULT 384
XX ADB81551/c
XX ID ADB81551 standard; DNA; 20 BP.
XX
XX ADB81551;
XX
XX 04-DEC-2003 (first entry)
XX
XX Antisense oligo (SeqID 68) used to inhibit human EIF2C1 DNA.
XX
XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
XX gene therapy; hyperproliferative disorder;
XX familial hypercholesterolemia; cancer; polycystic kidney disease;
XX cystic fibrosis; progeroid syndrome; cytosstatic; antipapemic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= a
XX /mod_base= OTHER
XX /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX 5-methylcytidines"
XX
XX WO2003040321-A2.
XX
XX 15-MAY-2003.
XX
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XX PF 04-NOV-2002; 2002MO-US035324.
XX PR 08-NOV-2001; 2001US-00007078.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ward DT, Walt AT;
XX DR WPI; 2003-449448/42.
XX PT New compound, having a sequence targeted to a nucleic acid encoding human
XX PT collapse response mediator protein 2, useful for preparing a composition
XX PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX PT cancer.
XX PS Claim 3; Page 77; 120pp; English.
XX CC This invention relates to novel antisense oligonucleotides that modulate
XX CC the expression of human eukaryotic translation initiation factor 2C 1
XX CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
XX CC Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
XX CC intracellular membrane associated protein thought to be involved in
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XX CC affect cell growth, morphology and tumorigenicity. Accordingly,
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XX CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX CC progeroid syndrome. As such, the oligos of the present invention can be
XX CC described as having cytostatic and antiproliferative activities. This
XX CC oligonucleotide sequence is an antisense oligo used to inhibit expression
XX CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX CC of the invention.
XX SQ Sequence 20 BP; 8 A; 2 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6727 CTGGAATACCTCTCTCTTA 6746
XX DB 20 CTGGAATACCTCTCTCTTA 1
XX
XX RESULT 385
XX ADB81495/c
XX ID ADB81495 standard; DNA; 20 BP.
XX AC ADB81495;
XX DT 04-DEC-2003 (first entry)
XX XX
XX DE Antisense oligo (SeqID 12) used to inhibit human EIF2C1 DNA.
XX KW antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX KW EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99;
XX KW gene therapy; hyperproliferative disorder;
XX KW familial hypercholesterolemia; cancer; polycystic kidney disease;
XX KW cystic fibrosis; progeroid syndrome; cytostatic; antiproliferative.
XX OS Homo sapiens.
XX XX
XX Key Location/Qualifiers
XX FH modified_base 1..20
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX FT 5-methylcytidines"
XX PN WO2003040321-A2.

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XX PD 15-MAY-2003.
XX PF 04-NOV-2002; 2002MO-US035324.
XX PR 08-NOV-2001; 2001US-00007078.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ward DT, Walt AT;
XX DR WPI; 2003-449448/42.
XX PT New compound, having a sequence targeted to a nucleic acid encoding human
XX PT collapse response mediator protein 2, useful for preparing a composition
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XX PS Claim 3; Page 76; 120pp; English.
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XX CC the expression of human eukaryotic translation initiation factor 2C 1
XX CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
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XX CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX CC progeroid syndrome. As such, the oligos of the present invention can be
XX CC described as having cytostatic and antiproliferative activities. This
XX CC oligonucleotide sequence is an antisense oligo used to inhibit expression
XX CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX CC of the invention.
XX SQ Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 163 CGCTGACCTTCACAGTCTCC 182
XX DB 20 CGCTGACCTTCACAGTCTCC 1
XX
XX RESULT 386
XX ADB81499/c
XX ID ADB81499 standard; DNA; 20 BP.
XX AC ADB81499;
XX DT 04-DEC-2003 (first entry)
XX XX
XX DE Antisense oligo (SeqID 16) used to inhibit human EIF2C1 DNA.
XX KW antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX KW EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99;
XX KW gene therapy; hyperproliferative disorder;
XX KW familial hypercholesterolemia; cancer; polycystic kidney disease;
XX KW cystic fibrosis; progeroid syndrome; cytostatic; antiproliferative.
XX OS Homo sapiens.
XX XX
XX Key Location/Qualifiers
XX FH modified_base 1..20
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX FT 5-methylcytidines"

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XX PN WO2003040321-A2.
XX FT
XX PD 15-MAY-2003.
XX PF 04-NOV-2002; 2002WO-US035324.
XX PR 08-NOV-2001; 2001US-00007078.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ward DT, Watt AT,
XX DR WPI; 2003-449448/42.
XX PT New compound, having a sequence targeted to a nucleic acid encoding human
XX PT collapsin response mediator protein 2, useful for preparing a composition
XX PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX PS cancer.
XX PS Claim 3; Page 76; 120pp; English.
XX CC This invention relates to novel antisense oligonucleotides that modulate
XX CC the expression of human eukaryotic translation initiation factor 2C 1
XX CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
XX CC Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
XX CC intracellular membrane associated protein thought to be involved in
XX CC cellular differentiation, such that altered expression of EIF2C1 can
XX CC affect cell growth, morphology and tumorigenicity. Accordingly,
XX CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
XX CC or tissues can be used in gene therapy to treat various conditions
XX CC including hyperproliferative disorders, familial hypercholesterolemia
XX CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX CC progeria syndrome. As such, the oligos of the present invention can be
XX CC described as having cytostatic and antiproliferative activities. This
XX CC oligonucleotide sequence is an antisense oligo used to inhibit expression
XX CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX CC of the invention.
XX SQ Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
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QY Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 543 GGTGACTTGGAGTCAAA 562
Db 20 GGTGACTTGGAGTCAAA 1
XX
RESULT 387
ADB81515/c
XX ID ADB81515 standard; DNA; 20 BP.
XX AC ADB81515;
XX AC
XX DT 04-DEC-2003 (first entry)
XX DE Antisense oligo (SeqID 32) used to inhibit human EIF2C1 DNA.
XX XX
XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99;
XX gene therapy; hyperproliferative disorder;
XX familial hypercholesterolemia; cancer; polycystic kidney disease;
XX cystic fibrosis; progeria syndrome; cytostatic; antiproliferative.
XX OS Homo sapiens.
XX OS
XX Key Location/Qualifiers
XX modified_base 1..20
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= phosphorothioate backbone, where 1-5 and

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FT FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX XX 5-methylcytidines"
XX PN WO2003040321-A2.
XX FT
XX PD 15-MAY-2003.
XX PF 04-NOV-2002; 2002WO-US035324.
XX PR 08-NOV-2001; 2001US-00007078.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ward DT, Watt AT,
XX DR WPI; 2003-449448/42.
XX PT New compound, having a sequence targeted to a nucleic acid encoding human
XX PT collapsin response mediator protein 2, useful for preparing a composition
XX PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX PS cancer.
XX PS Claim 3; Page 76; 120pp; English.
XX CC This invention relates to novel antisense oligonucleotides that modulate
XX CC the expression of human eukaryotic translation initiation factor 2C 1
XX CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
XX CC Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
XX CC intracellular membrane associated protein thought to be involved in
XX CC cellular differentiation, such that altered expression of EIF2C1 can
XX CC affect cell growth, morphology and tumorigenicity. Accordingly,
XX CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
XX CC or tissues can be used in gene therapy to treat various conditions
XX CC including hyperproliferative disorders, familial hypercholesterolemia
XX CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX CC progeria syndrome. As such, the oligos of the present invention can be
XX CC described as having cytostatic and antiproliferative activities. This
XX CC oligonucleotide sequence is an antisense oligo used to inhibit expression
XX CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX CC of the invention.
XX SQ Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
XX
QY Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1629 GCGGAAGATTTCCAGATG 1648
Db 20 GCGGAAGATTTCCAGATG 1
XX
RESULT 388
ADB81540/c
XX ID ADB81540 standard; DNA; 20 BP.
XX AC ADB81540;
XX AC
XX DT 04-DEC-2003 (first entry)
XX DE Antisense oligo (SeqID 57) used to inhibit human EIF2C1 DNA.
XX XX
XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99;
XX gene therapy; hyperproliferative disorder;
XX familial hypercholesterolemia; cancer; polycystic kidney disease;
XX cystic fibrosis; progeria syndrome; cytostatic; antiproliferative.
XX OS Homo sapiens.
XX OS
XX Key Location/Qualifiers
XX modified_base 1..20
XX FT /tag= a
XX FT

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FT      /mod_base= OTHER
FT      /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT      16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT      5-methylcytidines"
FT      MO2003040321-A2.
XX
XX      15-MAY-2003.
XX
XX      04-NOV-2002; 2002MO-US035324.
XX
XX      08-NOV-2001; 2001US-00007078.
XX
XX      (ISIS-) ISIS PHARM INC.
XX      Ward DT, Watt AT;
XX      WPI; 2003-449448/42.
XX
XX      New compound, having a sequence targeted to a nucleic acid encoding human
XX      collagen response mediator protein 2, useful for preparing a composition
XX      for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX      cancer.
XX
XX      Claim 3; Page 76; 120pp; English.
XX
XX      This invention relates to novel antisense oligonucleotides that modulate
XX      the expression of human eukaryotic translation initiation factor 2C 1
XX      (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
XX      Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
XX      intracellular membrane associated protein thought to be involved in
XX      cellular differentiation, such that altered expression of EIF2C1 can
XX      affect cell growth, morphology and tumorigenicity. Accordingly,
XX      antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
XX      or tissues can be used in gene therapy to treat various conditions
XX      including hyperproliferative disorders, familial hypercholesterolemia
XX      and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX      progeroid syndrome. As such, the oligos of the present invention can be
XX      described as having cytosolic and antipapemic activities. This
XX      oligonucleotide sequence is an antisense oligo used to inhibit expression
XX      of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX      of the invention.
XX
XX      Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX      Query Match      0.3%; Score 20; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX      QY      5052 CATTCTTACCAAGTGCCT 5071
XX      |||||||
XX      Db      20 CATTCTTACCAAGTGCCT 1
XX
XX      RESULT 389
XX      ADB81505/c
XX      ID      ADB81505 standard; DNA; 20 BP.
XX
XX      AC      ADB81505;
XX
XX      DT      04-DEC-2003 (first entry)
XX
XX      DE      Antisense oligo (SeqID 22) used to inhibit human EIF2C1 DNA.
XX
XX      KW      antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX      EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99;
XX      gene therapy; hyperproliferative disorder;
XX      familial hypercholesterolemia; cancer; polycystic kidney disease;
XX      cystic fibrosis; progeroid syndrome; cytosolic; antipapemic.
XX
XX      OS      Homo sapiens.
XX
XX      FH      Key      Location/Qualifiers

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FT      modified_base 1..20
FT      ;
FT      /mod_base= OTHER
FT      /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT      16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT      5-methylcytidines"
FT      MO2003040321-A2.
XX
XX      15-MAY-2003.
XX
XX      04-NOV-2002; 2002MO-US035324.
XX
XX      08-NOV-2001; 2001US-00007078.
XX
XX      (ISIS-) ISIS PHARM INC.
XX      Ward DT, Watt AT;
XX      WPI; 2003-449448/42.
XX
XX      New compound, having a sequence targeted to a nucleic acid encoding human
XX      collagen response mediator protein 2, useful for preparing a composition
XX      for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX      cancer.
XX
XX      Claim 3; Page 76; 120pp; English.
XX
XX      This invention relates to novel antisense oligonucleotides that modulate
XX      the expression of human eukaryotic translation initiation factor 2C 1
XX      (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
XX      Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
XX      intracellular membrane associated protein thought to be involved in
XX      cellular differentiation, such that altered expression of EIF2C1 can
XX      affect cell growth, morphology and tumorigenicity. Accordingly,
XX      antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
XX      or tissues can be used in gene therapy to treat various conditions
XX      including hyperproliferative disorders, familial hypercholesterolemia
XX      and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX      progeroid syndrome. As such, the oligos of the present invention can be
XX      described as having cytosolic and antipapemic activities. This
XX      oligonucleotide sequence is an antisense oligo used to inhibit expression
XX      of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX      of the invention.
XX
XX      Sequence 20 BP; 3 A; 5 C; 3 G; 9 T; 0 U; 0 Other;
XX
XX      Query Match      0.3%; Score 20; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      925 ATCAGGACATGATGACCA 944
XX      |||||||
XX      Db      20 ATCAGGACATGATGACCA 1
XX
XX      RESULT 390
XX      ADB81534/c
XX      ID      ADB81534 standard; DNA; 20 BP.
XX
XX      AC      ADB81534;
XX
XX      DT      04-DEC-2003 (first entry)
XX
XX      DE      Antisense oligo (SeqID 51) used to inhibit human EIF2C1 DNA.
XX
XX      KW      antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX      EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99;
XX      gene therapy; hyperproliferative disorder;
XX      familial hypercholesterolemia; cancer; polycystic kidney disease;
XX      cystic fibrosis; progeroid syndrome; cytosolic; antipapemic.
XX
XX      OS      Homo sapiens.

```

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XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
PN WO2003040321-A2.
XX
XX 15-MAY-2003.
XX
XX 04-NOV-2002; 2002WO-US035324.
XX
XX 08-NOV-2001; 2001US-00007078.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ward DT, Walt AT;
XX
XX WPI; 2003-449448/42.
XX
XX New compound, having a sequence targeted to a nucleic acid encoding human
XX collapsin response mediator protein 2, useful for preparing a composition
XX for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX cancer.
XX
XX Claim 3; Page 76; 120pp; English.
XX
XX This invention relates to novel antisense oligonucleotides that modulate
XX the expression of human eukaryotic translation initiation factor 2C 1
XX (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
XX Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
XX intracellular membrane associated protein thought to be involved in
XX cellular differentiation, such that altered expression of EIF2C1 can
XX affect cell growth, morphology and tumorigenicity. Accordingly,
XX antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
XX or tissues can be used in gene therapy to treat various conditions
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XX and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX progeroid syndrome. As such, the oligos of the present invention can be
XX described as having cytosolic and antipneumatic activities. This
XX oligonucleotide sequence is an antisense oligo used to inhibit expression
XX of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX of the invention.
XX
XX Sequence 20 BP; 6 A; 8 C; 2 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4522 AGAAGTGTGGTCTTACTGCT 4541
XX |||||||||||||||||||
XX DB 20 AGAAGTGTGGTCTTACTGCT 1
XX
XX RESULT 391
XX ADB81538/c
XX ID ADB81538 standard; DNA; 20 BP.
XX
XX AC ADB81538;
XX
XX DT 04-DEC-2003 (first entry)
XX
XX Antisense oligo (SeqID 55) used to inhibit human EIF2C1 DNA.
XX
XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99;
XX gene therapy; hyperproliferative disorder;
XX familial hypercholesterolemia; cancer; polycystic kidney disease;
XX cystic fibrosis; progeroid syndrome; cytosolic; antipneumatic.
XX

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XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
PN WO2003040321-A2.
XX
XX 15-MAY-2003.
XX
XX 04-NOV-2002; 2002WO-US035324.
XX
XX 08-NOV-2001; 2001US-00007078.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ward DT, Walt AT;
XX
XX WPI; 2003-449448/42.
XX
XX New compound, having a sequence targeted to a nucleic acid encoding human
XX collapsin response mediator protein 2, useful for preparing a composition
XX for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX cancer.
XX
XX Claim 3; Page 76; 120pp; English.
XX
XX This invention relates to novel antisense oligonucleotides that modulate
XX the expression of human eukaryotic translation initiation factor 2C 1
XX (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
XX Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
XX intracellular membrane associated protein thought to be involved in
XX cellular differentiation, such that altered expression of EIF2C1 can
XX affect cell growth, morphology and tumorigenicity. Accordingly,
XX antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
XX or tissues can be used in gene therapy to treat various conditions
XX including hyperproliferative disorders, familial hypercholesterolemia
XX and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX progeroid syndrome. As such, the oligos of the present invention can be
XX described as having cytosolic and antipneumatic activities. This
XX oligonucleotide sequence is an antisense oligo used to inhibit expression
XX of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX of the invention.
XX
XX Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4965 CTACAGCATGGGTCCTCA 4984
XX |||||||||||||||||||
XX DB 20 CTACAGCATGGGTCCTCA 1
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XX RESULT 392
XX ADB81494/c
XX ID ADB81494 standard; DNA; 20 BP.
XX
XX AC ADB81494;
XX
XX DT 04-DEC-2003 (first entry)
XX
XX Antisense oligo (SeqID 11) used to inhibit human EIF2C1 DNA.
XX
XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;
XX EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99;
XX gene therapy; hyperproliferative disorder;
XX

```

KM familial hypercholesterolaemia; cancer; polycystic kidney disease;
 KM cystic fibrosis; progeria syndrome; cytostatic; antilipemic.
 OS Homo sapiens.
 XX
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 FT Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 FT 5-methylcytidines"
 XX
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 PN WO2003040321-A2.
 PD
 PD 15-MAY-2003.
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 PF 04-NOV-2002; 2002WO-US035324.
 XX
 XX
 PR 08-NOV-2001; 2001US-00007078.
 XX
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 XX
 PI Ward DT, Watt AT;
 XX
 PI WPI; 2003-449448/42.
 DR
 XX
 XX
 PT New compound, having a sequence targeted to a nucleic acid encoding human
 PT collapse response mediator protein 2, useful for preparing a composition
 PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
 PT cancer.
 XX
 XX
 PS Claim 3; Page 76; 120pp; English.
 XX
 XX
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 CC the expression of human eukaryotic translation initiation factor 2C 1
 CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
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 CC cellular differentiation, such that altered expression of EIF2C1 can
 CC affect cell growth, morphology and tumorigenicity. Accordingly,
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 CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
 CC progeria syndrome. As such, the oligos of the present invention can be
 CC described as having cytostatic and antilipemic activities. This
 CC oligonucleotide sequence is an antisense oligo used to inhibit expression
 CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
 CC of the invention.
 CC
 CC
 SQ Sequence 20 BP; 4 A; 9 C; 5 G; 2 T; 0 U; 0 Other;
 XX
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 Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 26 GTGGAGCTGCTGAGGCTC 45
 DB 20 GTGGAGCTGCTGAGGCTC 1
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 RESULT 393
 ADB81533/c
 ID ADB81533 standard; DNA; 20 BP.
 XX
 AC ADB81533;
 XX
 XX
 DT 04-DEC-2003 (first entry)
 XX
 XX
 DE Antisense oligo (SeqID 50) used to inhibit human EIF2C1 DNA.
 XX
 XX
 KM antisense; ss; human; eukaryotic translation initiation factor 2C 1;

KM EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP5; Q99;
 KM gene therapy; hyperproliferative disorder;
 KM familial hypercholesterolaemia; cancer; polycystic kidney disease;
 KM cystic fibrosis; progeria syndrome; cytostatic; antilipemic.
 OS Homo sapiens.
 XX
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 FT Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 FT 5-methylcytidines"
 XX
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 PN WO2003040321-A2.
 PD
 PD 15-MAY-2003.
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 PF 04-NOV-2002; 2002WO-US035324.
 XX
 XX
 PR 08-NOV-2001; 2001US-00007078.
 XX
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 XX
 PI Ward DT, Watt AT;
 XX
 PI WPI; 2003-449448/42.
 DR
 XX
 XX
 PT New compound, having a sequence targeted to a nucleic acid encoding human
 PT collapse response mediator protein 2, useful for preparing a composition
 PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
 PT cancer.
 XX
 XX
 PS Claim 3; Page 76; 120pp; English.
 XX
 XX
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 CC the expression of human eukaryotic translation initiation factor 2C 1
 CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
 CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP5 and Q99. It is an
 CC intracellular membrane associated protein thought to be involved in
 CC cellular differentiation, such that altered expression of EIF2C1 can
 CC affect cell growth, morphology and tumorigenicity. Accordingly,
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 CC or tissues can be used in gene therapy to treat various conditions
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 CC progeria syndrome. As such, the oligos of the present invention can be
 CC described as having cytostatic and antilipemic activities. This
 CC oligonucleotide sequence is an antisense oligo used to inhibit expression
 CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
 CC of the invention.
 CC
 CC
 SQ Sequence 20 BP; 4 A; 9 C; 3 G; 4 T; 0 U; 0 Other;
 XX
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 Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4162 TGACCTGGCTAGGAGGAG 4181
 DB 20 TGACCTGGCTAGGAGGAG 1
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 XX
 RESULT 394
 ADB81559/c
 ID ADB81559 standard; DNA; 20 BP.
 XX
 AC ADB81559;
 XX
 XX
 DT 04-DEC-2003 (first entry)
 XX
 XX
 DE Antisense oligo (SeqID 76) used to inhibit human EIF2C1 DNA.

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XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;
KM EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
KM gene therapy; hyperproliferative disorder;
KM familial hypercholesterolaemia; cancer; polycystic kidney disease;
KM cystic fibrosis; progeria syndrome; cytostatic; antihypertensive.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
PN WO2003040321-A2.
XX
PD 15-MAY-2003.
XX
PP 04-NOV-2002; 2002WO-US035324.
XX
PR 08-NOV-2001; 2001US-00007078.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ward DT, Watt AT;
XX
PI WPI; 2003-449448/42.
XX
PT New compound, having a sequence targeted to a nucleic acid encoding human
PT collapsin response mediator protein 2, useful for preparing a composition
PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT cancer.
XX
PS Claim 3; Page 77; 120pp; English.
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XX the expression of human eukaryotic translation initiation factor 2C 1
XX (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
XX Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
XX intracellular membrane associated protein thought to be involved in
XX cellular differentiation, such that altered expression of EIF2C1 can
XX affect cell growth, morphology and tumorigenicity. Accordingly,
XX antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
XX or tissues can be used in gene therapy to treat various conditions
XX including hyperproliferative disorders, familial hypercholesterolaemia
XX and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX progeria syndrome. As such, the oligos of the present invention can be
XX described as having cytostatic and antihypertensive activities. This
XX oligonucleotide sequence is an antisense oligo used to inhibit expression
XX of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX of the invention.
XX
SQ Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 7239 CAAGTCACAGCATGATGAGG 7258
XX ||||||||||||||||||
DB 20 CAAGTCACAGCATGATGAGG 1

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XX antisense oligo (Seqid 23) used to inhibit human EIF2C1 DNA.
DE
XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;
KM EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
KM gene therapy; hyperproliferative disorder;
KM familial hypercholesterolaemia; cancer; polycystic kidney disease;
KM cystic fibrosis; progeria syndrome; cytostatic; antihypertensive.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
PN WO2003040321-A2.
XX
PD 15-MAY-2003.
XX
PP 04-NOV-2002; 2002WO-US035324.
XX
PR 08-NOV-2001; 2001US-00007078.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ward DT, Watt AT;
XX
PI WPI; 2003-449448/42.
XX
PT New compound, having a sequence targeted to a nucleic acid encoding human
PT collapsin response mediator protein 2, useful for preparing a composition
PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT cancer.
XX
PS Claim 3; Page 76; 120pp; English.
XX
XX This invention relates to novel antisense oligonucleotides that modulate
XX the expression of human eukaryotic translation initiation factor 2C 1
XX (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
XX Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
XX intracellular membrane associated protein thought to be involved in
XX cellular differentiation, such that altered expression of EIF2C1 can
XX affect cell growth, morphology and tumorigenicity. Accordingly,
XX antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
XX or tissues can be used in gene therapy to treat various conditions
XX including hyperproliferative disorders, familial hypercholesterolaemia
XX and cancer, as well as polycystic kidney disease, cystic fibrosis and
XX progeria syndrome. As such, the oligos of the present invention can be
XX described as having cytostatic and antihypertensive activities. This
XX oligonucleotide sequence is an antisense oligo used to inhibit expression
XX of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX of the invention.
XX
SQ Sequence 20 BP; 3 A; 8 C; 3 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 989 AGATCAAGGCGCTGAAGTG 1008
XX ||||||||||||||||||
DB 20 AGATCAAGGCGCTGAAGTG 1

```

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RESULT 395
ADB81506/c
ID ADB81506 standard; DNA; 20 BP.
XX
AC ADB81506,
XX
DT 04-DEC-2003 (first entry)

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```

RESULT 396
ADB81508/c
ID ADB81508 standard; DNA; 20 BP.
XX
AC ADB81508,

```


XX	04-DEC-2003	(first entry)
DT	Antisense oligo (Seqid 25) used to inhibit human EIF2C1 DNA.	
XX		
DE	Antisense; ss; human; eukaryotic translation initiation factor 2C 1;	
XX	EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GBRP95; Q99;	
KW	gene therapy; hyperproliferative disorder;	
KW	familial hypercholesterolaemia; cancer; polycystic kidney disease;	
KW	cystic fibrosis; progeria syndrome; cytoskeletal; antihypertensive.	
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	modified_base	1..20
FT	/*tag= a	/mod_base= OTHER
FT	/note= "OTHER= phosphorothioate backbone, where 1-5 and	16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT	5-methylcytidines"	
XX		
PN	WO2003040321-A2.	
XX		
PD	15-MAY-2003.	
XX		
PF	04-NOV-2002; 2002WO-US035324.	
XX		
PR	08-NOV-2001; 2001US-00007078.	
XX		
PA	(ISIS-) ISIS PHARM INC.	
XX		
PI	Ward DT, Watt AT;	
DR	WPI; 2003-449448/42.	
XX		
PT	New compound, having a sequence targeted to a nucleic acid encoding human	
PT	collapsin response mediator protein 2, useful for preparing a composition	
PT	for treating hypercholesterolemia or hyperproliferative disorder, e.g.,	
PT	cancer.	
XX		
PS	Claim 3; Page 76; 120pp; English.	
XX		
CC	This invention relates to novel antisense oligonucleotides that modulate	
CC	the expression of human eukaryotic translation initiation factor 2C 1	
CC	(EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as	
CC	Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GBRP95 and Q99. It is an	
CC	intracellular membrane associated protein thought to be involved in	
CC	cellular differentiation, such that altered expression of EIF2C1 can	
CC	affect cell growth, morphology and tumorigenicity. Accordingly,	
CC	antisense oligonucleotides that inhibit the expression of EIF2C1 in cells	
CC	or tissues can be used in gene therapy to treat various conditions	
CC	including hyperproliferative disorders, familial hypercholesterolaemia	
CC	and cancer, as well as polycystic kidney disease, cystic fibrosis and	
CC	progeria syndrome. As such, the oligos of the present invention can be	
CC	described as having cytostatic and antihypertensive activities. This	
CC	oligonucleotide sequence is an antisense oligo used to inhibit expression	
CC	of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA	
CC	of the invention.	
XX		
SQ	Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;	
XX		
QY	Query Match	0.3%; Score 20; DB 1; Length 20;
DB	Best Local Similarity	100.0%; Pred. No. 2.7e+02;
DB	Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
DB	1258 CGCTGTATTAGAGCTGAC 1277	
DB	CGCTGTATTAGAGCTGAC 1	

XX	AD81518;
AC	04-DEC-2003 (first entry)
DT	
XX	
DE	Antisense oligo (SegID 35) used to inhibit human EIF2C1 DNA.
XX	
KM	antisense; ser; human; eukaryotic translation initiation factor 2C 1;
XX	EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99;
KW	gene therapy; hyperproliferative disorder;
KW	familial hypercholesterolemia; cancer; polycystic kidney disease;
KW	cystic fibrosis; progeria syndrome; cytosolic; antihypertensive.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	modified_base
FT	1..20
FT	/*tag= a
FT	/mod_base= OTHER
FT	/note= "OTHER= phosphothioate backbone, where 1-5 and
FT	16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT	5-methylcytidines"
PN	WO2003040321-A2.
PD	15-MAY-2003.
XX	
PF	04-NOV-2002; 2002WO-US035324.
XX	
PR	08-NOV-2001; 2001US-00007078.
PA	(ISIS-) ISIS PHARM INC.
PI	Ward DT, Watt AT;
XX	
DR	WPI: 2003-449448/42.
XX	
PT	New compound, having a sequence targeted to a nucleic acid encoding human
PT	collapsin response mediator protein 2, useful for preparing a composition
PT	for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT	cancer.
XX	
PS	Claim 3; Page 76; 120pp; English.
XX	
XX	This invention relates to novel antisense oligonucleotides that modulate
CC	the expression of human eukaryotic translation initiation factor 2C 1
CC	(EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC	Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC	intracellular membrane associated protein thought to be involved in
CC	cellular differentiation, such that altered expression of EIF2C1 can
CC	affect cell growth, morphology and tumorigenicity. Accordingly,
CC	antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC	or tissues can be used in gene therapy to treat various conditions
CC	including hyperproliferative disorders, familial hypercholesterolemia
CC	and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC	progeria syndrome. As such, the oligos of the present invention can be
CC	described as having cytostatic and antiproliferative activities. This
CC	oligonucleotide sequence is an antisense oligo used to inhibit expression
CC	of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC	of the invention.
XX	
SQ	Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
XX	
XX	Query Match 0.3%; Score 20; DB 1; Length 20;
XX	Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX	Matches 20; Conservative 0; Mismatches 0; Gaps 0;
XX	
XX	2038 ATCACAGCAGTCGTAGGCG 2057
XX	
XX	
XX	
XX	
XX	
XX	20 ATCACAGCAGTCGTAGGCG 1

```
ADB81535/c
ID ADB81535 standard; DNA; 20 BP.
XX
AC ADB81535;
XX
DT 04-DEC-2003 (first entry)
XX
DE Antisense oligo (SeqID 52) used to inhibit human EIF2C1 DNA.
XX
KM antisense; ss; human; eukaryotic translation initiation factor 2C 1;
KM EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
KM gene therapy; hyperproliferative disorder;
KM familial hypercholesterolaemia; cancer; polycystic kidney disease;
KM cystic fibrosis; progeria syndrome; cytostatic; antihypertensive.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
PN MO2003040321-A2.
XX
PD 15-MAY-2003.
XX
PF 04-NOV-2002; 2002WO-US035324.
XX
PR 08-NOV-2001; 2001US-00007078.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ward DT, Watt AT;
XX
PI WPI; 2003-449448/42.
XX
DR
XX
PT New compound, having a sequence targeted to a nucleic acid encoding human
PT collapsin response mediator protein 2, useful for preparing a composition
PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT cancer.
XX
PS Claim 3; Page 76; 120pp; English.
XX
CC This invention relates to novel antisense oligonucleotides that modulate
CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
CC affect cell growth, morphology and tumorigenicity. Accordingly,
CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC or tissues can be used in gene therapy to treat various conditions
CC including hyperproliferative disorders, familial hypercholesterolaemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC progeria syndrome. As such, the oligos of the present invention can be
CC described as having cytostatic and antihypertensive activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC of the invention.
XX
SQ Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4823 TTGCTATGCAAAACATCT 4842
DB 20 TTGCTATGCAAAACATCT 1
```

```
RESULT 399
ADB81544/c
ID ADB81544 standard; DNA; 20 BP.
XX
AC ADB81544;
XX
DT 04-DEC-2003 (first entry)
XX
DE Antisense oligo (SeqID 61) used to inhibit human EIF2C1 DNA.
XX
KM antisense; ss; human; eukaryotic translation initiation factor 2C 1;
KM EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
KM gene therapy; hyperproliferative disorder;
KM familial hypercholesterolaemia; cancer; polycystic kidney disease;
KM cystic fibrosis; progeria syndrome; cytostatic; antihypertensive.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
PN MO2003040321-A2.
XX
PD 15-MAY-2003.
XX
PF 04-NOV-2002; 2002WO-US035324.
XX
PR 08-NOV-2001; 2001US-00007078.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ward DT, Watt AT;
XX
PI WPI; 2003-449448/42.
XX
DR
XX
PT New compound, having a sequence targeted to a nucleic acid encoding human
PT collapsin response mediator protein 2, useful for preparing a composition
PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT cancer.
XX
PS Claim 3; Page 76; 120pp; English.
XX
CC This invention relates to novel antisense oligonucleotides that modulate
CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
CC affect cell growth, morphology and tumorigenicity. Accordingly,
CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC or tissues can be used in gene therapy to treat various conditions
CC including hyperproliferative disorders, familial hypercholesterolaemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC progeria syndrome. As such, the oligos of the present invention can be
CC described as having cytostatic and antihypertensive activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC of the invention.
XX
SQ Sequence 20 BP; 7 A; 2 C; 9 G; 2 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5332 CTTGGCTCAGCTCTCCAG 5351
DB 20 CTTGGCTCAGCTCTCCAG 1
```

Db 20 CTTTGCTCACTGCTCCAG 1

RESULT 400
ADB81556/c
ID ADB81556 standard; DNA; 20 BP.
XX
AC ADB81556;
XX
DT 04-DEC-2003 (first entry)
XX
DE Antisense oligo (SeqID 73) used to inhibit human EIF2C1 DNA.
XX
KM antisense; ss; human; eukaryotic translation initiation factor 2C 1;
KW EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
KM gene therapy; hyperproliferative disorder;
KW familial hypercholesterolaemia; cancer; polycystic kidney disease;
KM cystic fibrosis; progeria syndrome; cytostatic; antilipaeamic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
PN WO2003040321-A2.
XX
PD 15-MAY-2003.
XX
PE 04-NOV-2002; 2002WO-US035324.
XX
PR 08-NOV-2001; 2001US-00007078.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ward DT, Watt AT;
XX
PI WPI; 2003-449448/42.
XX
DR New compound, having a sequence targeted to a nucleic acid encoding human
XX PT collapsin response mediator protein 2, useful for preparing a composition
XX PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX PT cancer.
XX
PS Claim 3; Page 77; 120pp; English.
XX
CC This invention relates to novel antisense oligonucleotides that modulate
CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
CC affect cell growth, morphology and tumorigenicity. Accordingly,
CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC or tissues can be used in gene therapy to treat various conditions
CC including hyperproliferative disorders, familial hypercholesterolaemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC progeria syndrome. As such, the oligos of the present invention can be
CC described as having cytostatic and antilipaeamic activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC of the invention.
XX
SQ Sequence 20 BP; 8 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7067 TTTTGTGAATGCACTGAGTC 7086
|||
Db 20 TTGTGTGAATGCACTGAGTC 1

RESULT 401
ADB81558/c
ID ADB81558 standard; DNA; 20 BP.
XX
AC ADB81558;
XX
DT 04-DEC-2003 (first entry)
XX
DE Antisense oligo (SeqID 75) used to inhibit human EIF2C1 DNA.
XX
KM antisense; ss; human; eukaryotic translation initiation factor 2C 1;
KW EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
KM gene therapy; hyperproliferative disorder;
KW familial hypercholesterolaemia; cancer; polycystic kidney disease;
KM cystic fibrosis; progeria syndrome; cytostatic; antilipaeamic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
PN WO2003040321-A2.
XX
PD 15-MAY-2003.
XX
PE 04-NOV-2002; 2002WO-US035324.
XX
PR 08-NOV-2001; 2001US-00007078.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ward DT, Watt AT;
XX
PI WPI; 2003-449448/42.
XX
DR New compound, having a sequence targeted to a nucleic acid encoding human
XX PT collapsin response mediator protein 2, useful for preparing a composition
XX PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX PT cancer.
XX
PS Claim 3; Page 77; 120pp; English.
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CC This invention relates to novel antisense oligonucleotides that modulate
CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
CC affect cell growth, morphology and tumorigenicity. Accordingly,
CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC or tissues can be used in gene therapy to treat various conditions
CC including hyperproliferative disorders, familial hypercholesterolaemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC progeria syndrome. As such, the oligos of the present invention can be
CC described as having cytostatic and antilipaeamic activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC of the invention.
XX
SQ Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;

XX WPI; 2003-328499/31.
 DR
 XX New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as
 PT pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying
 PT modulators of receptor-ligand interactions.
 XX
 PS Disclosure; SEQ ID NO 213; 55pp; English.
 XX
 CC The invention relates to an isolated secreted and transmembrane
 CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful
 CC in PRO polypeptide detection methods. The PRO polypeptide is useful for
 CC linking a bioactive molecule to a cell. The PRO polypeptide or an
 CC antibody against it is useful for modulating a biological activity of a
 CC cell. The PRO polypeptide is useful in industrial applications including
 CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO
 CC polypeptide is also useful as a thrombolytic agent, interferon,
 CC interleukin, erythropoietin, colony stimulating factor and other
 CC cytokines. The PRO polypeptide is useful for treating disease such as
 CC cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,
 CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,
 CC atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,
 CC Parkinson's disease; cardiovascular disease e.g. hypertension and
 CC myocardial ischaemia; kidney disease e.g. renal failure and
 CC glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial
 CC asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory
 CC bowel disease; reproductive disorders e.g. premature labour and
 CC preeclampsia; carcinogenesis. The present sequence represents a PRO
 CC polypeptide associated oligonucleotide of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?docid=20020177553
 XX
 SQ Sequence 24 BP; 6 A; 10 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 0.28; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 7.2e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2551 CTGACGTCACGCTGTCACAC 2573
 Db 2 CTGACCTTCACGTCGACAC 24
 RESULT 856
 ABX92443 standard; DNA; 24 BP.
 ID ABX92443
 AC ABX92443;
 XX
 DT 08-MAY-2003 (first entry)
 XX
 DE Human PRO DNA PCR primer SEQ ID NO 213.
 XX
 KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
 KW cardiac insufficiency; nervous system disorder; kidney disorder;
 KW bone disorder; cartilage disorder; arthritis; tumour wound healing;
 KW genetic disorder; cytotoxic; antidiabetic; anti-inflammatory;
 KW antidiabetic; anti-tumour; vulnary; antianaemic; dermatological;
 KW cardiant; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2002169284-A1.
 XX
 PD 14-NOV-2002.
 XX
 PF 16-OCT-2001; 2001US-00978697.
 XX
 XX 26-MAY-1981; 81US-00267213.
 PR 17-OCT-1997; 97US-0062250P.
 PR 03-NOV-1997; 97US-0064249P.

PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 17-MAR-1998; 98US-0080420P.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0078939P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 26-MAR-1998; 98US-0079656P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 27-MAR-1998; 98US-0079786P.
 PR 30-MAR-1998; 98US-0079920P.
 PR 30-MAR-1998; 98US-0079923P.
 PR 26-JUN-1998; 98US-00105413.
 PR 07-OCT-1998; 98US-00168978.
 PR 07-OCT-1998; 98US-0021141.
 PR 02-NOV-1998; 98US-00184216.
 PR 06-NOV-1998; 98US-00187368.
 PR 20-NOV-1998; 98US-00204855.
 PR 07-DEC-1998; 98US-00202054.
 PR 22-DEC-1998; 98US-0021517.
 PR 05-JAN-1999; 99US-00500106.
 PR 05-MAR-1999; 99US-00254465.
 PR 08-MAR-1999; 99US-00505028.
 PR 10-MAR-1999; 99US-00265686.
 PR 10-MAR-1999; 99US-00505190.
 PR 12-APR-1999; 99US-00284291.
 PR 14-MAY-1999; 99US-0031832.
 PR 14-MAY-1999; 99US-0010733.
 PR 02-JUN-1999; 99US-0012252.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380142.
 PR 30-NOV-1999; 99US-00285313.
 PR 02-DEC-1999; 99US-0028551.
 PR 02-DEC-1999; 99US-0028565.
 PR 16-DEC-1999; 99US-0030095.
 PR 30-DEC-1999; 99US-0031243.
 PR 30-DEC-1999; 99US-005031274.
 PR 05-JAN-2000; 2000US-0000219.
 PR 06-JAN-2000; 2000US-0000277.
 PR 06-JAN-2000; 2000US-0000376.
 PR 11-FEB-2000; 2000US-0003565.
 PR 18-FEB-2000; 2000US-0004341.
 PR 24-FEB-2000; 2000US-0005004.
 PR 02-MAR-2000; 2000US-0005841.
 PR 10-MAR-2000; 2000US-0006319.
 PR 21-MAR-2000; 2000US-0007532.
 PR 30-MAR-2000; 2000US-0008439.
 PR 17-MAY-2000; 2000US-0013705.
 PR 22-MAY-2000; 2000US-0014042.
 PR 30-MAY-2000; 2000US-0014941.
 PR 02-JUN-2000; 2000US-0015264.
 PR 28-JUL-2000; 2000US-0020710.
 PR 24-AUG-2000; 2000US-0023328.
 PR 08-NOV-2000; 2000US-00709238.
 PR 27-NOV-2000; 2000US-00723749.
 PR 01-DEC-2000; 2000US-00732678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000US-0074956.
 PR 28-FEB-2001; 2001US-00506520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 22-MAR-2001; 2001US-00816920.
 PR 23-MAR-2001; 2001US-00809552.

CC corresponding PRO polypeptide selected from 118 100-700 amino acid
CC sequences, all given in the specification. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS, cancer, or diabetic complications. The nucleic
CC acids are useful as hybridization probes, in chromosome and gene mapping,
CC and in generating antisense RNA or DNA. The polypeptides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful
CC in tissue typing. This sequence represents a novel human secreted and
CC transmembrane PRO polypeptide associated primer
XX
SQ Sequence 24 BP; 6 A; 10 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 7, 2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 2551 CTGACGTACAGCTGTGCCACAC 2573
DB 2 CTGACCTTCAGCTGACCCACAC 24
RESULT 855
ID ACA71803
ID ACA71803 standard; DNA; 24 BP.
XX
AC ACA71803;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human PRO polypeptide associated oligonucleotide SEQ ID NO 213.
XX
KM Human; ds; thrombolytic agent; interferon; interleukin; cytokine;
KM erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;
KM apoptosis related condition; AIDS; amyotrophic lateral sclerosis;
KM inflammatory disease; asbestosis; atherosclerosis; neurodegenerative disease;
KM gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;
KM hypertension; myocardial ischemia; kidney disease; carcinogenesis;
KM glomerulonephritis; lung disease; pulmonary hypertension; pre-eclampsia;
KM bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;
KM inflammatory bowel disease; reproductive disorder; premature labour.
XX
OS Homo sapiens.
XX
PN US2002177553-A1.
XX
PD 28-NOV-2002.
XX
PF 15-OCT-2001; 2001US-00798192.
XX
XX 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-006511P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-007791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-0004020.
PR 20-MAR-1998; 98US-0078866P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.

PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US0204855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
PR 12-MAR-1999; 99WO-US005190.
PR 12-APR-1999; 99US-00267213.
PR 14-MAY-1999; 99US-00284291.
PR 14-MAY-1999; 99WO-US011832.
PR 02-JUN-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US030955.
PR 16-DEC-1999; 99WO-US030955.
PR 30-DEC-1999; 99WO-US031273.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003555.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
XX
XX
XX (GENTH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
PI Ferrara N, Filvaroff E, Fong S, Gerber H, Gerritsen ME,
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
PI Klijavin IJ, Kuo SS, Napiet MA, Pan J, Paoni NF, Roy MA, Shelton DL,
PI Stewart TA, Tumas D, Williams PM, Wood WI;

PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 Query Match 0.24; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.08; Pred. No. 7.2e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2551 CTGACGTACCACTGTGCGCACAC 2573
 |||||
 Db 2 CTGACCTTCACGCTGAGCCACAC 24

RESULT 854
 ACA63639
 ID ACA63639 standard; DNA; 24 BP.
 XX ACA63639;
 AC
 XX 16-JUN-2003 (first entry)
 DT
 XX Novel human secreted and transmembrane protein related primer #104.
 DE
 XX Human: secreted and transmembrane protein; PRO; antiinflammatory;
 KM antiarteriosclerotic; cardiact; anti-infertility; anti-HIV; cytostatic;
 KM anti-diabetic; gene therapy; inflammatory disease; organ failure;
 KM atherosclerosis; cardiac injury; infertility; birth defect;
 KM premature aging; AIDS; cancer; diabetic complication; chromosome mapping;
 KM Gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;
 KM tissue typing; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2002192706-A1.
 XX
 PD 19-DEC-2002.
 XX
 PF 24-OCT-2001; 2001US-00999832.
 XX
 PR 17-OCT-1997; 97US-0062250P.
 PR 03-NOV-1997; 97US-0064249P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 17-MAR-1998; 98US-00040220.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0078939P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 26-MAR-1998; 98US-0079656P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 27-MAR-1998; 98US-0079786P.
 PR 30-MAR-1998; 98US-0079920P.
 PR 30-MAR-1998; 98US-0079923P.
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 PR 31-MAR-1998; 98US-0080107P.
 PR 31-MAR-1998; 98US-0080165P.
 PR 31-MAR-1998; 98US-0080194P.
 PR 01-APR-1998; 98US-0080327P.
 PR 01-APR-1998; 98US-0080328P.
 PR 01-APR-1998; 98US-0080333P.
 PR 01-APR-1998; 98US-0080344P.
 PR 08-APR-1998; 98US-0081049P.
 PR 08-APR-1998; 98US-0081070P.
 PR 08-APR-1998; 98US-0081071P.
 PR 09-APR-1998; 98US-0081195P.

PR 09-APR-1998; 98US-0081203P.
 PR 09-APR-1998; 98US-0081229P.
 PR 15-APR-1998; 98US-0081817P.
 PR 15-APR-1998; 98US-0081819P.
 PR 15-APR-1998; 98US-0081838P.
 PR 15-APR-1998; 98US-0081952P.
 PR 15-APR-1998; 98US-0081955P.
 PR 21-APR-1998; 98US-0082568P.
 PR 21-APR-1998; 98US-0082569P.
 PR 22-APR-1998; 98US-0082700P.
 PR 22-APR-1998; 98US-0082704P.
 PR 22-APR-1998; 98US-0082797P.
 PR 22-APR-1998; 98US-0082804P.
 PR 23-APR-1998; 98US-0082796P.
 PR 07-OCT-1998; 98US-00821141.
 PR 20-NOV-1998; 98US-00824855.
 PR 05-JAN-1999; 99US-00800106.
 PR 08-MAR-1999; 99US-00800528.
 PR 10-MAR-1999; 99US-00805190.
 PR 14-MAY-1999; 99US-00810733.
 PR 02-JUN-1999; 99US-00812252.
 PR 30-NOV-1999; 99US-00828313.
 PR 02-DEC-1999; 99US-00828551.
 PR 02-DEC-1999; 99US-00828565.
 PR 16-DEC-1999; 99US-00830095.
 PR 30-DEC-1999; 99US-00831243.
 PR 30-DEC-1999; 99US-00831274.
 PR 05-JAN-2000; 2000US-00800219.
 PR 06-JAN-2000; 2000US-00800277.
 PR 06-JAN-2000; 2000US-00800376.
 PR 11-FEB-2000; 2000US-00803565.
 PR 18-FEB-2000; 2000US-00804341.
 PR 24-FEB-2000; 2000US-00805804.
 PR 02-MAR-2000; 2000US-00805841.
 PR 10-MAR-2000; 2000US-00806319.
 PR 21-MAR-2000; 2000US-00807532.
 PR 30-MAR-2000; 2000US-00808439.
 PR 17-MAY-2000; 2000US-00813705.
 PR 22-MAY-2000; 2000US-00814042.
 PR 30-MAY-2000; 2000US-00814941.
 PR 02-JUN-2000; 2000US-00815264.
 PR 28-JUL-2000; 2000US-00820710.
 PR 24-AUG-2000; 2000US-00823328.
 PR 01-DEC-2000; 2000US-00823678.
 PR 20-FEB-2000; 2000US-00834956.
 PR 28-FEB-2001; 2001US-00805520.
 PR 22-MAR-2001; 2001US-00809552.
 PR 25-MAY-2001; 2001US-00817092.
 PR 01-JUN-2001; 2001US-00817800.
 PR 20-JUN-2001; 2001US-00819692.
 PR 29-JUN-2001; 2001US-00821066.
 PR 09-JUL-2001; 2001US-00821735.

(GETH) GENENTECH INC.
 PA
 XX
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Kijavain IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 DR WPI; 2003-328860/31.
 XX
 PT New secreted and transmembrane nucleic acids and polypeptides, designated
 PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
 PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
 PT cancer.
 XX
 XX Example 34; Page 143; 453pp; English.
 PS
 CC The invention describes an isolated nucleic acid (1) comprising, or which
 CC is at least 80 % sequence identity to, or the full-length coding sequence
 CC of, any of 118 300-2100 nucleotide sequences, which encodes its


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PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
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PR 22-APR-1998; 98US-0082797P.
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PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
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PR 22-MAY-1998; 98US-0086430P.
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PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
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PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090863P.
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PR 01-JUL-1998; 98US-0091359P.
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PR 07-OCT-1998; 98US-0016897P.
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PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98US-00202855.
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PR 22-DEC-1998; 98US-00218517.
PR 22-DEC-1998; 98US-0113296P.

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PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
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PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUN-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.

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(GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;

DR WPI, 2002-292882/34..
 XX New polypeptide-human macroprotein 21.78 and polynucleotide encoding it,
 PT for treating diseases such as embryo development teratogenesis and tumor.
 XX
 PS Example 2; Page 19 (Disclosure); 35pp; Chinese.
 XX
 CC The present invention describes human macroprotein 21.78 (I). Also
 CC described is a process for preparing (I) using DNA recombination
 CC techniques. (I) and the polynucleotide sequence encoding it (II) can be
 CC used in the treatment of diseases such as embryo development
 CC teratogenesis and tumors. The present sequence represents a PCR primer
 CC for (I), which is used in an example from the present invention
 CC
 XX Sequence 24 BP; 0 A; 1 C; 2 G; 21 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 7.2e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4464 TTTTGTGTTTGTGTC 4486
 DB 2 TTTTGTGTTTGTGTTTTC 24
 RESULT 852
 ABX03797/c
 ID ABX03797 standard; cDNA; 24 BP.
 XX
 AC ABX03797;
 XX
 DT 09-JAN-2003 (first entry)
 XX
 DE DNA encoding secreted protein signal peptide sequence #6.
 XX
 KW Differential display method; leucine-rich motif; transmembrane protein;
 KM secreted protein; secreted protein signal peptide; ss.
 XX
 OS Unidentified.
 XX
 PN WO200259259-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 23-JAN-2002; 2002WO-IL000071.
 XX
 PR 23-JAN-2001; 2001US-0263158P.
 XX
 PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
 XX
 PI Wreschner DH;
 XX
 DR WPI, 2002-559769/64.
 XX
 DR P-PSDB; ABG98326.
 XX
 PT Differential display method for identifying secreted or transmembrane
 PT protein, comprising contacting a DNA with a first primer that hybridizes
 PT to a sequence coding for a leucine-rich motif and with a second
 PT oligonucleotide primer.
 XX
 PS Disclosure; Fig 2; 37pp; English.
 XX
 CC The invention relates to a differential display comprising contacting
 CC cDNA with a first primer that hybridizes to an oligonucleotide sequence
 CC coding for a leucine-rich motif, and with a second oligonucleotide primer
 CC to form a cDNA-hybrid molecule. The method comprises obtaining mRNA from
 CC at least 2 samples, synthesizing cDNA from the RNA of each sample,
 CC contacting the cDNA with a first primer that hybridizes to an
 CC oligonucleotide sequence coding for a leucine-rich motif, and with a second
 CC oligonucleotide primer to form cDNA-hybrid molecules, amplifying the cDNA
 CC -hybrid molecules, detecting amplified products and comparing the
 CC amplified products from each sample to identify distinctive amplified
 CC products coding for at least one secreted or transmembrane protein. The

CC method is useful for discovering novel secreted and/or transmembrane
 CC proteins which are important for cell processes and play an important
 CC role in determining its phenotype, and which act as mediators for the
 CC transfer of signals from external environment into the cell itself, thus
 CC modulating gene expression. Sequences ABX03792-ABX03869 represent DNA
 CC encoding secreted protein signal peptide sequences
 XX
 SQ Sequence 24 BP; 0 A; 9 C; 8 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 7.2e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7402 GCAAGCACATCAGCAGCAGCAG 7424
 DB 23 GCCAGCACAGCAGCAGCAGCGG 1
 RESULT 853
 ACD42604
 ID ACD42604 standard; DNA; 24 BP.
 XX
 AC ACD42604;
 XX
 DT 09-SEP-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein related primer #104.
 XX
 DE Human; secreted and transmembrane protein; PEO; virulence; gene therapy;
 KW cell death; growth induction cascade; blood coagulation cascade;
 KM viral infection; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003050239-A1.
 XX
 PD 13-MAR-2003.
 XX
 PF 15-OCT-2001; 2001US-00978191.
 XX
 PR 17-OCT-1997; 97US-0062250P.
 PR 03-NOV-1997; 97US-0064249P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077532P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077919P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 17-MAR-1998; 98US-0080422P.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0078939P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 26-MAR-1998; 98US-0079656P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 27-MAR-1998; 98US-0079786P.
 PR 30-MAR-1998; 98US-0079920P.
 PR 30-MAR-1998; 98US-0079923P.
 PR 31-MAR-1998; 98US-0080105P.
 PR 31-MAR-1998; 98US-0080107P.
 PR 31-MAR-1998; 98US-0080156P.
 PR 31-MAR-1998; 98US-0080194P.
 PR 01-APR-1998; 98US-0080327P.
 PR 01-APR-1998; 98US-0080328P.
 PR 01-APR-1998; 98US-0080333P.
 PR 01-APR-1998; 98US-0080334P.
 PR 08-APR-1998; 98US-0081049P.

KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 XX Synthetic.
 OS
 XX WO200122972-A2.
 PN
 XX
 XX 05-APR-2001.
 PD
 XX
 XX 25-SEP-2000; 2000WO-US026383.
 PF
 XX
 XX 25-SEP-1999; 99US-0156113P.
 PR
 XX 27-SEP-1999; 99US-0156135P.
 PR 23-AUG-2000; 2000US-0227436P.
 XX
 XX (IOWA) UNIV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 XX
 XX Krieg AM, Schetter C, Vollmer J;
 PI
 XX WPI; 2001-273485/28.
 DR
 XX
 XX Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids.
 PR
 XX
 XX Disclosure; Page 39; 338pp; English.
 PS
 XX The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the
 CC present sequence may have a phosphorothioate backbone
 CC
 SQ Sequence 24 BP; 0 A; 0 C; 3 G; 21 T; 0 U; 0 Other;
 Query Match 0.2%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 7.2e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4466 TTTTGTGCTT 4488
 Db 1 TTGTTTGTGTTTGTGTTT 23
 RESULT 850
 ABS77576
 ID ABS77576 standard; DNA; 24 BP.
 XX
 AC ABS77576;
 XX
 XX 13-DEC-2002 (first entry)
 DT
 XX
 XX Angiogenesis inhibitory oligonucleotide #60.
 DE
 XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubella; Osler-Weber Syndrome; myocardial angiodysplasia;
 KW plaque neovascularisation; telangiectasia; haemophilic joint;
 KW angiodioma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.
 XX
 OS Synthetic.

XX
 PN WO200253141-A2.
 XX
 XX 11-JUL-2002.
 PD
 XX
 XX 14-DEC-2001; 2001WO-US048458.
 PF
 XX
 XX 14-DEC-2000; 2000US-0255534P.
 PR
 XX
 XX (COLE-) COLEY PHARM GROUP INC.
 PA
 XX
 XX Bratzler RL;
 PI
 XX WPI; 2002-566690/60.
 DR
 XX
 XX Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.
 PR
 XX
 XX Claim 2; Page 20; 276pp; English.
 PS
 XX The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubella, Osler-Weber Syndrome, myocardial angiodysplasia, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiodioma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 CC
 SQ Sequence 24 BP; 0 A; 0 C; 3 G; 21 T; 0 U; 0 Other;
 Query Match 0.2%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 7.2e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4466 TTTTGTGCTT 4488
 Db 1 TTGTTTGTGTTTGTGTTT 23
 RESULT 851
 ABR86902
 ID ABR86902 standard; DNA; 24 BP.
 XX
 AC ABR86902;
 XX
 XX 23-JUL-2002 (first entry)
 DT
 XX
 XX Human macroprotein 21.78 PCR primer 2 SEQ ID NO:4.
 DE
 XX
 XX Human; macroprotein 21.78; embryo development teratogenesis; tumour;
 KW PCR primer; ss.
 KW
 XX Homo sapiens.
 OS
 XX CN1331245-A.
 PN
 XX
 XX 16-JAN-2002.
 PD
 XX
 XX 30-JUN-2000; 2000CN-00116981.
 PF
 XX
 XX 30-JUN-2000; 2000CN-00116981.
 PR
 XX
 XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 PA
 XX
 XX Mao Y, Xie Y;
 PI
 XX

ID AACT8737
 AC AACT8737 standard; DNA; 24 BP.
 XX
 DT AACT8737;
 XX
 DE 08-FEB-2001 (first entry)
 XX
 XX Human PRO860 reverse PCR primer SEQ ID NO:213.
 XX
 OS Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
 XX expressed sequence tag; detection; cancer; PCR primer; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200053756-A2.
 PD
 PD 14-SEP-2000.
 XX
 PF 18-FEB-2000; 2000MO-US004341.
 XX
 PR 08-MAR-1999; 99WO-US005028.
 PR 12-MAR-1999; 99US-0123957P.
 PR 29-MAR-1999; 99US-0126773P.
 PR 21-APR-1999; 99US-0130232P.
 PR 28-APR-1999; 99US-0131445P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 23-JUL-1999; 99US-0141037P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000MO-US000219.
 PR 05-JAN-2000; 2000MO-US000277.
 PR 06-JAN-2000; 2000MO-US000376.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Bolstein D, Deenoyers L, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kljavin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 XX
 DR WPI; 2000-611443/58.
 XX
 PT Novel PRO polypeptides and polynucleotides used in detection methods, to
 PT target bioactive molecules to specific cells, and to modulate cellular
 PT activities.
 XX
 PS Example 34; Page 265; 636pp; English.
 XX
 CC AACT8458 to AACT8559 represent polynucleotide and EST (expressed sequences
 CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
 CC The PRO polynucleotides and polypeptides have cytosaric activity. The
 CC polynucleotides and polypeptides can be used for detecting the presence
 CC of PRO polypeptides in samples, for linking bioactive molecules to cells
 CC and for modulating biological activities of cells, using the polypeptides
 CC for specific targeting. The polypeptide targeting can be used to kill the
 CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
 CC provide specific targeting of bioactive molecules to cells. AACT8600 to
 CC AACT8987 represent PCR primers and probes used in the isolation of the
 CC PRO polynucleotide sequences
 XX
 SQ Sequence 24 BP; 6 A; 10 C; 4 G; 4 T; 0 U; 0 Other;

OY	2551	CTGACGTACCAGCTGTGCACAC	2573
Db	2	CTGACCTTCACGCTGAGCCACAC	24
RESULT 848			
ID	AAC90278	standard; DNA; 24 BP.	
XX			
AC	AAC90278;		
XX			
DT	14-MAR-2001	(first entry)	
XX			
DE	Primer BBI296 used to clone SNORF3.		
XX			
KW	SNORF3; inflammation; arthritis; neurological disorder; infection;		
RW	bone disease; respiratory disorder; asthma; cancer; cardiovascular; ss.		
OS	Mus musculus.		
XX			
FN	MO200073449-A1.		
XX			
PD	07-DEC-2000.		
XX			
PF	26-MAY-2000; 2000WO-US014654.		
XX			
PR	28-MAY-1999; 99US-00322257.		
PR	06-OCT-1999; 99US-00413433.		
XX			
PA	(SYNA-) SYNAPTIC PHARM CORP.		
XX			
PI	Borowsky BE, Ogozalek KL, Jones KA,		
DR	WPI; 2001-025252/03.		
XX			
Nucleic acid encoding a mammalian (human, rat and mouse) SNORF3 receptor			
PT	which is useful for designing drugs for treating conditions such as a		
PT	chronic and acute inflammation, arthritis, neurological disorders and		
PT	microbial infections.		
XX			
PS	Disclosure; Page 99; 227pp; English.		
XX			
CC	The present invention relates to a mammalian SNORF3 receptor. SNORF3		
CC	antagonists and agonists are used to treat abnormalities brought about by		
CC	increased or decreased activity of the mammalian SNORF3 receptor. The		
CC	receptor is useful as a tool for designing drugs for treating conditions		
CC	-such as a chronic and acute inflammation, arthritis, neurological		
CC	disorders, microbial infections, bone diseases, respiratory disorders		
CC	such as asthma, cancers, cardiovascular disorders		
XX			
SQ	Sequence 24 BP; 2 A; 10 C; 5 G; 7 T; 0 U; 0 Other;		
Query Match	0.2%; Score 18.2; DB 1; Length 24;		
Best Local Similarity	87.0%; Pred. No. 7,2e+02;		
Matches	20; Conservative 0; Mismatches 3; Indels 0; Gaps 0.		
OY	4267	TCTGCACTGTCTCGACTCTTTC	4289
Db	1	TCTGCACGCTCCTGACCCCTTC	23
RESULT 849			
ID	AAF98935	standard; DNA; 24 BP.	
XX			
AC	AAF98935;		
XX			
DT	12-JUN-2001	(first entry)	
XX			
DE	Immunostimulatory nucleic acid #51.		
XX			
Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;			
immunostimulatory; tumour; viral infection; bacterial infection;			

AAZ34071
 ID AAZ34071 standard; DNA; 24 BP.
 XX
 AC AAZ34071;
 XX
 DT 07-DEC-1999 (first entry)
 XX
 DE Human PRO860 PCR reverse primer.
 XX
 KM Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9946281-A2.
 PD 16-SBP-1999.
 XX
 PF 08-MAR-1999; 99WO-US005028.
 XX
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 17-MAR-1998; 98US-00040220.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0078939P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 26-MAR-1998; 98US-0079656P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 27-MAR-1998; 98US-0079786P.
 PR 30-MAR-1998; 98US-0079920P.
 PR 30-MAR-1998; 98US-0079923P.
 PR 31-MAR-1998; 98US-0080105P.
 PR 31-MAR-1998; 98US-0080107P.
 PR 31-MAR-1998; 98US-0080165P.
 PR 31-MAR-1998; 98US-0080194P.
 PR 01-APR-1998; 98US-0080327P.
 PR 01-APR-1998; 98US-0080328P.
 PR 01-APR-1998; 98US-0080333P.
 PR 01-APR-1998; 98US-0080334P.
 PR 08-APR-1998; 98US-0081049P.
 PR 08-APR-1998; 98US-0081070P.
 PR 08-APR-1998; 98US-0081071P.
 PR 09-APR-1998; 98US-0081195P.
 PR 09-APR-1998; 98US-0081203P.
 PR 09-APR-1998; 98US-0081229P.
 PR 15-APR-1998; 98US-0081817P.
 PR 15-APR-1998; 98US-0081838P.
 PR 15-APR-1998; 98US-0081952P.
 PR 15-APR-1998; 98US-0081955P.
 PR 21-APR-1998; 98US-0082568P.
 PR 21-APR-1998; 98US-0082569P.
 PR 22-APR-1998; 98US-0082700P.
 PR 22-APR-1998; 98US-0082704P.
 PR 23-APR-1998; 98US-0082804P.
 PR 23-APR-1998; 98US-0082767P.
 PR 23-APR-1998; 98US-0082796P.
 PR 27-APR-1998; 98US-0083336P.
 PR 28-APR-1998; 98US-0083322P.
 PR 29-APR-1998; 98US-0083392P.
 PR 29-APR-1998; 98US-0083495P.
 PR 29-APR-1998; 98US-0083496P.
 PR 29-APR-1998; 98US-0083499P.

PR 29-APR-1998; 98US-0083500P.
 PR 29-APR-1998; 98US-0083545P.
 PR 29-APR-1998; 98US-0083554P.
 PR 29-APR-1998; 98US-0083558P.
 PR 29-APR-1998; 98US-0083559P.
 PR 30-APR-1998; 98US-0083742P.
 PR 05-MAY-1998; 98US-0084366P.
 PR 06-MAY-1998; 98US-0084414P.
 PR 07-MAY-1998; 98US-0084441P.
 PR 07-MAY-1998; 98US-0084598P.
 PR 07-MAY-1998; 98US-0084600P.
 PR 07-MAY-1998; 98US-0084637P.
 PR 07-MAY-1998; 98US-0084639P.
 PR 07-MAY-1998; 98US-0084643P.
 PR 07-MAY-1998; 98US-0084643P.
 PR 13-MAY-1998; 98US-0085323P.
 PR 13-MAY-1998; 98US-0085338P.
 PR 13-MAY-1998; 98US-0085339P.
 PR 15-MAY-1998; 98US-0085573P.
 PR 15-MAY-1998; 98US-0085579P.
 PR 15-MAY-1998; 98US-0085580P.
 PR 15-MAY-1998; 98US-0085582P.
 PR 15-MAY-1998; 98US-0085689P.
 PR 15-MAY-1998; 98US-0085697P.
 PR 15-MAY-1998; 98US-0085700P.
 PR 15-MAY-1998; 98US-0085704P.
 PR 18-MAY-1998; 98US-0086023P.
 PR 22-MAY-1998; 98US-0086392P.
 PR 22-MAY-1998; 98US-0086414P.
 PR 22-MAY-1998; 98US-0086430P.
 PR 22-MAY-1998; 98US-0086486P.
 PR 28-MAY-1998; 98US-0087098P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 28-MAY-1998; 98US-0087208P.
 PR 30-JUL-1998; 98US-0094651P.
 PR 11-SEP-1998; 98US-0100038P.

XX (GENTECH) GENENTECH INC.

XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

XX WPI; 1999-551358/46.

PT New secreted and transmembrane polypeptides and their polynucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders.

XX Example 34; Page 210; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as sources
 CC of probes, primers, for chromosome mapping, and for generation of
 CC antisense sequences. They can also be used to create transgenic animals.
 CC The proteins can be used to treat a variety of diseases and disorders,
 CC depending on their function. Diseases that may be treated include blood
 CC coagulation disorders, cancers and cellular adhesion disorders. They may
 CC also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY1685 to
 CC AAY1774 represent polynucleotide and polypeptide sequence given in the
 CC exemplification of the present invention

XX Sequence 24 BP; 6 A; 10 C; 4 G; 4 T; 0 U; 0 Other;

SO Query Match 0.2%; Score 18.2; DB 1; Length 24;

Best Local Similarity 87.0%; Pred. No. 7.2e+02;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2551 CTGACGTACGAGCTGTGCACAC 2573

Db 2 CTGACCTTCAGCTGAGCCAC 24

RESULT 847


```
PR 22-JUN-2001; 2001US-0300135P.
XX
XX (CERE-) CERES INC.
XX
XX Dang V, Okamoto J;
XX
XX WPI; 2003-175280/17.
XX
XX
XX New chimeric polypeptide comprising a histone acetyltransferase
PT polypeptide segment and a segment comprising a histone deacetylase
PT chromatin-associated protein complex subunit, useful for modulating gene
PT expression in cells.
XX
XX Example 10; Page 54; 85pp; English.
XX
XX The specification describes chimeric histone acetyltransferase
CC polypeptides. The chimeric polypeptides comprise a polypeptide segment
CC that exhibits histone acetyltransferase activity, and a polypeptide
CC segment having 40% or greater sequence identity to a subunit of a histone
CC deacetylase chromatin-associated protein complex. The chimeric
CC polypeptide cells are useful for determining gene expression profiles in
CC specific cells, for modulating gene expression in specific cells, and for
CC making genetically modified eukaryotes. The present sequence represents a
CC reverse transcription primer used in the method of the invention
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
SQ
Query Match 0.2%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 5.2e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4466 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
RESULT 840
ACCT9402
ID ACC79402 standard; DNA; 19 BP.
XX
XX ACC79402;
AC
XX
XX 04-AUG-2003 (first entry)
XX
XX M13 sequencing primer 3' primer SEQ ID NO:84.
XX
XX Pathological condition; ataxia telangiectasia; AT; tumour; cancer;
XX cytostatic; vaccine; gene therapy; PCR primer; ss.
XX
XX Enterobacteria phage M13.
OS Synthetic.
XX
XX WO2003033668-A2.
XX
XX 24-APR-2003.
XX
XX 17-OCT-2002; 2002WO-US033311.
XX
XX 17-OCT-2001; 2001US-0330206P.
XX
XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
XX Barlow C, Winrow CJ, Callahan MLA, Pankratz DG, Vibat CRT;
XX Warren AJ;
XX
XX WPI; 2003-393520/37.
XX
XX Preventing or treating a pathological condition e.g., ataxia
PT telangiectasia (AT), AT tumors or other cancers comprises administering
PT polynucleotides.
XX
XX Example 1; Page 76; 184pp; English.
XX
```

```
CC The present invention describes a method for preventing or treating a
CC pathological condition (comprising ataxia telangiectasia (AT), AT tumors
CC or other cancers), which comprises administering to a mammalian subject
CC at least one of: (a) a first polynucleotide comprising a sequence having
CC 38-889 bp (consisting of the sequences in ACC79319 to ACC79392 (1)) or a
CC second polynucleotide at least 95% identical to the first polynucleotide;
CC (b) a third polynucleotide comprising at least 10-bp sequence that is
CC hybridizable to the first polynucleotide under stringent conditions; or
CC (c) a gene corresponding to any of (1)-(2) or another gene at least 95%
CC identical to the gene (1) have cytosolic activities, and can be used in
CC vaccines and in gene therapy. The method is useful for preventing or
CC treating e.g., ataxia telangiectasia (AT), AT tumors or other cancers.
CC ACC79393 to ACC79423 represent primers used in the exemplification of the
CC present invention
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
SQ
Query Match 0.2%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 5.2e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4466 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
RESULT 841
AAD49149
ID AAD49149 standard; DNA; 19 BP.
XX
XX AAD49149;
AC
XX
XX 07-MAR-2003 (first entry)
XX
XX 3' sequencing primer #1 used in the invention.
XX
XX Atherosclerosis; vaccine; nervous system disorder; Alzheimer's disease;
XX Parkinson's disease; multiple sclerosis; immune disorder; gene therapy;
XX autoimmune disorder; rheumatoid arthritis; hyperproliferative disorder;
XX haemolytic anaemia; graft-versus-host disease; inflammation; infection;
XX epilepsy; Addison's disease; neoplasm; tissue regeneration; Chemotaxis;
XX food additive; food preservative; primer; ss.
XX
XX Unidentified.
XX
XX WO200281726-A2.
XX
XX 17-OCT-2002.
XX
XX 15-NOV-2001; 2001WO-US043741.
XX
XX 15-NOV-2000; 2000US-0248892P.
XX
XX 28-NOV-2000; 2000US-0253623P.
XX
XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
XX Leonard A, Sartani A, Glas J, Sutcliffe JG, Hasel KW;
XX
XX WPI; 2003-058561/05.
XX
XX New polypeptide associated with atherosclerosis, useful for treating
PT atherosclerosis, nervous system disorders, immune disorders,
PT hyperproliferative disorders and infectious diseases.
XX
XX Disclosure; Page 139; 146pp; English.
XX
XX The invention relates to polynucleotides and polypeptides associated with
CC atherosclerosis. Polynucleotides of the invention are useful for delivery
CC of genes, DNA vaccines, diagnostic reagents, peptides, proteins or
CC macromolecules. Sequences of the invention are useful for treating
CC nervous system disorders (e.g., Alzheimer's disease, Parkinson's disease,
CC multiple sclerosis, epilepsy), immune disorders (e.g., autoimmune
CC disorders such as rheumatoid arthritis, Addison's disease, haemolytic
```


XX	Hepatitis B virus; HBV infection; chronic hepatitis; toxicity; virulence;
KM	acute hepatitis; therapeutic; gene therapy; vaccine; infectious disease;
KM	TOGA; Total Gene expression Analysis; PCR; primer; ss.
XX	
OS	unidentified.
XX	
PN	WO20022783-A2.
XX	
PD	21-MAR-2002.
XX	
PF	17-SEP-2001; 2001WO-US029123.
XX	
PR	15-SEP-2000; 2000US-0233176P.
XX	
PA	(DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX	
PI	Chisari FV, Wieland SF, Guidotti LGDVM, Mueller R, Hilbush BS;
XX	
DR	WPI, 2002-339865/37.
XX	
PT	Preventing and treating hepatitis viral infection in a mammal, comprises
PT	administering nucleic acid molecules that up- or down-regulate in
PT	hepatitis B virus infection or polypeptides encoded by the nucleic acid
XX	molecules.
XX	
PS	Disclosure; Page 28; 125pp; English.
XX	
CC	The present invention relates to a method for preventing, treating,
CC	modulating or ameliorating a medical condition. The method involves
CC	administering one or more nucleic acid molecules up- or down-regulated in
CC	hepatitis B virus (HBV) infection or polypeptides encoded by the nucleic
CC	acid molecules or antibodies that bind to the polypeptide. The method is
CC	useful for preventing, treating, modulating or ameliorating a medical
CC	condition. It is also useful for determining the presence or absence of a
CC	mutation in the nucleic acid molecules or detecting an alteration in
CC	expression of the polypeptide which is useful for the diagnosis of
CC	hepatitis viral infection. The method is useful for assessing the stage
CC	of hepatitis viral infection (e.g., acute hepatitis versus chronic
CC	hepatitis) or assessing the efficacy or toxicity of therapeutic treatment
CC	for hepatitis viral infection and a gene expression profile is useful for
CC	identifying polypeptides and polynucleotides which are associated with
CC	hepatitis viral infection. Sequences of the invention are used in gene
CC	therapy and as vaccines. Nucleic acid sequences are useful as a
CC	diagnostic markers for HBV infection and for treating infectious
CC	diseases. The present DNA sequence is a PCR primer which is used for
CC	direct sequencing of TOGA (Total Gene expression Analysis) generated PCR
XX	products
XX	
SQ	Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
XX	
Query Match	0.2%; Score 18.2; DB 1; Length 19;
Best Local Similarity	94.7%; Pred. No. 5.2e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0	
OY	4466 TTTT TTTT TTTT TTTT TTTT TTTT G 4484
DB	1 TTTT TTTT TTTT TTTT TTTT TTTT V 19
XX	
RESULT 838	
AAAD40279	
ID	AAAD40279 standard; DNA; 19 BP.
XX	
AC	AAAD40279;
XX	
DT	22-OCT-2002 (first entry)
XX	
DE	HOOK PCR primer used to isolate pumpkin 2beta-3beta hydroxylase cDNA.
XX	
XX	Gibberellin; transgenic plant; seed germination; seedling growth; GA;
XX	transgenic; 2beta-3beta hydroxylase; enzyme; pumpkin; PCR; primer; ss.
XX	

OS	Cucurbita pepo.
XX	!
PN	US2002053095-A1.
XX	
PD	02-MAY-2002.
XX	
PE	10-AUG-1999; 99US-00371307.
XX	
PR	10-AUG-1999; 99US-00371307.
XX	
PA	(BROW/) BROWN S M.
PI	Brown SM, Ellich TD, Heck GR, Kishore GM, Lognuech EW, Lognuech SJ;
PI	Piller KU, Rao S, Ream JE;
XX	
DR	WPI; 2002-489107/52.
XX	
PT	Control of gibberellin levels in plants useful to avoid unfavorable
PT	conditions in crops to increase yields, using transgenic plants having
PT	reduced seed germination and early seedling growth then treatment to
PT	restore these properties.
XX	
PS	Example 19; Page 104; 155pp; English.
XX	
CC	The invention relates to control of gibberellin (GA) levels in plants.
CC	The method involves producing transgenic plants having a phenotype of
CC	reduced seed germination and reduced early seedling growth, then
CC	restoring seed germination and early seedling growth by treating plants
CC	with an appropriate compound when conditions are favourable. The method
CC	is useful to control seed germination and/or early seedling growth in
CC	agricultural production so that unfavorable environmental conditions
CC	normally reducing agronomic output can be avoided and yields increased.
CC	Plants also demonstrate increased uniformity of germination, emergence
CC	and seedling vigor, so increasing yields at harvest. The method is
CC	especially useful in crop plants such as e.g. canola, soybean, cotton,
CC	etc., and is also useful in storage and transport of seeds to reduce
CC	premature germination which may affect agronomic or food quality of the
CC	seeds. The present sequence is a PCR primer used to isolate pumpkin beta
CC	-beta hydroxylase cDNA. This primer is used in the exemplification of
CC	the invention
XX	
SQ	Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
	Query Match 0.2%; Score 18.2; DB 1; Length 19;
	Best Local Similarity 94.7%; Pred. No. 5.2e+02;
	Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY	4466 TTTT TTTT TTTT TTTT TTTG 4484
DB	1 TTTT TTTT TTTT TTTT TV 19
RESULT 839	
ID	ABZ68389 standard; DNA; 19 BP.
XX	
AC	ABZ68389;
XX	
DT	22-APR-2003 (first entry)
XX	
DE	Reverse transcription primer used to produce yeast cDNA.
XX	
KM	Histone acetyltransferase; histone deacetylase; gene expression profile;
KW	chromatin-associated protein; gene expression; primer; ss.
OS	Synthetic.
XX	
FN	WO2003000715-A1.
XX	
PD	03-JAN-2003.
XX	
PF	21-JUN-2002; 2002WO-USO19750.
XX	

KM neuropsychiatric disorder; psychiatric disorder; Alzheimer's disease;
 KM Pick's disease; Binswanger's disease; senile dementia; encephalopathy;
 KM Parkinson's disease; obsessive compulsive disorder; epilepsy; ischaemia;
 KM addiction; multiple sclerosis; depression; manic-depressive disorder;
 KM primer; ss.
 OS Synthetic.
 XX
 XX WO200226936-A2.
 XX
 XX PD 04-APR-2002.
 XX
 XX PF 01-OCT-2001; 2001WO-US030695.
 XX
 XX PR 29-SEP-2000; 2000US-0236790P.
 XX PR 18-JAN-2001; 2001US-0263084P.
 XX
 XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
 XX
 XX PI Thomas BA, Sutcliffe JG, Pribyl TM, Hilbush BS, Haeel KW;
 XX WPI; 2002-363271/41.
 DR
 XX PT New polynucleotide useful in gene therapy for preventing, treating
 PT modulating or ameliorating a medical condition such as psychoses or a
 PT neuro psychiatric disorder e.g. schizophrenia, or a bipolar disorder in a
 PT mammal.
 XX
 XX PS Example 1; Page 40; 254pp; English.
 XX
 CC This invention relates to the cDNA sequences of novel isolated
 CC polynucleotides associated with psychoses or other neuropsychiatric
 CC disorders. The sequences of the invention may act as blockers of D 2
 CC receptors in the meso-limbic dopamine system. The nucleotide sequences of
 CC the invention and the polypeptides encoded by them are useful in the
 CC manufacture of a medicament useful for preventing, treating, modulating
 CC or ameliorating a medical condition e.g. a neuropsychiatric disorder. An
 CC antibody that binds the proteins of the invention is useful for
 CC preventing, treating, modulating or ameliorating neurological disorders
 CC such as psychoses or other neuropsychiatric disorders in a subject. The
 CC sequences are also useful for diagnosing neurological disorders or a
 CC susceptibility to a neurological disorder such as psychoses and other
 CC neuro psychiatric disorders in a subject by determining the presence or
 CC absence of mutation in the nucleotide sequence of apolipoprotein D or by
 CC determining the alteration (increase or decrease) in the expression of
 CC apolipoprotein D. The sequences of the invention are useful in treating
 CC deficiencies or disorders of the central nervous system or peripheral
 CC nervous system by activating or inhibiting the proliferation,
 CC differentiation or mobilization (chemotaxis) of neuroblasts, stem cells
 CC or glial cells. The sequences are useful as a marker or detector of a
 CC particular nervous system disease or disorder such as Alzheimer's
 CC disease, Pick's disease, Binswanger's disease, other senile dementia,
 CC Parkinson's disease, obsessive compulsive disorders, epilepsy,
 CC encephalopathy, ischaemia, addiction, multiple sclerosis, depression and
 CC manic-depressive disorder. The present sequence represents an
 CC oligonucleotide primer used in the identification of the cDNA sequences
 CC of the invention
 XX
 XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
 XX
 XX
 Query Match 0.2%; Score 18.2; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 5.2e+02;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4466 TTTT TTTT TTTT TTTT TTTT TTTT G 4484
 DB 1 TTTT TTTT TTTT TTTT TTTT TTTT V 19
 RESULT 836
 ABQ73231
 ID ABQ73231 standard; DNA; 19 BP.
 XX

AC ABQ73231;
 XX
 XX DT 27-SEP-2002 (first entry)
 XX
 DE Rabbit atherosclerosis related TOGA primer SEQ ID NO:26.
 XX
 XX KW Rabbit; Oryctolagus cuniculus; atherosclerosis; intimal hyperplasia;
 XX TOGA primer; ss.
 XX
 XX OS Oryctolagus cuniculus.
 OS Synthetic.
 XX
 XX PN WO200242420-A2.
 XX
 XX PD 30-MAY-2002.
 XX
 XX PF 21-NOV-2001; 2001WO-US044072.
 XX
 XX PR 21-NOV-2000; 2000US-0252216P.
 XX
 XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
 XX
 XX PA Leonard A, Sartani A, Glaes JR, Haeel KW;
 XX PT WPI; 2002-575233/61.
 DR
 XX PT New polynucleotides related to regulated genes characteristic of
 PT atherosclerosis, useful for diagnosing, preventing, treating, modulating
 PT or ameliorating atherosclerosis in a mammalian subject.
 XX
 XX PS Disclosure; Page 28; 130pp; English.
 XX
 CC The present invention describes an isolated polynucleotide (I) and its
 CC complements, and degenerate variants, comprising a sequence selected from
 CC those given in ABQ73206 to ABQ73222 (NS), which is a digital sequence tag
 CC (UST) corresponding to mRNAs whose expression is regulated by
 CC proliferative lesion development caused by mechanically induced intimal
 CC hyperplasia, or by lecanidipine treatment, or by proliferative lesions
 CC and reversed by lecanidipine treatment. (I) has antiatherosclerotic
 CC activity and can be used in gene therapy. (I) can be used for diagnosing
 CC a medical condition (e.g. atherosclerosis) in a subject which involves
 CC determining the presence or absence of a mutation in (I) and diagnosing
 CC the medical condition based on the presence or absence of the mutation.
 CC (I) is also useful for diagnosing atherosclerosis, or the susceptibility
 CC to atherosclerosis in a subject which involves detecting an alteration
 CC (an increase or decrease) in amount of expression of (I). (I) is also
 CC useful for diagnosing or monitoring the effects of treating a subject
 CC with dihydropyridine calcium antagonist e.g., lecanidipine. (I) can also
 CC be used for preventing, treating, modulating, or ameliorating a medical
 CC condition such as atherosclerosis in a mammalian subject. The present
 CC sequence represents a TOGA primer which is used in the exemplification of
 CC the present invention
 XX
 XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
 XX
 XX
 Query Match 0.2%; Score 18.2; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 5.2e+02;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4466 TTTT TTTT TTTT TTTT TTTT TTTT G 4484
 DB 1 TTTT TTTT TTTT TTTT TTTT TTTT V 19
 RESULT 837
 AAD34663
 ID AAD34663 standard; DNA; 19 BP.
 XX
 XX AC AAD34663;
 XX
 XX DT 16-JUL-2002 (first entry)
 XX
 DE PCR primer #4 used for direct sequencing of TOGA generated PCR products.
 XX


```

SQ      Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
Query Match      0.2%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 5.2e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0
Qy      4466 TTTTTTTTTTTTTTTTG 4484
      |||||
Db      1 TTTTTTTTTTTTTTTT 19

RESULT 831
AADI5201
AADI5201 standard; DNA; 19 BP.
XX      AADI5201;
XX      DT      01-NOV-2001 (first entry)
DE      3' sequencing primer #1 to identify and characterise polynucleotides.
XX
XX      Fatty lesion development; atherosclerosis; Alzheimer's disease;
KW      nervous system disorder; Parkinson's disease; immune system disorder;
KW      ischaemia; lymphopenia; leukocyte adhesion deficiency syndrome;
KW      haemoglobinuria; anaemia; hyperproliferative disorder; Gaucher's disease;
KW      coagulation disorder; blood platelet disorder; autoimmune disorder;
KW      dermatitis; herpes simplex; Addison's disease; rheumatoid arthritis;
KW      Grave's disease; gene therapy; antileukostatic; immunostimulant;
KW      cardiovascular; antiviral; primer; ss.
XX
XX      Unidentified.
XX
XX      WO200154651-A2.
XX      PN
XX      PD      02-AUG-2001.
XX
XX      25-JAN-2001; 2001WO-US002439.
XX      PF
XX      25-JAN-2000; 2000US-0177963P.
XX      PR
XX      PA      (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
XX      Leonard A, Sartani A, Glass JR, Sutcliffe JG, Hasel KW;
XX      PI      WPI; 2001-514526/56.
XX      DR
XX      PT      New polynucleotides regulated by fatty lesion development and their
XX      PT      encoded polypeptides, useful for preventing, treating or ameliorating
XX      PT      atherosclerosis, as well as for immune or hyperproliferative disorders.
XX
XX      Example 1; Page 79; 188pp; English.
XX      PS
XX
XX      The present invention relates to an isolated nucleic acid regulated by
XX      CC      fatty lesion development, which comprises any of 55 polynucleotide
XX      CC      sequences from Oryctolagus cuniculus. The polynucleotide, polypeptide or
XX      CC      antibody is useful for preventing, treating, modulating or ameliorating a
XX      CC      medical condition, particularly atherosclerosis. The invention is used as
XX      CC      a marker or detector of nervous system disorder or disease (e.g.
XX      CC      Parkinson's disease, Alzheimer's disease, ischaemia, dementia). The
XX      CC      invention may also be useful for treating deficiencies or disorders of
XX      CC      the immune system (e.g. lymphopenia, leukocyte adhesion deficiency
XX      CC      syndrome or haemoglobinuria, anaemia), hyperproliferative disorders
XX      CC      (e.g. Gaucher's disease), infectious disease (e.g. herpes simplex),
XX      CC      coagulation disorders, blood platelet disorders and autoimmune disorders
XX      CC      (Addison's disease, rheumatoid arthritis, dermatitis, Grave's disease).
XX      CC      The polynucleotide sequence is also used in gene therapy. The present
XX      CC      sequence is a 3' sequencing primer used in the identification and
XX      CC      characterisation of polynucleotides up-regulated by fatty lesion
XX      CC      development
XX
XX      Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
XX

```

Best Local Similarity 94.7%; Pred. No. 5.2e+02; Indels 0; Gaps 0; Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4466 TTTTTTTTTTTTTTTTTTG 4484
|||||
ID 1 TTTTTTTTTTTTTTTTTTV 19

RESULT 832
AAH21968
AAH21968 standard; DNA, 19 BP.
AC
XX AAH21968;
DE
DT 16-AUG-2001 (first entry)
XX
XX Mouse total gene expression analysis (TOGA) 3' sequencing primer SEQ:92.
XX
XX Mouse; human; total gene expression analysis; TOGA; DST; EST;
KM digital sequence tag; expressed sequence tag; neuroleptic; antimanic;
KM central nervous system; antidepressant; gene therapy; diagnosis;
KM neuropsychiatric disorder; schizophrenia; bipolar disorder;
KM addiction-related behaviour; chromosome identification; immune response;
XX PCR primer; probe; ss.
XX
XX Mus musculus.
OS
XX
XX Mus musculus.
PN
XX MO200130972-A2.
PD
XX 03-MAY-2001.
PF
XX 26-OCT-2000; 2000MO-US029690.
PR
XX 26-OCT-1999; 99US-0161379P.
XX
XX
XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
PA
XX Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush B, Hasel KW;
XX
XX WPI; 2001-300499/31.
DR
XX
XX New neuroleptic-regulated polynucleotides expressed in the central
PT nervous system for diagnosing and treating neuropsychiatric disorders
PT such as schizophrenia, bipolar disorder and addiction-related behavior.
FT
XX
XX
XX Example 1; Page 87; 210pp; English.

The present invention describes isolated neuroleptic-regulated nucleic acid molecules. (I) have neuroleptic, antimanic and antidepressant activities, and can be used in gene therapy. (II), polypeptides (II) encoded by (I), or a host cell (III) comprising (I), are useful for preventing, treating, modulating or ameliorating a medical condition such as a neuropsychiatric disorder. (I) are useful as diagnostic agents for diagnosing a pathological condition or susceptibility to a pathological condition such as neuropsychiatric disorder e.g. schizophrenia, a bipolar disorder or addiction-related behaviour. (I) are useful for detecting the presence of a nucleic acid encoding a protein in a mammalian tissue sample. (I) can be used as probes and primers, for chromosome identification, to control gene expression through triple helix formation or antisense DNA or RNA, in gene therapy to treat the above mentioned disorders, identifying individuals from minute biological samples, as an alternative to restriction fragment length polymorphism (RFLP) and as polymorphic markers for forensic purposes. (I) is also useful as molecular weight markers on Southern gels, diagnostic probes for the presence of specific mRNA in a particular cell type, as a probe to subtract-out known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a gene chip or other support, to raise anti-DNA antibodies using DNA immunisation technique, and as an antigen to elicit an immune response. AAH2197 to AAH2198, AAB98083 and AAB98084 represent sequences used in the exemplification of the present invention

Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

PT Calibration of molecular array data by employing calibration probes that
 PT generate signals proportional to total concentrations of labeled target
 PT molecules, and molecular arrays incorporating sets of calibration probes.
 XX
 XX Disclosure; Page 14; 32pp; English.
 XX
 CC The invention relates to a method for calibrating data scanned from a
 CC molecular array. The method involves employing calibration probes that
 CC generate signals proportional to the total concentrations of labelled
 CC target molecules to which the molecular array probes are directed over an
 CC entire range of sample solutions and molecular arrays incorporating sets
 CC of calibration probes. Method is useful for calibrating different types
 CC of signals scanned from a molecular array, or calibrating signals scanned
 CC from different molecular arrays. The present sequence is poly (A)
 CC normalization probe used in calibration of molecular array data
 XX
 XX SQ Sequence 28 BP; 22 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 18.4; DB 1; Length 28;
 Best Local Similarity 78.6%; Pred. No. 8.2e+02;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 6452 TGTTCGATCTTTTCTGTTT 6479
 Db 28 TTTTGGGAGATTTTCTTTT 1
 XX
 RESULT 829
 AAX06572
 ID AAX06572 standard; DNA; 19 BP.
 XX
 AC AAX06572;
 XX
 DT 06-APR-1999 (first entry)
 XX
 DE (-)-limonene-6-hydroxylase primer 3.B.
 XX
 XX (-)-limonene-6-hydroxylase; (-)-limonene-3-hydroxylase; L3H; L6H;
 KM speak mint; peppermint; enzyme; limonene hydroxylase; trans-carveol;
 KM trans-isopiperitenol; pathogen defense mechanism; attractant;
 KM environmental signal; monoterpene hydroxylase; PCR primer; ss.
 XX
 OS Synthetic.
 OS Mentha spicata.
 XX
 PN WO9859042-A1.
 XX
 PD 30-DEC-1998.
 XX
 PF 15-JUN-1998; 98WO-US012581.
 XX
 PR 24-JUN-1997; 97US-00881784.
 XX
 PA (UNIV) UNIV WASHINGTON STATE RES FOUND.
 XX
 PI Croteau RB, Lupien SL, Karp F;
 XX
 DR WPI; 1999-105618/09.
 XX
 PT New isolated limonene hydroxylase nucleic acids - which encode limonene-6
 PT hydroxylase and limonene-3-hydroxylase, which can be used to produce
 PT trans-carveol and trans-isopiperitenol.
 XX
 PS Example 4; Page 27; 80pp; English.
 XX
 CC The invention relates to nucleotide sequences encoding spearmint (-)-
 CC limonene-6-hydroxylase (L6H) and peppermint (-)-limonene-3-hydroxylase
 CC (L3H). Host cells containing a vector comprising the nucleotide sequences
 CC can be used for the recombinant production of limonene hydroxylases or of
 CC primary enzyme products. The primary enzyme products are trans-carveol in
 CC the case of (-)-L6H or trans-isopiperitenol in the case of (-)-L3H, which
 CC are of subsequent use, to obtain enhanced expression of limonene
 CC hydroxylase in plants to attain enhanced trans-carveol or trans-

CC isopiperitenol production as a predator or pathogen defense mechanism,
 CC attractant or environmental signal. The limonene hydroxylase cDNAs also
 CC provide a useful tool for isolating other monoterpene hydroxylase genes
 CC and for examining the developmental regulation of monoterpene
 CC biosynthesis. Sequences AAX06564-73 represent primers for the PCR
 CC amplification of (-)-limonene-6-hydroxylase cDNA
 XX
 XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
 XX
 Query Match 0.2%; Score 18.2; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 5.2e+02;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTTCTTTTCTTTTCTTTT 4482
 Db 1 TTTTCTTTTCTTTTCTTTT 19
 XX
 RESULT 830
 AAZ99489
 ID AAZ99489 standard; DNA; 19 BP.
 XX
 AC AAZ99489;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE Primer HOOK for cDNA encoding a C-20 oxidase polypeptide.
 XX
 XX Gibberellic acid; copalyl diphosphate synthase; beta-hydroxylase;
 KM 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
 KM seed germination; seedling growth; gibberellin biosynthetic pathway;
 KM transgenic plant; hypocotyl; epicotyl; PCR primer; ss.
 XX
 OS Cucurbita maxima.
 OS
 PN WO200009722-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 10-AUG-1999; 99WO-US018066.
 XX
 PR 10-AUG-1998; 98US-0096111P.
 PR 07-JUN-1999; 99US-0137977P.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Brown SM, Ellich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
 PI Pillar KJ, Rao S, Ream JR;
 XX
 DR WPI; 2000-224351/19.
 XX
 PT Obtaining transgenic plant useful for controlling seed germination and
 PT seedling growth comprises transgene comprising a sequence expressing
 PT altered levels of an essential hormone.
 XX
 PS Example 17; Page 262; 267pp; English.
 XX
 CC The present primer was used to reverse transcribe cDNA encoding a C-20
 CC oxidase. The amplify fragment is used in the method of the invention.
 CC The specification describes methods for the inhibition and control of
 CC gibberellic acid levels. Gibberellic acid levels may be inhibited or
 CC controlled by use of a chimeric expression construct expressing a RNA or
 CC protein which suppresses the gibberellin biosynthetic pathway sequence,
 CC diverts substrate from the pathway, or degrades pathway substrates or
 CC products. The method uses copalyl diphosphate synthase, 3beta-
 CC hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a
 CC 2beta,3beta-hydroxylase polynucleotides to achieve this. The method is
 CC used to control seed germination and seedling growth especially to
 CC regulate gene products of gibberellin biosynthetic pathway and
 CC restoration of normal seed germination, in transgenic plants. The plants
 CC produced are gibberellin deficient, and have shortened hypocotyl and/or
 CC epicotyl phenotypes compared to normal plants
 XX

KW	chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM	developmental disorder; ss.
XX	
OS	Homo sapiens.
PV	EP1281758-A2.
PN	
PD	05-FEB-2003.
PF	30-JUL-2002; 2002EP-00016874.
XX	
PR	02-AUG-2001; 2001US-00922181.
XX	
PA	(AECOM-) AECOMICA INC.
PI	Shannon M, Gu Y, Nguyen C;
XX	
DR	WPI; 2003-423107/40.
XX	
PT	New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX	
PS	Example 8; SEQ ID NO 5557; 103bp; English.
XX	
CC	The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2, MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy, or in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acids can also be used as probes to detect and characterize gross alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as vaccines. The present sequence was used to illustrate the invention.
XX	
SQ	Sequence 25 BP; 3 A; 1 C; 3 G; 18 T; 0 U; 0 Other;
	Query Match 0.2%; Score 18.4; DB 1; Length 25; Best Local Similarity 95.0%; Pred. No. 7,1e+02; Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	4465 TTTTCTTTTTTTTTTTTTTG 4484 3 TTCTTTTTTTTTTTTTTG 22
DB	
RESULT 822	
AAD57848	
ID	AAD57848 standard; DNA; 25 BP.
XX	
AC	AAD57848;
XX	
DT	20-NOV-2003 (first entry)
XX	
DE	Oligonucleotide related to the invention.
XX	
KM	Nonlinear optical technique; screening; ss.
OS	unidentified.
XX	
PN	WO2003064991-A2.
XX	
PD	07-AUG-2003.
XX	
PF	17-JUL-2002; 2002WO-US022681.
XX	

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PR 17-JUL-2001; 2001US-0306040P.
PR 23-OCT-2001; 2001US-0347821P.
PR 06-FEB-2002; 2002US-0354668P.
XX
XX
PA (SALA/) SALAFSKY J S.
XX
XX
PI Salafsky JS;
XX
XX
DR WPI; 2003-646172/61.
XX
XX
PT Screening candidate binding partner(s) for binding to test molecule by
PT applying external force field to sample in homogeneous phase, and
PT illuminating sample with light beam(s) at fundamental frequencies, and
PT measuring physical properties.
XX
XX
PS Disclosure; Page 146; 146pp; English.
XX
XX
CC The present invention relates to a method for detecting interactions
CC between biological components using a nonlinear optical technique. The
CC invention is used for screening candidate binding partner(s) for binding
CC to test molecule. It can also be used to detect changes in orientation or
CC conformation of the probe and/or target. The present sequence is an
CC oligonucleotide related to the invention
XX
XX
SQ Sequence 25 BP, 1 A, 5 C, 3 G, 16 T, 0 U, 0 Other;
XX
XX
Query Match 0.2%; Score 18.4; DB 1; Length 25;
Best Local Similarity 95.0%; Pred. No. 7.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4461 GACCTTTTTTTTTTTTTTTT 4480
|||
3 GACCTTTTTTTTTTTTTTCT 22
XX
XX
RESULT 823
ID ADC38191
XX ADC38191 standard; DNA; 25 BP.
XX AC ADC38191;
XX DT 18-DEC-2003 (first entry)
XX
XX Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:540.
XX
XX human; angiotensin-like protein 1; AMLP1, cytotactic; gene therapy;
XX AMLP1a; se.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX WO2003037931-A2.
XX
XX PD 08-MAY-2003.
XX
XX 01-NOV-2002; 2002WO-US035129.
XX PF 01-NOV-2001; 2001US-0334773P.
XX
XX BR 01-NOV-2001; 2001US-0334773P.
XX
XX (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX PA
XX Shannon M, Phan T;
XX
XX WPI; 2003-430501/40.
XX
XX New isolated nucleic acid molecule encoding a human angiotensin-like
XX protein, useful for treating or preventing a disorder associated with
XX decreased or increased expression or activity of AMLP1.
XX
XX Example 2; SEQ ID NO 540; 172bp; English.
XX
XX The present invention describes the human angiotensin-like protein 1
XX (AMLP1), human AMLP1 has cytotactic activity, and can be used in gene

```


CC insects. The lectin polypeptide is also useful for targeting neutrophil
 CC glycoproteins for diagnostic and therapeutic applications, including
 CC evaluating the nature of immune cells and can also be used in typing,
 CC e.g. blood group typing of polymorphonuclear cells
 XX
 SQ Sequence 25 BP; 1 A; 3 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 25;
 Best Local Similarity 95.0%; Pred. No. 7.1e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTGTGTTTTTTTTTTT 4481
 DB 6 AGTTTTTTTTTTTTTTTT 25

RESULT 819
 AAF74925/C
 ID AAF74925 standard; DNA; 25 BP.
 XX
 AC AAF74925;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE CD40L poly-A tract sequence SEQ ID NO:22.

XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
 KW diagnosis; anarthritic; antirheumatic; immunosuppressive;
 KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
 XX

OS Homo sapiens.

XX WO200119844-A1.

XX 22-MAR-2001.

XX 13-SEP-2000; 2000WO-US024966.

XX 13-SEP-1999; 99US-0153625P.

XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

XX Crow MK, Li Y;

XX WPI; 2001-244776/25.

XX New altered CD40L promoter for use in the study, diagnosis and treatment
 PT of a variety of inflammatory disorders and autoimmune diseases, such as
 PT rheumatoid arthritis.

XX Example 1; Fig 3; 90pp; English.

XX The present invention describes an isolated, purified nucleic acid, which
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
 CC residues 331-455 of the sequence comprising 455 nucleotides given in
 CC AAF74905 where A in the wild type sequence at position 331 (corresponding
 CC to position -125) is replaced with C. (I) has antirheumatic,
 CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
 CC be used in gene therapy. (I) is useful in the study, diagnosis and
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in
 CC which elevated expression of CD40L is a factor, e.g., rheumatoid
 CC arthritis. The present sequence represents a CD40L poly-A tract sequence
 CC which is used in an example from the present invention

XX Sequence 25 BP; 19 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 25;
 Best Local Similarity 95.0%; Pred. No. 7.1e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTGTGTTTTTTTTTTT 4483
 DB 20 TTTTGTGTTTTTTTTTTT 1

RESULT 820
 AAF74930/C
 ID AAF74930 standard; DNA; 25 BP.

XX AAF74930;

XX 23-MAY-2001 (first entry)

XX CD40L poly-A tract sequence SEQ ID NO:27.

XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
 KW diagnosis; anarthritic; antirheumatic; immunosuppressive;
 KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
 XX

OS Homo sapiens.

XX WO200119844-A1.

XX 22-MAR-2001.

XX 13-SEP-2000; 2000WO-US024966.

XX 13-SEP-1999; 99US-0153625P.

XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

XX Crow MK, Li Y;

XX WPI; 2001-244776/25.

XX New altered CD40L promoter for use in the study, diagnosis and treatment
 PT of a variety of inflammatory disorders and autoimmune diseases, such as
 PT rheumatoid arthritis.

XX Example 1; Fig 3; 90pp; English.

XX The present invention describes an isolated, purified nucleic acid, which
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
 CC residues 331-455 of the sequence comprising 455 nucleotides given in
 CC AAF74905 where A in the wild type sequence at position 331 (corresponding
 CC to position -125) is replaced with C. (I) has antirheumatic,
 CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
 CC be used in gene therapy. (I) is useful in the study, diagnosis and
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in
 CC which elevated expression of CD40L is a factor, e.g., rheumatoid
 CC arthritis. The present sequence represents a CD40L poly-A tract sequence
 CC which is used in an example from the present invention

XX Sequence 25 BP; 19 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 25;
 Best Local Similarity 95.0%; Pred. No. 7.1e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTGTGTTTTTTTTTTT 4483
 DB 20 TTTTGTGTTTTTTTTTTT 1

RESULT 821

ID ADB04571 standard; DNA; 25 BP.

XX ADB04571;

XX 20-NOV-2003 (first entry)

XX Human MD27 scanning oligonucleotide SEQ ID 5557.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Db 4 CTTTCTCTTTT 23

RESULT 816

ABL53569/c

ID ABL53569 standard; DNA; 24 BP.

AC ABL53569;

DT 10-JUN-2002 (first entry)

DE Human calcitonin 15.18 PCR primer #1.

XX Calcitonin 15.18; human; foetal abnormality; autoimmune disease; tumour;

KM ageing; immunomodulator; cytostatic; gene therapy; PCR; primer; ss.

OS Homo sapiens.

PN WO200220778-A1.

PD 14-MAR-2002.

PF 02-JUL-2001; 2001WO-CN001124.

PR 07-JUL-2000; 2000CN-00117059.

PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

PI Mao Y, Xie Y;

DR WPI; 2002-269626/31.

PT Human calcitonin 15.18 and encoding polynucleotide, used in diagnosis and treatment of malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and inflammation.

PS Example 2; Page 11; 32pp; Chinese.

CC The present invention relates to human calcitonin 15.18 (see ABB75631).

CC The calcitonin protein and its coding sequence are useful for the

CC diagnosis and treatment of foetal abnormality, autoimmune disease,

CC tumours, and for the study of human ageing. The present sequence is a PCR

CC primer, which was used in an example from the invention

SO Sequence 24 BP; 3 A; 7 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 24;

Best Local Similarity 95.0%; Pred. No. 6.7e+02; Mismatches 1; Indels 0; Gaps 0;

QY 5773 GGCGGCTGCTGCTGCC 5792

Db 23 GGCGAGCTGCTGCTGCC 4

RESULT 817

ABV77669

ID ABV77669 standard; DNA; 24 BP.

AC ABV77669;

DT 03-FEB-2003 (first entry)

DE Human zinc finger protein 9.79 PCR primer #1.

XX Human; zinc finger protein 9.79; cancer; HIV infection; cytostatic;

KM anti-HIV; PCR; primer; ss.

OS Homo sapiens.

PN CN1343710-A.

PD 10-APR-2002.

XX 19-SEP-2000; 2000CN-00125246.

XX 19-SEP-2000; 2000CN-00125246.

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

PI Mao Y, Xie Y;

DR WPI; 2002-548879/59.

PT A novel human zinc finger protein 9.79 polypeptide, useful for treating several diseases e.g. cancer and HIV infection.

PS Example 2; Page 16 (Disclosure); 31pp; Chinese.

CC The present invention relates to human zinc finger protein 9.79 (see

CC ABP59011). The zinc finger protein is useful for treating several

CC diseases e.g. cancer and HIV infection. The present sequence is a PCR

CC primer, which was used in an example from the invention

SO Sequence 24 BP; 1 A; 2 C; 1 G; 20 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 24;

Best Local Similarity 95.0%; Pred. No. 6.7e+02; Mismatches 1; Indels 0; Gaps 0;

QY 4461 GACTTTTTTTTTTTTTT 4480

Db 1 GTCTTTTTTTTTTTTTTT 20

RESULT 818

AAA47833

ID AAA47833 standard; DNA; 25 BP.

AC AAA47833;

DT 16-NOV-2000 (first entry)

DE Adapter sequence for 3' end of lectin cDNA.

KM Lectin; mannosyl; sugar; transgenic plant; crop protection; resistance;

KM bacteria; virus; fungus; insect; targeting; neutrophil glycoprotein;

KM polymorphonuclear cell; blood typing; primer; ss.

OS Hernandia moerenhoutiana.

PN WO200044780-A1.

PD 03-AUG-2000.

PF 28-JAN-2000; 2000WO-AU000039.

PR 29-JAN-1999; 99AU-00008395.

PA (AURE-) AUSTRALIAN RED CROSS BLOOD SERVICE.

PI Clark TR, Minchinton RM;

DR WPI; 2000-532807/48.

PT New polypeptide, capable of binding to mannosyl, isolated from the plant

PT Hernandia is useful for the generation of transgenic plants which exhibit

PS enhanced resistance to micro-organisms, fungi, viruses and insects.

XX Example 8; Page 35; 63pp; English.

CC The Hernandia lectin is capable of binding and/or interacting with

CC mannosyl or a sugar chemically related to mannosyl. The genetic sequence

CC encoding lectin can be used for the generation of transgenic plants which

CC exhibit enhanced resistance to micro-organisms, fungi, viruses and

CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic
 CC marker prediction of ubiquitous simple sequences, POMPUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to understand, treat or eliminate genetic
 CC diseases, predispositions or adverse drug-treatment reactions. Examples
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,
 CC myotonic dystrophy, hyperandrogenemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs

SO Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 5.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
 Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 812

AA064706 standard; cDNA to mRNA, 22 BP.

AA064706;

25-MAR-2003 (revised)

04-JAN-1995 (first entry)

2',5'-linked tetraadenylate-antisense oligonucleotide chimeric mol.

antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator;

RNA cleavage; antiviral therapy; chimeric molecule; ss.

Synthetic.

Location/Qualifiers

misc_feature

1..4

/*tag= a

/label= 2',5'-linked tetraadenylate

/note= "nucleotides linked through phosphodiester bonds
 at hydroxyl groups of 2' and 5' carbons"

misc_feature

5..22

/*tag= b

/note= "antisense region"

WO9409129-A2.

28-APR-1994.

20-OCT-1993; 93WO-US010103.

21-OCT-1992; 92US-00965666.

17-SEP-1993; 93US-00123449.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

(CLEV-) CLEVELAND CLINIC RES INST.

Torrence P, Silverman R, Maitra R, Lesiak K;

WPI; 1994-151315/18.

Specific cleavage of RNA, useful partic. for treating viral infection,

cancers, etc. - by using anti-sense oligo:nucleotide coupled to activator

of 2-5A dependent RNase.

Example 1; Page 68; 86pp; English.

CC This sequence is an example of a 2-5A-antisense oligonucleotide chimeric
 CC molecule. The antisense region targets the chimeric molecule to a
 CC particular region of RNA to be specifically cleaved and the 2',5'-linked
 CC tetraadenylate tail activates the 2-5A RNase. Typical applications are
 CC treatment of viral infections (esp. for cleavage of an RNA virus genome),
 CC cancer; leukaemia, cardiovascular disorders (e.g. restenosis after
 CC angioplasty), genetic disorders, osteoarthritis or rheumatoid arthritis.
 CC (Updated on 25-MAR-2003 to correct PN field.)

SO Sequence 22 BP; 4 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 22;
 Best Local Similarity 95.0%; Pred. No. 5.9e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTT TTTT TTTT TTTT TTTT 4481
 Db 3 AATTTT TTTT TTTT TTTT TTTT 22

RESULT 813

AAT92356 standard; DNA; 22 BP.

AAT92356;

26-JAN-1998 (first entry)

Amino modified oligodeoxyribonucleotide.

Amino modified oligodeoxyribonucleotide; oligonucleotide;

achiral linker reagent; 5-(aminomethyl)-1,3-benzenedimethanol;

N-fluoreceyl-5-(aminomethyl)-1,3-benzenedimethanol;

hybridisation probe; PCR primer; nucleic acid sequencing;

affinity matrix; cloning recombinant DNA; in-vitro mutagenesis; ss.

Synthetic.

Location/Qualifiers

misc_difference 11

/*tag= a

/note= "n = 5-(aminomethyl)-1,3-benzenedimethanol"

misc_difference 12

/*tag= b

/note= "n = 5-(aminomethyl)-1,3-benzenedimethanol"

WO9705156-A1.

13-FEB-1997.

26-JUL-1996; 96WO-DK000330.

27-JUL-1995; 95DK-00000863.

(BEHR/) BEHRENS C.

(PETE/) PETERSEN K H.

(EGHO/) EGHOLM M.

(NIEL/) NIELSEN J.

(DAHL/) DAHL O.

Behrens C, Petersen KH, Egholm M, Nielsen J, Dahl O;

WPI; 1997-145615/13.

New achiral linker reagents - useful for incorporation of multiple amino

gps. or reporter gps. into oligo:nucleotide(s).

Disclosure; Page 20; 42pp; English.

Achiral linker reagents have been developed for the incorporation of

multiple amino groups into oligonucleotides. The present sequence

represents a modified oligodeoxyribonucleotide. The achiral linker

reagents can be used for incorporation of multiple primary amino groups

OS	Homo sapiens.
XX	
PN	W09841648-A2.
PD	24-SEP-1998.
PP	19-MAR-1998;
PR	98WO-US005419.
PS	20-MAR-1997; 9TUS-0041057P.
PA	(VARI-) VARIAGENICS INC.
P1	Housman D, Ledley FD, Stanton VP,
DR	WPI; 1998-521232/44.
PT	Identifying target genes for allele-specific drugs - used for diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic plaque, dysplastic lesions, endometriosis or graft versus host disease.
XX	
PS	Disclosure; Fig 7; 605pp; English.
CC	This invention describes a novel method for identifying an inhibitor potentially useful for treatment of cancer, where the inhibitor is active on a gene vital for cell growth or viability, and where the gene is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is used for preventing the development of cancer in a patient having a precancerous condition, by administering to the patient a first allele specific inhibitor (ASI) targeted to an allele of a first essential gene present in cells of the precancerous condition where the normal somatic cells of the patient are heterozygous for the first gene, the inhibitor is active on at least one but less than all allelic forms of the gene present in a population and targets only one allelic form present in the normal somatic cells, and the first gene. The products and methods can be used in the diagnosis, prevention and treatment of LOH disorders, e.g. cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic lesions, benign tumors, endometriosis, polycystic kidney disease, and graft versus host disease. The method can also be used to remove malignant cells from bone marrow transplants. AAZ5812-Z26825 represent human polymorphic sites described in the method of the invention
SO	Sequence 21 BP; 19 A; 1 C; 1 G; 0 T; 0 U; 0 Other;
OY	Query Match 0.2%; Score 18.4; DB 1; Length 21; Best Local Similarity 95.0%; Pred. No. 5.5e+02; Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
Db	4466 TTTTTTTTTTTTTTTTGCT 4485 21 TTTTTTTTTTTTCTTGT 2
RESULT 810	
ID	AAF24290
XX	AAF24290 standard; DNA; 21 BP.
AC	AAF24290;
DT	03-APR-2001 (first entry)
DE	Complementary nucleic acid detection method related sequence #5.
KM	Complementary nucleic acid; gene analysis; polymorphism; variation; DNA chip; primer; ss.
OS	Unidentified.
XX	
PN	EPI065278-A2.
PD	03-JAN-2001.
PF	07-JUN-2000; 2000EP-00112235.
XX	

```

PR 07-JUN-1999; 99JP-00159339.
XX
XX PA (FUGF ) FUJI PHOTO FILM CO LTD.
XX
XX P1 Makino Y, Abe Y, Ogawa M, Takagi M, Takenaka S, Yamashita K;
XX
XX DR WPI; 2001-140003/15.
XX
XX PT Determining complementarity of nucleotide fragment for gene analysis, by
XX PT comparing flow of electric current from or to electroconductive substrate
XX PT through DNA fragment, with reference obtained from its complement.
XX
XX PS Example 1; Page 12; 28pp; English.
XX
XX CC The present invention provides a method for analysing a nucleic acid
XX CC strand to determine the degree of complementarity between two sequences.
XX CC This involves the measurement of an electric current along the annealed
XX CC strands compared to a standard. This is useful in the analysis of genetic
XX CC polymorphisms and variation between genes
XX
XX SQ Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 18.4; DB 1; Length 21;
XX Best Local Similarity 95.0%; Pred. No. 5.5e+02;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 4464 TTTTTTTTTTTTTTTTTTTT 4483
XX |||||
XX 1 TTTTTTTTTTTATTTTTTTT 20
XX
XX Db
XX
XX RESULT 811
XX ABX79794
XX ID ABX79794 standard; cDNA; 21 BP.
XX
XX AC ABX79794;
XX
XX DT 17-APR-2003 (first entry)
XX
XX DE EST polymorphic DNA repeat polynucleotide #119.
XX
XX ESF expressed sequence tag; ss; polymorphic repeat; tandem repeat;
XX KW polymorphic marker prediction of ubiquitous simple sequences; POMPUS;
XX KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
XX KW Haw River syndrome; Huntington's disease; Fragile-X syndrome;
XX KW Friedrich's ataxis; myotonic dystrophy; hyperandrogenaemia;
XX KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
XX OS Homo sapiens.
XX
XX FN US6472154-B1.
XX
XX PD 29-OCT-2002.
XX
XX PF 31-DEC-1999; 99US-00475947.
XX
XX PR 31-DEC-1999; 99US-00475947.
XX
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX
XX PI Garner HR, Wren JD, Minna JD, Fondon JW;
XX
XX DR WPI; 2003-208818/20.
XX
XX PT Identifying a candidate polymorphic repeat within a coding sequence, for
XX PT understanding or treating genetic disease, comprises detecting tandem
XX PT repeats in a target coding sequence and scoring the repeats for
XX PT polymorphic probability.
XX
XX PS Example; Col 495; 588pp; English.
XX
XX CC The invention discloses a method for identifying a candidate polymorphic
XX CC repeat within a coding sequence (expressed sequence tag, EST), which

```

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 by digestion with restriction enzymes.
 XX
 XX
 PS Disclosure; Page 9; 11pp; Japanese.
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily.
 XX
 SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
 Query Match 0.2%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 5.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4465 TTTTCTTTTCTTTCTG 4484
 1 TTTTCTTTTCTTTCTG 20
 Db
 RESULT 807
 ID AAQ75711 standard; DNA; 21 BP.
 AC AAQ75711;
 XX
 XX 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 7; 11pp; Japanese.
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily.
 XX
 SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
 Query Match 0.2%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 5.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4466 TTTTCTTTTCTTTCTG 4485

Db
 1 TTTTCTTTTCTTTCTG 20
 RESULT 808
 ID AAQ75744 standard; DNA; 21 BP.
 AC AAQ75744;
 XX
 XX 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 8; 11pp; Japanese.
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily.
 XX
 SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
 Query Match 0.2%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 5.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4466 TTTTCTTTTCTTTCTG 4485
 1 TTTTCTTTTCTTTCTG 20
 Db
 RESULT 809
 ID AAZ26563/C standard; DNA; 21 BP.
 AC AAZ26563;
 XX
 XX 30-NOV-1999 (first entry)
 DE Human polymorphic region 752.
 XX
 XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
 KM cell viability; loss of heterozygosity; precancerous condition; ASI;
 KM allele specific inhibitor; somatic cell; diagnosis; prevention;
 KM atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
 KM dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
 KM graft versus host disease; malignant cell removal; bone marrow; ss.
 XX

CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 21;

Best Local Similarity 95.0%; Pred. No. 5.5e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4467 TTTTGTGTC 4486

DB 1 TTTTGTGTC 20

RESULT 804

AAQ75683

ID AAQ75683 standard; DNA; 21 BP.

XX AAQ75683;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PD 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

PS Disclosure; Page 7; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENSEQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 21;

Best Local Similarity 95.0%; Pred. No. 5.5e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4467 TTTTGTGTC 4486

DB 1 TTTTGTGTC 20

RESULT 805

AAQ75745

ID AAQ75745 standard; DNA; 21 BP.

XX AAQ75745;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PD 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

PS Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENSEQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 21;

Best Local Similarity 95.0%; Pred. No. 5.5e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4466 TTTTGTGTC 4485

DB 1 TTTTGTGTC 20

RESULT 806

AAQ75770

ID AAQ75770 standard; DNA; 21 BP.

XX AAQ75770;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PD 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 801
 ID AAQ75782 standard; DNA; 21 BP.
 AC AAQ75782;
 XX
 DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 9; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 5.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTT TTTT TTTT TTTT TTTT 4486
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 802
 ID AAQ75616 standard; DNA; 21 BP.
 AC AAQ75616;
 XX
 DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.

XX 01-NOV-1994.
 PD
 XX 16-APR-1993; 93JP-00112515.
 PF
 XX 16-APR-1993; 93JP-00112515.
 PR
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA
 XX WPI; 1995-018287/03.
 DR
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 6; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 5.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4466 TTTT TTTT TTTT TTTT TTTT 4485
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 803
 ID AAQ75638 standard; DNA; 21 BP.
 AC AAQ75638;
 XX
 DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 6; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX


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XX 04-AUG-1995 (first entry)
DT Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI, 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
PS
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
Query Match 0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4467 TTTTCTTTTCTTTCTG 4486
DB 1 TTTTCTTTTCTTTCTG 20
RESULT 739
AAQ75768
ID AAQ75768 standard; DNA; 21 BP.
AC
XX AAQ75768;
XX
XX 04-AUG-1995 (first entry)
DT Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI, 1995-018287/03.
DR
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XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
DE
XX
XX Disclosure; Page 9; 11pp; Japanese.
PS
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4465 TTTTCTTTTCTTTCTG 4484
DB 1 TTTTCTTTTCTTTCTG 20
RESULT 800
AAQ75777
ID AAQ75777 standard; DNA; 21 BP.
AC
XX AAQ75777;
XX
XX 04-AUG-1995 (first entry)
DT Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX 16-APR-1993; 93JP-00112515.
PA
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
DR
XX WPI, 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
DE
XX
XX Disclosure; Page 9; 11pp; Japanese.
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XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX
SQ Sequence 21 BP; 0 A; 1 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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PN JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESKO files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTTGTGTC 4486
XX 1 TTTTGTGTC 20

RESULT 796
AAQ75672
ID AAQ75672 standard; DNA; 21 BP.
XX
XX AAQ75672;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESKO files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTTGTGTC 4486
XX 1 TTTTGTGTC 20

RESULT 797
AAQ75617
ID AAQ75617 standard; DNA; 21 BP.
XX
XX AAQ75617;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESKO files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4466 TTTTGTGTC 4485
XX 1 TTTTGTGTC 20

RESULT 798
AAQ75635
ID AAQ75635 standard; DNA; 21 BP.
XX
XX AAQ75635;
XX

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CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4465 TTTTGTGTC 4484
XX 1 TTTTGTGTC 20

RESULT 797
AAQ75617
ID AAQ75617 standard; DNA; 21 BP.
XX
XX AAQ75617;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESKO files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4466 TTTTGTGTC 4485
XX 1 TTTTGTGTC 20

RESULT 798
AAQ75635
ID AAQ75635 standard; DNA; 21 BP.
XX
XX AAQ75635;
XX

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DR  WPI; 1995-018287/03.
XX  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
XX  Disclosure; Page 7; 11pp; Japanese.
XX
CC  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
SQ  Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
XX
Query Match      0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  4467 TTTT TTTT TTTT TTTT TTTT GTC 4486
    |||||
Db  1 TTTT TTTT TTTT TTTT TTTT ATC 20

RESULT 793
AAQ75712
ID  AAQ75712 standard; DNA; 21 BP.
XX
XX  AAQ75712;
XX
DT  04-AUG-1995 (first entry)
XX
DE  Reverse transcription primer used in cDNA analysis technique.
XX
XX  Analysis; gene expression; reverse transcription; primer; cDNA;
XX  aggregate; restriction enzyme; ss.
XX
XX  Synthetic.
XX
XX  JP06303997-A.
XX
XX  01-NOV-1994.
XX
XX  16-APR-1993; 93JP-00112515.
XX
XX  16-APR-1993; 93JP-00112515.
XX
XX  16-APR-1993; 93JP-00112515.
XX
XX  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX  WPI; 1995-018287/03.
XX
PT  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
XX  Disclosure; Page 7; 11pp; Japanese.
XX
XX
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CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
SQ  Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match      0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy  4466 TTTT TTTT TTTT TTTT TTTT TGT 4485
    |||||
Db  1 TTTT TTTT TTTT TTTT TTTT TGT 20

RESULT 794
AAQ75776
ID  AAQ75776 standard; DNA; 21 BP.
XX
XX  AAQ75776;
XX
DT  04-AUG-1995 (first entry)
XX
DE  Reverse transcription primer used in cDNA analysis technique.
XX
XX  Analysis; gene expression; reverse transcription; primer; cDNA;
XX  aggregate; restriction enzyme; ss.
XX
XX  Synthetic.
XX
XX  JP06303997-A.
XX
XX  01-NOV-1994.
XX
XX  16-APR-1993; 93JP-00112515.
XX
XX  16-APR-1993; 93JP-00112515.
XX
XX  16-APR-1993; 93JP-00112515.
XX
XX  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX  WPI; 1995-018287/03.
XX
PT  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
XX  Disclosure; Page 9; 11pp; Japanese.
XX
XX
CC  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
SQ  Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
XX
Query Match      0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  4464 TTTT TTTT TTTT TTTT TTTT TTT 4483
    |||||
Db  1 TTTT TTTT TTTT TTTT TTTT TTT 20

RESULT 795
AAQ75619
ID  AAQ75619 standard; DNA; 21 BP.
XX
XX  AAQ75619;
XX
DT  04-AUG-1995 (first entry)
XX
DE  Reverse transcription primer used in cDNA analysis technique.
XX
XX  Analysis; gene expression; reverse transcription; primer; cDNA;
XX  aggregate; restriction enzyme; ss.
XX
XX  Synthetic.
XX

```

CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX
 SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 5.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4466 TTTT TTTT TTTT TTTT TTTT GT 4485
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT GT 20

RESULT 790
 AAQ75779
 ID AAQ75779 standard; DNA; 21 BP.

XX
 AC AAQ75779;

XX
 DT 04-AUG-1995 (first entry)

XX
 DE Reverse transcription primer used in cDNA analysis technique.

XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 aggregate; restriction enzyme; ss.

XX
 OS Synthetic.

XX
 PN JP06303997-A.

XX
 PD 01-NOV-1994.

XX
 PF 16-APR-1993; 93JP-00112515.

XX
 PR 16-APR-1993; 93JP-00112515.

XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX
 DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

XX
 PS Disclosure; Page 9; 11pp; Japanese.

XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
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XX
 SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 5.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTT TTTT TTTT TTTT TTTT GT 4486
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT GT 20

RESULT 791
 AAQ75636
 ID AAQ75636 standard; DNA; 21 BP.

AC AAQ75636;
 XX
 DT 04-AUG-1995 (first entry)

XX
 DE Reverse transcription primer used in cDNA analysis technique.

XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 aggregate; restriction enzyme; ss.

XX
 OS Synthetic.

XX
 PN JP06303997-A.

XX
 PD 01-NOV-1994.

XX
 PF 16-APR-1993; 93JP-00112515.

XX
 PR 16-APR-1993; 93JP-00112515.

XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX
 DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

XX
 PS Disclosure; Page 6; 11pp; Japanese.

XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX
 SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 5.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTT TTTT TTTT TTTT TTTT GT 4486
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT GT 20

RESULT 792

AAQ75686
 ID AAQ75686 standard; DNA; 21 BP.

XX
 AC AAQ75686;

XX
 DT 04-AUG-1995 (first entry)

XX
 DE Reverse transcription primer used in cDNA analysis technique.

XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 aggregate; restriction enzyme; ss.

XX
 OS Synthetic.

XX
 PN JP06303997-A.

XX
 PD 01-NOV-1994.

XX
 PF 16-APR-1993; 93JP-00112515.

XX
 PR 16-APR-1993; 93JP-00112515.

XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX


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XX AAQ75682;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX
XX Disclosure; Page 7; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX
SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
Db 1 TTTT TTTT TTTT TTTT TTTT 20

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XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX
XX Disclosure; Page 9; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4465 TTTT TTTT TTTT TTTT TTTT 4484
Db 1 TTTT TTTT TTTT TTTT TTTT 20

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RESULT 785
AAQ75767
ID AAQ75767 standard; DNA; 21 BP.
XX
XX AAQ75767;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX
XX 16-APR-1993; 93JP-00112515.
PA
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

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RESULT 786
AAQ75713
ID AAQ75713 standard; DNA; 21 BP.
XX
XX AAQ75713;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX
XX 16-APR-1993; 93JP-00112515.
PA
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX
XX Disclosure; Page 7; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
Query Match 0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.5e+02;

```

```

OS Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENSEQ files AAQ75547-075798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c) the
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4467 TTTTTCCTTTTTCCTTC 4486
Db 1 TTTTTCCTTTTTCCTTC 20

RESULT 782
AAQ75684
ID AAQ75684 standard; DNA; 21 BP.
XX
XX AAQ75684;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENSEQ files AAQ75547-075798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c) the
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

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XX labelled reverse transcription primers (GENSEQ files AAQ75547-075798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4467 TTTTTCCTTTTTCCTTC 4486
Db 1 TTTTTCCTTTTTCCTTC 20

RESULT 783
AAQ75667
ID AAQ75667 standard; DNA; 21 BP.
XX
XX AAQ75667;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENSEQ files AAQ75547-075798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c) the
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4467 TTTTTCCTTTTTCCTTC 4486
Db 1 TTTTTCCTTTTTCCTTC 20

RESULT 784
AAQ75682
ID AAQ75682 standard; DNA; 21 BP.

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PA      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX      WPI, 1995-018287/03.
XX
PT      Analysis of cDNA and gene expression - by amplification of mRNA followed
PT      by digestion with restriction enzymes.
XX
XX      Disclosure; Page 7; 11pp; Japanese.
PS
CC      A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC      labelled reverse transcription primers (GENSEQ files AAQ75547-075798)
CC      and using the aggregate of mRNAs as the template for each reverse
CC      transcription primer; (b) digesting each of the prepared aggregates of
CC      the double-stranded cDNAs with restriction enzyme and; (c)
CC      electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC      method can be used to analyse gene expression rapidly and easily
XX
XX
SQ      Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
SQ
Query Match          0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pied. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY      4465 TTTT TTTT TTTT TTTT TTTT TTTT G 4484
Db      1 TTTT TTTT TTTT TTTT TTTT TTTT ATG 20
RESULT 779
AAQ75681
ID      AAQ75681 standard; DNA; 21 BP.
XX
XX      AAQ75681;
XX
DT      04-AUG-1995 (first entry)
DE      Reverse transcription primer used in cDNA analysis technique.
XX
XX      Analysis; gene expression; reverse transcription; primer; cDNA;
KW      aggregate; restriction enzyme; ss.
XX
XX      Synthetic.
OS
FN      JP06303997-A.
PD      01-NOV-1994.
XX
XX      16-APR-1993; 93JP-00112515.
PF      16-APR-1993; 93JP-00112515.
PR      16-APR-1993; 93JP-00112515.
PA      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX      WPI, 1995-018287/03.
XX
PT      Analysis of cDNA and gene expression - by amplification of mRNA followed
PT      by digestion with restriction enzymes.
XX
XX      Disclosure; Page 7; 11pp; Japanese.
PS
CC      A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC      labelled reverse transcription primers (GENSEQ files AAQ75547-075798)
CC      and using the aggregate of mRNAs as the template for each reverse
CC      transcription primer; (b) digesting each of the prepared aggregates of
CC      the double-stranded cDNAs with restriction enzyme and; (c)
CC      electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC      method can be used to analyse gene expression rapidly and easily
XX
XX
SQ      Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
SQ
Query Match          0.2%; Score 18.4; DB 1; Length 21;

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	Best Local Similarity	95.0%	Pred.	No. 5.5e+02;	Mismatches	1;	Indels	0;	Gaps	0;
	Matches	19;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
OY	4464	TTTTTTT	TTTTTTT	TTTTTTT	TAT	4483				
Dd	1	TTTTTTTTTTTTTTTT	TATT	20						
	RESULT 780									
ID	AAQ75778	standard; DNA; 21 BP.								
XX	AAQ75778;									
AC	AAQ75780;									
DT	04-AUG-1995	(first entry)								
DE	Reverse transcription primer used in cDNA analysis technique.									
DS	Analysis; gene expression; reverse transcription; primer; cDNA;									
KM	aggregate; restriction enzyme; ss.									
OS	Synthetic.									
PN	JP06303997-A.									
XX	01-NOV-1994:									
PD	16-APR-1993;	93JP-00112515.								
PF	16-APR-1993;	93JP-00112515.								
PR	(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.									
PA	WPI; 1995-018287/03.									
DR	Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.									
PT	Disclosure; Page 9; 11pp; Japanese.									
XK	A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENBSEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily									
CC	Sequence	21 BP;	0 A;	2 C;	0 G;	19 T;	0 U;	0 Other;		
SQ										
	Query Match	0.2%;	Score	18.4;	DB	1;	Length	21;		
	Best Local Similarity	95.0%;	Pred.	No. 5.5e+02;						
	Matches	19;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
OY	4464	TTTTTTTTTTTTTTTT	TTTTTT	4483						
Dd	1	TTTTTTTTTTTTTTTTCT	T	20						
	RESULT 781									
ID	AAQ75780	standard; DNA; 21 BP.								
XX	AAQ75780;									
AC	AAQ75780;									
DT	04-AUG-1995	(first entry)								
DE	Reverse transcription primer used in cDNA analysis technique.									
DS	Analysis; gene expression; reverse transcription; primer; cDNA;									
KM	aggregate; restriction enzyme; ss.									
OS										

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 5.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTTGTGTC 4486
 DB 1 TTTTGTGTC 20

RESULT 776

AAQ75671
 ID AAQ75671 standard; DNA; 21 BP.

AC AAQ75671;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

PS Disclosure; Page 7; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 5.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4465 TTTTGTGTC 4484
 DB 1 TTTTGTGTC 20

RESULT 777

AAQ75668

ID AAQ75668 standard; DNA; 21 BP.

AC AAQ75668;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

PS Disclosure; Page 7; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 5.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTTGTGTC 4486
 DB 1 TTTTGTGTC 20

RESULT 778

AAQ75674
 ID AAQ75674 standard; DNA; 21 BP.

AC AAQ75674;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

Query Match 0.2%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 5.2e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4465 TTTT TTTT TTTT TTTT TTTT TTTT G 4484
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT TTTT AG 20

RESULT 773

AAQ75622
 ID AAQ75622 standard; DNA; 21 BP.

XX AAQ75622;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

KM aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed

XX by digestion with restriction enzymes.

PS Disclosure; Page 6; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 18.4; DB 1; Length 21;

Best Local Similarity 95.0%; Pred. No. 5.5e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTT TTTT TTTT TTTT TTTT TTTT GTC 4486
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT TTTT GGC 20

RESULT 774

AAQ75670
 ID AAQ75670 standard; DNA; 21 BP.

XX AAQ75670;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

KM aggregate; restriction enzyme; ss.

XX Synthetic.

OS JP06303997-A.

XX 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed

XX by digestion with restriction enzymes.

PS Disclosure; Page 7; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 18.4; DB 1; Length 21;

Best Local Similarity 95.0%; Pred. No. 5.5e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTT TTTT TTTT TTTT TTTT TTTT GTC 4486
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT TTTT GCC 20

RESULT 775

AAQ75620
 ID AAQ75620 standard; DNA; 21 BP.

XX AAQ75620;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed

XX by digestion with restriction enzymes.

PS Disclosure; Page 6; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

Db 20 CTGCAGCAGCAGCAGCA 1

RESULT 771

AD52462
ID ADE52462 standard; DNA; 20 BP.

AC ADE52462;

DT 29-JAN-2004 (first entry)

DE Stem cell factor (SCF) related DNA #33.

XX Stem cell factor; SCF; haematopoietic activity; infertility;

KW intestinal damage; myeloproliferative disorder; leucopenia;

KW thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;

KW myelodysplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;

KW myeloid leukaemia; haematopoietic progenitor cell; ss.

OS Synthetic.

PN US2002031491-A1.

PD 14-MAR-2002.

PF 31-DEC-1998; 98US-00224683.

PR 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 01-OCT-1990; 90US-00589701.

PR 10-APR-1991; 91US-00684535.

PR 25-NOV-1992; 92US-00982255.

PR 21-DEC-1993; 93US-00172329.

PR 24-MAY-1995; 95US-00449653.

PR 12-JAN-1998; 98US-00005893.

XX (ZSEB/) ZSEBO K M.

PA (BOSS/) BOSSSELMAN R A.

PA (SUGS/) SUGGS S V.

PA (MART/) MARTIN F H.

PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

DR WPI; 2003-851459/79.

XX New non-natural stem cell factor, useful for treating e.g. leucopenia or

PT immune deficiency, also related nucleic acid and antibodies.

XX Disclosure; SEQ ID NO 34; 217pp; English.

PS The invention relates to stem cell factor (SCF) polypeptides with

XX haematopoietic activity and the polynucleotides encoding them. The

CC polypeptides are used for treating infertility, intestinal damage,

CC myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,

CC for improving engraftment of bone marrow transplants, for enhancing bone

CC marrow recovery after radiotherapy or chemotherapy and in treatment of

CC immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic

CC carcinoma, leukaemia and myeloid leukaemia. The SCF polypeptides are

CC also used to expand haematopoietic progenitor cells for transplantation

CC and to prepare such cells for transfection with a gene. The SCF

CC polynucleotides can be used for recombinant expression of the

CC polypeptides and also as probes for mapping of the SCF gene, for

CC identifying SCF-related diseases and as a marker for neighbouring genes.

CC Antibodies raised against the polypeptides are useful in diagnosis and to

CC remove SCF from blood. This sequence represents SCF related DNA of the

CC invention.

XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

SQ

Query Match 0.2%; Score 18.4; DB 1; Length 20;

Best Local Similarity 95.0%; Pred. No. 5.2e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy. 4465 TTTT TTTT TTTT TTTT TTTG 4484
Db 1 TTTT TTTT TTTT TTTT TTTG 20

RESULT 772

AD52461
ID ADE52461 standard; DNA; 20 BP.

AC ADE52461;

DT 29-JAN-2004 (first entry)

DE Stem cell factor (SCF) related DNA #32.

XX Stem cell factor; SCF; haematopoietic activity; infertility;

KW intestinal damage; myeloproliferative disorder; leucopenia;

KW thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;

KW neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;

KW myeloid leukaemia; haematopoietic progenitor cell; ss.

OS Synthetic.

PN US2002031491-A1.

PD 14-MAR-2002.

PF 31-DEC-1998; 98US-00224683.

PR 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 01-OCT-1990; 90US-00589701.

PR 10-APR-1991; 91US-00684535.

PR 25-NOV-1992; 92US-00982255.

PR 21-DEC-1993; 93US-00172329.

PR 24-MAY-1995; 95US-00449653.

PR 12-JAN-1998; 98US-00005893.

XX (ZSEB/) ZSEBO K M.

PA (BOSS/) BOSSSELMAN R A.

PA (SUGS/) SUGGS S V.

PA (MART/) MARTIN F H.

PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

DR WPI; 2003-851459/79.

XX New non-natural stem cell factor, useful for treating e.g. leucopenia or

PT immune deficiency, also related nucleic acid and antibodies.

XX Disclosure; SEQ ID NO 33; 217pp; English.

PS The invention relates to stem cell factor (SCF) polypeptides with

XX haematopoietic activity and the polynucleotides encoding them. The

CC polypeptides are used for treating infertility, intestinal damage,

CC myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,

CC for improving engraftment of bone marrow transplants, for enhancing bone

CC marrow recovery after radiotherapy or chemotherapy and in treatment of

CC immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic

CC carcinoma, leukaemia and myeloid leukaemia. The SCF polypeptides are

CC also used to expand haematopoietic progenitor cells for transplantation

CC and to prepare such cells for transfection with a gene. The SCF

CC polynucleotides can be used for recombinant expression of the

CC polypeptides and also as probes for mapping of the SCF gene, for

CC identifying SCF-related diseases and as a marker for neighbouring genes.

CC Antibodies raised against the polypeptides are useful in diagnosis and to

CC remove SCF from blood. This sequence represents SCF related DNA of the

CC invention.

XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

SQ

Query Match 0.2%; Score 18.4; DB 1; Length 20;

Best Local Similarity 95.0%; Pred. No. 5.2e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 20 TTTT TTTT TTTT TTTT TTTCT 1

RESULT 769
AB289240/C
ID AB289240 standard; DNA; 20 BP.
XX
XX AB289240;
AC
XX 17-OCT-2003 (first entry)
DT
XX
XX Human oligonucleotide sequence.
DE
XX Human; antisease; lung dysfunction; nasal airway dysfunction;
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antiaesthetic; hypotensive; immunosuppressive; cytoskeletal; gene therapy;
KM antisease gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KM lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX NO200285308-A2.
PN
XX 31-OCT-2002.
PD
XX 23-APR-2002; 2002MO-US013135.
PF
XX 24-APR-2001; 2001US-0286137P.
PR
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX NYce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
XX WPI; 2003-229219/22.
DR
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisease to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 4482; 872bp; English.
PS
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisease to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiaesthetic, hypotensive,
CC immunosuppressive, and cytoskeletal activity. The composition may have a
CC use in antisease gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 18 A; 1 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4465 TTTT TTTT TTTT TTTT TTTTG 4484
|||||

Db 20 TTTT TTTT TTTT TTTT TTTAG 1

RESULT 770
AB286076/C
ID AB286076 standard; DNA; 20 BP.
XX
XX AB286076;
AC
XX 17-OCT-2003 (first entry)
DT
XX
XX Human oligonucleotide sequence.
DE
XX Human; antisease; lung dysfunction; nasal airway dysfunction;
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antiaesthetic; hypotensive; immunosuppressive; cytoskeletal; gene therapy;
KM antisease gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KM lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX NO200285308-A2.
PN
XX 31-OCT-2002.
PD
XX 23-APR-2002; 2002MO-US013135.
PF
XX 24-APR-2001; 2001US-0286137P.
PR
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX NYce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
XX WPI; 2003-229219/22.
DR
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisease to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Claim 15; SEQ ID NO 1318; 872bp; English.
PS
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisease to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiaesthetic, hypotensive,
CC immunosuppressive, and cytoskeletal activity. The composition may have a
CC use in antisease gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 1 A; 6 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7413 CAGCAGCAGCAGCAGCAGCA 7432
|||||

Db 20 TTTT TTTT TTTT TTTT CTGC 1

RESULT 767
AB285532/c
ID AB285532 standard; DNA; 20 BP.
XX
XX AB285532;
AC
XX 17-OCT-2003 (first entry)
XX
XX Human oligonucleotide sequence.
DE
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KM antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KM lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX WO200285308-A2.
PN
XX 31-OCT-2002.
PD
XX 23-APR-2002; 2002WO-US013135.
PF
XX 24-APR-2001; 2001US-0286137P.
PR
XX (EPIC-) EPIGENESIS PHARM INC.
PA
XX Nyce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
DR
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX
XX Claim 15; SEQ ID NO 774; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 BP; 17 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 20 TTTT TTTT TTTT TTTT TGCT 1

RESULT 768
AB289085/c
ID AB289085 standard; DNA; 20 BP.
XX
XX AB289085;
AC
XX 17-OCT-2003 (first entry)
XX
XX Human oligonucleotide sequence.
DE
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KM antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KM lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX WO200285308-A2.
PN
XX 31-OCT-2002.
PD
XX 23-APR-2002; 2002WO-US013135.
PF
XX 24-APR-2001; 2001US-0286137P.
PR
XX (EPIC-) EPIGENESIS PHARM INC.
PA
XX Nyce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
DR
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX
XX Disclosure; SEQ ID NO 4327; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 BP; 19 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4468 TTTT TTTT TTTT TTTT TGTCT 4487
|||||

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
|||||

Db 20 CTTTCTTTTCTTTTCTTTT 1

RESULT 765
ABZ88938/c
ID ABZ88938 standard; DNA; 20 BP.
XX
AC ABZ88938;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
PI WPI; 2003-229219/22.
XX
DR
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4180; 872pp; English.
XX
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTTCTTTTCTTTTCTTTGTC 4486
|||||

Db 20 TTTTCTTTTCTTTTCTTTGAC 1

RESULT 766
ABZ88564/c
ID ABZ88564 standard; DNA; 20 BP.
XX
AC ABZ88564;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
PI WPI; 2003-229219/22.
XX
DR
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3806; 872pp; English.
XX
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 17 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTTCTTTTCTTTTCTTTGTC 4486
|||||

RESULT 763
AB231489/C
ID AB231489 standard; DNA; 20 BP.
XX
XX AB231489;
AC
XX
XX 30-JAN-2003 (first entry)
XX
XX
XX Candida albicans GRACE strain PCR primer SEQ ID NO 5708.
DE
XX
XX Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
KM signal transduction; DNA replication; cell division; growth;
KM proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
XX
XX Candida albicans.
OS
XX
XX WO200253728-A2.
XX
XX 11-JUL-2002.
XX
XX 26-DEC-2001; 2001WO-US049486.
XX
XX 29-DEC-2000; 2000US-0259128P.
XX 20-FEB-2001; 2001US-00792024.
XX 22-AUG-2001; 2001US-0314050P.
XX
XX (ELIT-1) ELITRA PHARM INC.
XX
XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL,
PI WPI; 2002-566694/60.
XX
XX Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele of
PT a gene and placing other allele of the gene under conditional expression.
XX
XX Claim 36; SEQ ID NO 5708; 167pp + Sequence listing; English.
XX
XX The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, or a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of a PCR
CC primer used in the method of the invention. Note: The sequence data for
CC this patent is not represented in the printed specification but is based
CC on sequence information supplied to Derwent by the European Patent Office
XX
XX Sequence 20 BP; 0 A; 5 C; 7 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7409 ACATCAGCAGCAGCAGCAGC 7428
|||||

DB 20 ACAACAGCAGCAGCAGCAGC 1
RESULT 764
AB285534/C
ID AB285534 standard; DNA; 20 BP.
XX
XX AB285534;
AC
XX
XX 17-OCT-2003 (first entry)
XX
XX
XX Human oligonucleotide sequence.
DE
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antiinflammatory; hypotensive; immunosuppressive; cytostatic; gene therapy;
KM antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KM lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIC-1) EPICGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Claim 15; SEQ ID NO 776; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4463 CTTTCTTTCTTTCTTTCTTTT 4482
|||||

```

OY      4465  TTTT|TTTTTTTTTTTGG  4484
Db      1  TTTT|TTTTTTTTTTTGG  20

RESULT 761
ID      ABS73850  standard; DNA; 20 BP.
AC      ABS73850;
DT      05-DEC-2002  (first entry)
DE      SCF universal oligonucleotide 220-11.
XX
XX      Stem cell factor; SCF; blood-forming system; blood cell disorder;
KM      haematopoietic system; metastatic carcinoma; acute leukaemia;
KM      multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
KM      refractory erythroblastic anaemia; milary tuberculosis; cytostatic;
KM      disseminated fungus disease; haematopoietic; tuberculosis;
KM      antianemic; antifungal; antimarial; dermatological; se.
XX
XX      Synthetic.
OS
XX      EP1241258-A2.
XX
XX      18-SEP-2002.
PD
XX      04-OCT-1990; 2002EP-00008587.
XX
XX      16-OCT-1989; 89US-00422383.
XX      PR 11-JUN-1990; 90US-00537198.
XX      PR 24-AUG-1990; 90US-00573616.
XX      PR 28-SEP-1990; 90MO-US005548.
XX      PR 01-OCT-1990; 90US-00589701.
XX      PR 04-OCT-1990; 90EP-00310899.
XX      PR 04-OCT-1990; 95EP-00105391.
XX
XX      (AMGE-) AMGEN INC.
XX
XX      Zeebo KM, Suggs SV, Bosseلمان RA, Martin FH;
PI      WPI; 2002-684093/74.
XX
XX      Production of a human stem cell factor (SCF) polypeptide for treating
PT      disorders involving blood cells, such as leukemia, comprises culturing
PT      mammalian cells comprising non-human SCF promoter DNA linked to DNA
PT      encoding the human SCF.
XX
XX      Example 3; Fig 12C; 120pp; English.
XX
XX      The present invention relates to novel stem cell factors (SCFs),
XX      polynucleotide sequences encoding the SCFs, and methods of producing
XX      them. SCFs are involved in the blood-forming (haematopoietic) system in
XX      mammals, particularly humans. The method of the invention is useful for
XX      the production of human SCF. The stem cell factors are useful to treat
XX      disorders involving blood cells e.g. metastatic carcinoma, acute
XX      leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory
XX      erythroblastic anaemia, milary tuberculosis, disseminated fungus
XX      disease, malaria, and vitiligo. The present sequence representing a
XX      universal oligonucleotide for SCF DNA is used in the examples of the
XX      present invention
XX
XX      Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
SQ
Query Match      0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      4465  TTTT|TTTTTTTTTTTGG  4484
Db      1  TTTT|TTTTTTTTTTTGG  20

```

[illegible]

```

RESULT 762
ABZ30516/c
ID ABZ30516 standard; DNA; 20 BP.
XX
AC ABZ30516;
XX
DT 30-JAN-2003 (first entry)
XX
DE Candida albicans GRACE strain PCR primer SEQ ID NO 4667.
XX
KW Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
XX signal transduction; DNA replication; cell division; growth;
XX proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
OS Candida albicans.
XX
PN WO200253728-A2.
XX
PD 11-JUL-2002.
XX
PF 26-DEC-2001; 2001WO-US049486.
XX
PR 29-DEC-2000; 2000US-0259128P.
XX PR 20-FEB-2001; 2001US-00792024.
XX PR 22-AUG-2001; 2001US-0314050P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX WPI; 2002-566694/60.
XX
PT Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele of
PT a gene and placing other allele of the gene under conditional expression.
XX
PS Claim 36; SEQ ID NO 4667; 167bp + Sequence Listing; English.
XX
CC The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of a PCR
CC primer used in the method of the invention. Note: The sequence data for
CC this patent is not represented in the printed specification but is based
CC on sequence information supplied to Derwent by the European Patent Office
XX
Sequence 20 BP; 0 A; 4 C; 7 G; 9 T; 0 U; 0 Other;
Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
GY 7407 CAACATCAGCAGCGACGACA 7446
db 20 CAACACGACGCGACGACGA 1

```


AC AAD35466;
 XX
 XX 25-JUL-2002 (first entry)
 XX
 XX
 DE Rat SCF 5' cDNA amplifying PCR primer, 220-11.
 XX
 XX Rat; stem cell factor; SCF protein; leucopenia; thrombocytopenia;
 XX anemia; myelosuppression; nerve damage; myeloproliferative disorder;
 XX myelofibrosis; myeloid leukemia; myeloid leukemia; osteoporosis;
 XX metastatic carcinoma; acute leukemia; multiple myeloma; sarcomas;
 XX Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
 XX Letterer-Siwe disease; refractory erythroblastic anemia; Kala azar;
 XX Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;
 XX disseminated fungus disease; fulminating septicemia; pibaldism; AIDS;
 XX acquired immune deficiency syndrome; malaria; military tuberculosis;
 XX pyridoxine deficiency; vitamin B12 deficiency; folate deficiency;
 XX Diamond Blackfan anemia; hypopigmentation disorder; vitiligo; PCR;
 XX primer; ss.
 XX
 OS Rattus sp.
 XX
 XX US2002018763-A1.
 XX
 XX 14-FEB-2002.
 XX
 XX 12-JAN-1998; 98US-00005243.
 XX
 XX 24-MAY-1995; 95US-0049653.
 XX
 XX (ZSEB/ ZSEBO K. M.
 XX (BOSS/ BOSSLMAN R. A.
 XX (SUGG/ SUGGS S. V.
 XX (MART/ MARTIN F. H.
 XX
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX
 XX WPI, 2002-350789/38.
 XX
 XX Novel non-naturally-occurring stem cell factor polypeptide, useful for
 XX treating leucopenia, thrombocytopenia, anemia and for enhancing
 XX engraftment of bone marrow during transplantation in a mammal.
 XX
 PS Example 3; Fig 12C; 217pp; English.
 XX
 XX The present invention relates to novel non-naturally-occurring stem cell
 XX factor (SCF) polypeptides having an amino acid sequence sufficiently
 XX duplicative of that of naturally-occurring SCF to allow possession of
 XX haematopoietic biological activity of naturally occurring SCF. Sequences
 XX of the invention are useful for treating leucopenia, thrombocytopenia,
 XX anaemia and for enhancing bone marrow recovery in treatment of radiation,
 XX or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
 XX are also useful for treating acquired immune deficiency in a human, nerve
 XX damage, neoplasia, infertility, myeloproliferative disorder, intestinal
 XX damage in a mammal. SCF sequences are useful for preparing biologically
 XX active polymer polypeptide adduct, for enhancing transfection of early
 XX haematopoietic progenitor cells with a gene, and transfer of a gene into
 XX a mammal. They are useful for treating myelofibrosis, myelocytosis,
 XX osteoporosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
 XX Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
 XX Letterer-Siwe disease, refractory erythroblastic anemia, Di Guglielmo
 XX syndrome, congestive splenomegaly, Kala azar, sarcomas, primary
 XX splenic pancytopenia, disseminated fungus disease, malaria, military
 XX tuberculosis, fulminating septicemia, pyridoxine deficiency, vitamin B12
 XX and folate acid deficiency, Diamond Blackfan anemia, hypopigmentation
 XX disorders such as pibaldism, AIDS (acquired immune deficiency syndrome)
 XX and vitiligo. The present sequence is a PCR primer which is used for
 XX amplifying the 5' end of rat SCF cDNA. This sequence is used in the
 XX exemplification of the invention
 XX
 XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

```

Query Match          0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      4465 TTTT TTTT TTTT TTTT TTTT TTTT G 4484
      ||||| ||||| ||||| ||||| ||||| |||||
Db      1 TTTT TTTT TTTT TTTT TTTT TTTT CG 20

RESULT 760
ID      ABS73849
XX      ABS73849 standard; DNA; 20 BP.
AC      ABS73849;
XX      ABS73849;
DT      05-DEC-2002 (first entry)
XX      SCF universal oligonucleotide 220-7.
DE

KM      Stem cell factor; SCF; blood-forming system; blood cell disorder;
KM      haematopoietic system; metastatic carcinoma; acute leukemia;
KM      multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
KM      refractory erythroblastic anaemia; milary tuberculosis; cytostatic;
KM      disseminated fungus disease; haematopoietic; tuberculous;
KM      antinaemic; antifungal; antimalarial; dermatological; ss.
XX      Synthetic.
OS      EP1241258-A2.
XX      EP1241258-A2.
XX      18-SEP-2002.
PD      04-OCT-1990; 2002EP-00008587.
XX      04-OCT-1990; 89US-00422383.
PF      11-JUN-1990; 90US-00537198.
XX      24-AUG-1990; 90US-00573616.
PR      28-SEP-1990; 90MO-US0005548.
XX      01-OCT-1990; 90US-00589701.
PR      04-OCT-1990; 90EP-00310899.
XX      04-OCT-1990; 95EP-00105391.
PR      04-OCT-1990; 95EP-00105391.
XX      (AMGE-) AMGEN INC.
PA      Zsebo KM, Suggs SV, Bossejman RA, Martin FH;
XX      WPI; 2002-684093/74.
XX      WPI; 2002-684093/74.
DR      Production of a human stem cell factor (SCF) polypeptide for treating
PT      disorders involving blood cells, such as leukemia, comprises culturing
PT      mammalian cells comprising non-human SCF promoter DNA linked to DNA
PT      encoding the human SCF.
XX      Example 3; Fig 12C; 120pp; English.
XX      The present invention relates to novel stem cell factors (SCFs),
XX      polynucleotide sequences encoding the SCFs, and methods of producing
XX      them. SCFs are involved in the blood-forming (haematopoietic) system in
XX      mammals, particularly humans. The method of the invention is useful for
XX      the production of human SCF. The stem cell factors are useful to treat
XX      disorders involving blood cells e.g. metastatic carcinoma, acute
XX      leukemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory
XX      erythroblastic anaemia, milary tuberculosis, disseminated fungus
XX      disease, malaria, and vitiligo. The present sequence representing a
XX      universal oligonucleotide for SCF DNA is used in the examples of the
XX      present invention
XX      Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
SQ
Query Match          0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

KW		hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
XX		
OS	Homo sapiens.	
XX		
FN	US6248319-B1.	
XX		
PD	19-JUN-2001.	
XX		
XX	24-MAY-1995;	95US-00449653.
XX		
PR	16-OCT-1989;	89US-00422383.
PR	11-JUN-1990;	90US-00537198.
PR	24-AUG-1990;	90US-00573616.
PR	01-OCT-1990;	90US-00589701.
PR	10-APR-1991;	91US-00684535.
PR	25-NOV-1992;	92US-00982255.
PR	21-DEC-1993;	93US-00172329.
XX		
PA	(ZSERB/) ZSEBO K M.	
PA	(BOSS/) BOSSSELMAN R A.	
PA	(SUGG/) SUGGS S V.	
PA	(MART/) MARTIN F H.	
P1	Zsebo KM, Bosselman RA, Sugge SV, Martin FH;	
XX		
DR	WPI, 2001-407312/43.	
XX		
PT	Increasing the number of early hematopoietic progenitor cells in the	
PT	peripheral blood useful for the treatment of blood disorders including	
PT	Hodgkin's disease comprises the administration of human stem cell factor.	
XX		
PS	Example 3; Fig 12C; 210pp; English.	
XX		
CC	The present sequence for universal PCR primer 220-7 is 1 of 19 PCR	
CC	primers (AAS10435-AAS10453) used to amplify various portions of the human	
CC	SCF cDNA sequence. The sequence is described in an invention relating to	
CC	novel stem cell factors, the polynucleotides encoding them and methods	
CC	for producing the stem cell factors. The methods involve increasing the	
CC	number of early haematopoietic progenitor cells in human peripheral blood	
CC	by administering a haematopoietically effective human stem cell factor	
CC	polypeptide. The methods are useful for the treatment of blood disorders,	
CC	including myelofibrosis, myelocytosis, osteopetrosis, metastatic	
CC	carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,	
CC	lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,	
CC	malaria, vitamin B12 and folic acid deficiency, hypopigmentation	
CC	disorders i.e. plebaldism and viral induced disorders, including AIDS	
XX		
SQ	Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;	
	Query Match	0.2%; Score 18.4; DB 1; Length 20;
	Best Local Similarity	95.0%; Pred. No. 5.2e+02;
	Matches 19; Conservative	0; Mismatches 1; Indels 0; Gaps 0
OY	4465 TTTTTCCTTTTTTTTTTTTG 4484	
DB	1 TTTTTCCTTTTTTTTTTAG 20	
	RESULT 758	
ID	AAD35465 standard; DNA; 20 BP.	
AC	AAD35465;	
XX		
DT	25-JUL-2002 (first entry)	
XX		
RAT	Rat SCF 5' cDNA amplifying PCR primer, 220-7.	
XX		
KW	Rat; stem cell factor; SCF protein; leucopenia; thrombocytopoenia;	
KW	anaemia; myelosuppression; nerve damage; myeloproliferative disorder;	
KW	infertility; neoplasia; myelofibrosis; myelocytosis; osteopetrosis;	
KW	metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;	
KW	Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;	

XX Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
KM Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;
KM disseminated fungus disease; Fulminating septicæmia; plebaldism, AIDS,
KM acquired immune deficiency syndrome; malaria; military tuberculosis;
KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
KM Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
KW primer, ss.

OS Rattus sp.
PN US3002018763-A1.
PP 14-FEB-2002.
PD
PE 12-JAN-1998; 98US-00005243.
PF
PR 24-MAY-1995; 95US-00449653.
PS

(ZSEB/) ZSEHO K M.
PA (BOSS/) BOSSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.

P1 Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
P2 WPI; 2002-350789/38.
PT Novel non-naturally-occurring stem cell factor polypeptide, useful for
PT treating leucopenia, thrombocytopenia, anemia and for enhancing
PT engraftment of bone marrow during transplantation in a mammal.

Example 3; Fig 12C, 217bp; English.

XX The present invention relates to novel non-naturally-occurring stem cell
XX factor (SCF) polypeptides having an amino acid sequence sufficiently
CC duplicative of that of naturally-occurring SCF to allow possession of
CC haematopoietic biological activity of naturally occurring SCF. Sequences
CC of the invention are useful for treating leucopaenia, thrombocytopenia,
CC anaemia and for enhancing bone marrow recovery in treatment of radiation,
CC engraftment of bone marrow during transplantation in mammals and chemical
CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
CC are also useful for treating acquired immune deficiency in a human, nerve
CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal
CC damage in a mammal. SCF sequences are useful for preparing biologically
CC active polymer polypeptide adduct, for enhancing transfection of early
CC haematopoietic progenitor cells with a gene, and transfer of a gene into
CC a mammal. They are useful for treating myelofibrosis, myelosclerosis,
CC osteoporosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
CC splenic pancytopenia, disseminated fungus disease, malaria, military
CC tuberculosis, Fulminating septicæmia, pyridoxine deficiency, vitamin B12
CC and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
CC disorders such as plebaldism, AIDS (acquired immune deficiency syndrome)
CC and vitiligo. The present sequence is a PCR primer which is used for
CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the
CC exemplification of the invention

XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4465 TTTT TTTTTTTTTTTTTTTTG 4464
DB 1 TTTT TTTTTTTTTTTTTTTTAG 20

RESULT 759
AAD35466
ID AAD35466 standard; DNA; 20 BP.

AC	AAS04214;
XX	
DT	29-AUG-2001 (first entry)
XX	
DE	Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
XX	
KM	Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW	blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KV	anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
XX	PCR primer; ss.
OS	Homo sapiens..
XX	
FN	US6218148-BL.
XX	
PD	17-APR-2001.
XX	
PE	21-DEC-1993; 93US-00172329.
XX	
PR	16-OCT-1989; 89US-00422383.
PR	11-JUN-1990; 90US-00537198.
PR	24-AUG-1990; 90US-00573616.
PR	01-OCT-1990; 90US-00589701.
PR	25-NOV-1992; 92US-00982255.
XX	
PA	(AMGE-) AMGEN INC.
XX	
P1	Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
XX	
DR	WPI; 2001-281051/29.
XX	
PT	Isolated DNA sequence, encoding polypeptide product useful for
XX	stimulating growth of early hematopoietic progenitor cells.
PS	Example 3; Fig 12C; 167pp; English.
CC	The present sequence for universal PCR primer 220-11 is 1 of 8 universal
CC	oligonucleotides (AAS04211-AAS04218) used in the isolation of the human
CC	SCF (stem cell factor) cDNA sequence. The present invention relates to
CC	a novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)
CC	and the polynucleotides encoding them. SCF stimulate primitive progenitor
CC	cells including early haematopoietic progenitor cells. The invention also
CC	describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
CC	(AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.
CC	The polynucleotide encoding SCF is useful for producing SCF and useful in
CC	gene therapy. It is useful for treating disorders involving blood cells
CC	such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC	myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC	congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC	diseminated fungus disease, fulminating septicemia, malaria, vitamin B12
CC	and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
CC	disorders such as prebaldism and vitiligo
XX	
SQ	Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
OY	Query Match 0.2%; Score 18.4; DB 1; Length 20;
	Best Local Similarity 95.0%; Pred. No. 5.2e+02;
	Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0
DB	1 TTTT TTTT TTTT TTTT TTG 4484 TTTTTTTTTTTTTTTTTCG 20
RESULT 756	
AAS10449	
ID	AAS10449 standard; DNA; 20 BP.
XX	
AC	AAS10449;
XX	
DT	24-OCT-2001 (first entry)
XX	
DE	Human stem cell factor (SCF) cDNA universal PCR primer 220-11.

[illegible]

Db 1 |||||
1 TTTTTCG 20

RESULT 753

AAH23890
ID AAH23890 standard; DNA; 20 BP.

XX AAH23890;

XX 07-AUG-2001 (first entry)

XX Human SCF (stem cell factor) cDNA universal PCR primer 220-7.

XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;

XX blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;

XX anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;

XX PCR primer; ss.

XX Homo sapiens.

XX US6204363-B1.

XX 20-MAR-2001.

XX 25-NOV-1992; 92US-00982255.

XX 16-OCT-1989; 89US-00422383.

XX 11-JUN-1990; 90US-00537198.

XX 24-AUG-1990; 90US-00573616.

XX 01-OCT-1990; 90US-00589701.

XX 10-APR-1991; 91US-00684535.

XX (AMGE-) AMGEN INC.

XX Zeebo KM, Bosselman RA, Suggs SV, Martin FH;

XX WPI; 2001-256683/26.

XX New stem cell factor polypeptides and their analogs which stimulate

XX growth of early hematopoietic progenitors, useful for treating aplastic

XX PT anemia, carcinoma, multiple myeloma, vitiligo, Kala azar, Hodgkin's

XX disease.

XX Example 3; Fig 12C; 166pp; English.

XX The present sequence for universal PCR primer 220-7 is 1 of 8 universal

XX oligonucleotides (AAH23888-AAH23895) used in the isolation of the human

XX SCF (stem cell factor) cDNA sequence. The present invention relates to

XX novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the

XX polynucleotides encoding them. SCF stimulate primitive progenitor cells

XX including early haematopoietic progenitor cells. The invention also

XX describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides

XX (AAH23889-AAH23897) used in the isolation of human and rat SCF sequences.

XX The polynucleotide encoding SCF is useful for producing SCF and useful in

XX gene therapy. It is useful for treating disorders involving blood cells

XX such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple

XX myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,

XX congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,

XX disseminated fungus disease, fulminating septicemia, malaria, vitamin

XX B12 and folic acid deficiency, pyridoxine deficiency, and

XX hypopigmentation disorders such as piebaldism and vitiligo

XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 18.4; DB 1; Length 20;

XX Best Local Similarity 95.0%; Pred. No. 5.2e+02;

XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX 4465 TTTTTCG 4484

XX 1 TTTTTCG 20

RESULT 754

AAH23890
ID AAH23890 standard; DNA; 20 BP.

XX AAH23890;

XX 29-AUG-2001 (first entry)

XX Human SCF (stem cell factor) cDNA universal PCR primer 220-7.

XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;

XX blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;

XX anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;

XX PCR primer; ss.

XX Homo sapiens.

XX US6218148-B1.

XX 17-APR-2001.

XX 21-DEC-1993; 93US-00172329.

XX 16-OCT-1989; 89US-00422383.

XX 11-JUN-1990; 90US-00537198.

XX 24-AUG-1990; 90US-00573616.

XX 01-OCT-1990; 90US-00589701.

XX 25-NOV-1992; 92US-00982255.

XX (AMGE-) AMGEN INC.

XX Zeebo KM, Bosselman RA, Suggs SV, Martin FH;

XX WPI; 2001-281051/29.

XX Isolated DNA sequence, encoding polypeptide product useful for

XX stimulating growth of early hematopoietic progenitor cells.

XX Example 3; Fig 12C; 167pp; English.

XX The present sequence for universal PCR primer 220-7 is 1 of 8 universal

XX oligonucleotides (AAS04211-AAS04218) used in the isolation of the human

XX SCF (stem cell factor) cDNA sequence. The present invention relates to

XX novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)

XX and the polynucleotides encoding them. SCF stimulate primitive progenitor

XX cells including early haematopoietic progenitor cells. The invention also

XX describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides

XX (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.

XX The polynucleotide encoding SCF is useful for producing SCF and useful in

XX gene therapy. It is useful for treating disorders involving blood cells

XX such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple

XX myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,

XX congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,

XX disseminated fungus disease, fulminating septicemia, malaria, vitamin

XX B12 and folic acid deficiency, pyridoxine deficiency, and hypopigmentation

XX disorders such as piebaldism and vitiligo

XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 18.4; DB 1; Length 20;

XX Best Local Similarity 95.0%; Pred. No. 5.2e+02;

XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX 4465 TTTTTCG 4484

XX 1 TTTTTCG 20

XX RESULT 755

XX AAS04214

XX ID AAS04214 standard; DNA; 20 BP.

CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
 CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
 CC and intestinal damage, infertility, AIDS and severe combined
 CC immunodeficiency (SCID). The present sequence is primer used to amplify
 CC an SCF in the exemplification of the invention

XX
 SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 5.2e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4465 TTTT TTTT TTTT TTTT TTTT G 4484
 DB 1 TTTT TTTT TTTT TTTT TAG 20

RESULT 751

AAH23891
 ID AAH23891 standard; DNA; 20 BP.

XX
 AC AAH23891;

XX
 DT 13-JUL-2001 (first entry)

DE Mammalian stem cell factor PCR primer SEQ ID NO: 34.

XX Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
 KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
 KW neurological damage; intestinal damage; infertility; AIDS; SCID;
 KW severe combined immunodeficiency; PCR primer; ss.

XX Mammalia.

XX US6207802-B1.

XX 27-MAR-2001.

XX 09-NOV-1994; 94US-00336728.

XX 16-OCT-1989; 89US-00422383.

XX 11-JUN-1990; 90US-00537198.

XX 24-AUG-1990; 90US-00573616.

XX 01-OCT-1990; 90US-00589701.

XX 25-NOV-1992; 92US-00982255.

XX (AMGE-) AMGEN INC.

XX Zsebo KM, Bosselman RA, Sugge SV, Martin FH;

XX WPI; 2001-353108/37.

XX Novel isolated non-human mammalian stem cell factor polypeptide
 PT stimulating growth of early hematopoietic progenitor cells, useful for
 PT treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
 PT sarcoidosis.

XX Example 3; Fig 12C; 209pp; English.

XX The present invention provides the protein and coding sequences of
 CC mammalian stem cell factors (SCFs). These are capable of stimulating the
 CC growth of early haematopoietic progenitor cells, neural stem cells and
 CC primordial germ stem cells. The sequences are useful in the treatment of
 CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
 CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
 CC and intestinal damage, infertility, AIDS and severe combined
 CC immunodeficiency (SCID). The present sequence is primer used to amplify
 CC an SCF in the exemplification of the invention

XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 5.2e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4465 TTTT TTTT TTTT TTTT TTTT G 4484
 DB 1 TTTT TTTT TTTT TTTT TCG 20

RESULT 752

AAH23891
 ID AAH23891 standard; DNA; 20 BP.

XX
 AC AAH23891;

XX 07-AUG-2001 (first entry)

DE Human SCF (stem cell factor) cDNA universal PCR primer 220-11.

XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
 KW PCR primer; ss.

XX Homo sapiens.

XX US6204363-B1.

XX 20-MAR-2001.

XX 25-NOV-1992; 92US-00982255.

XX 16-OCT-1989; 89US-00422383.

XX 11-JUN-1990; 90US-00537198.

XX 24-AUG-1990; 90US-00573616.

XX 01-OCT-1990; 90US-00589701.

XX 10-APR-1991; 91US-00684535.

XX (AMGE-) AMGEN INC.

XX Zsebo KM, Bosselman RA, Sugge SV, Martin FH;

XX WPI; 2001-256683/26.

XX Example 3; Fig 12C; 166pp; English.

XX The present sequence for universal PCR primer 220-11 is 1 of 8 universal
 CC oligonucleotides (AAH23888-AAH23895) used in the isolation of the human
 CC SCF (stem cell factor) cDNA sequence. The present invention relates to
 CC novel stem cell factors (AAH73561-AAH73568, AAH73571-AAH73576) and the
 CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
 CC including early haematopoietic progenitor cells. The invention also
 CC describes SCF peptides (AAH73578-AAH73597) and the oligonucleotides
 CC (AAH23859-AAH23887) used in the isolation of human and rat SCF sequences.
 CC The polynucleotide encoding SCF is useful for producing SCF and useful in
 CC gene therapy. It is useful for treating disorders involving blood cells
 CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
 CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
 CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
 CC disseminated fungus disease, fulminating septicemia, malaria, vitamin
 CC B12 and folic acid deficiency, pyridoxine deficiency, and
 CC hypopigmentation disorders such as piebaldism and vitiligo

XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 5.2e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4465 TTTT TTTT TTTT TTTT TTTT G 4484

CC The present sequence for universal PCR primer 220-7 is 1 of 8 universal
 CC oligonucleotides (AAS04110-AAS04117) used in the isolation of the human
 CC SCF (stem cell factor) cDNA sequence. The present invention relates to
 CC SCF (stem cell factor) cDNA sequence. The present invention relates to
 CC novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the
 CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
 CC including early haematopoietic progenitor cells. The invention also
 CC describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
 CC (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.
 CC The polynucleotide encoding SCF is useful for producing SCF and useful in
 CC gene therapy. It is useful for treating disorders involving blood cells
 CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
 CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
 CC congenitive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
 CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
 CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
 CC disorders such as plebaldism and vitiligo

XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
 SQ

Query Match 0.2%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 5.2e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4465 TTTT TTTT TTTT TTTT TTTT TTTT G 4484
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT TTTT G 20

RESULT 749
 AAS04113
 ID AAS04113 standard; DNA; 20 BP.
 XX
 AC AAS04113;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
 XX
 KM Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KM blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KM anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
 KM PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6207417-B1.
 XX
 PD 27-MAR-2001.
 XX
 PF 07-JUN-1995; 95US-00482918.
 XX
 PR 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 01-OCT-1990; 90US-00589701.
 PR 21-DEC-1993; 93US-00172329.
 XX
 PA (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX
 PI Zeebo KM, Bosseelman RA, Suggs SV, Martin FH;
 XX
 DR WPI; 2001-298941/31.
 XX
 PT Novel nucleic acids encoding stem cell factor useful for treating
 PT disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's
 PT disease, Kala azar, anemia and septicemia.
 XX
 PS Example 3; Fig 12C; 209pp; English.
 CC The present sequence, for universal PCR primer 220-11 is 1 of 8 universal

CC oligonucleotides (AAS04110-AAS04117) used in the isolation of the human
 CC SCF (stem cell factor) cDNA sequence. The present invention relates to
 CC SCF (stem cell factor) cDNA sequence. The present invention relates to
 CC novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the
 CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
 CC including early haematopoietic progenitor cells. The invention also
 CC describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
 CC (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.
 CC The polynucleotide encoding SCF is useful for producing SCF and useful in
 CC gene therapy. It is useful for treating disorders involving blood cells
 CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
 CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
 CC congenitive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
 CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
 CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
 CC disorders such as plebaldism and vitiligo

XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
 SQ

Query Match 0.2%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 5.2e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4465 TTTT TTTT TTTT TTTT TTTT TTTT G 4484
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT TTTT G 20

RESULT 750
 AAF89092
 ID AAF89092 standard; DNA; 20 BP.
 XX
 AC AAF89092;
 XX
 DT 13-JUL-2001 (first entry)
 XX
 DE Mammalian stem cell factor PCR primer SEQ ID NO: 33.
 XX
 KM Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
 KM gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
 KM neurological damage; intestinal damage; infertility; AIDS; SCID;
 KM severe combined immunodeficiency; PCR primer; ss.
 XX
 OS Mammalia.
 XX
 PN US6207802-B1.
 XX
 PD 27-MAR-2001.
 XX
 PF 09-NOV-1994; 94US-0036728.
 XX
 PR 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 01-OCT-1990; 90US-00589701.
 PR 25-NOV-1992; 92US-00982255.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Zeebo KM, Bosseelman RA, Suggs SV, Martin FH;
 XX
 DR WPI; 2001-353108/37.
 XX
 PT Novel isolated non-human mammalian stem cell factor polypeptide
 PT stimulating growth of early hematopoietic progenitor cells, useful for
 PT treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
 PT sarcoidosis.
 XX
 PS Example 3; Fig 12C; 209pp; English.
 CC The present invention provides the protein and coding sequences of
 CC mammalian stem cell factors (SCFs). These are capable of stimulating the
 CC growth of early haematopoietic progenitor cells, neural stem cells and
 CC primordial germ stem cells. The sequences are useful in the treatment of

PA	(AMGE-) AMGEN INC.
XX	
P1	Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX	
DR	WPI; 2001-366062/38.
XX	
PT	Enhancing efficiency of transfer of polynucleotide into a target
PT	mammalian cell in vitro, involves exposing cell that expresses a stem
PT	cell factor receptor to stem cell factor, and introducing polynucleotide
XX	into cell in vitro.
XX	
PS	Example 3; Fig 12C; 210pp; English.
XX	
CC	The present invention describes a method for enhancing (E) the efficiency
CC	of transfer of a polynucleotide (I) into a target mammalian cell (II) in
CC	vitro, comprising exposing (II) that expresses a stem cell factor (SCF)
CC	receptor to a biologically active SCF, its analogue or fragment, which
CC	induces cell proliferation, and introducing (I) to (II) in vitro.
CC	Exposure of SCF to (II) results in increased uptake of (I) into the cell.
CC	The method is useful for enhancing the efficiency of the transfer of a
CC	polynucleotide into a target mammalian cell in vitro. The method is
CC	useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to
CC	AAB98350 represent sequences used in the exemplification of the present
XX	invention
SQ	Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
Query Match	0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity	95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	4465 TTTTTTTTTTTTTTTTG 4484 1 TTTTTTTTTTTTTTTTAG 20
Db	
RESULT 747	
ID	AAH41333 standard; DNA; 20 BP.
XX	
AC	AAH41333;
XX	
D7	21-AUG-2001 (first entry)
XX	
DE	Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:34.
XX	
KM	Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
KM	gene therapy; PCR primer; mutagenesis; probe; ss.
XX	
OS	Synthetic.
XX	
PN	US6207454-B1.
PD	
DD	27-MAR-2001.
XX	
PF	31-DEC-1998; 98US-00224681.
XX	
PR	16-OCT-1989; 89US-00422383.
PR	11-JUN-1990; 90US-00537198.
PR	24-AUG-1990; 90US-00573616.
PR	01-OCT-1990; 90US-00589701.
PR	25-NOV-1992; 92US-00982255.
PR	21-DEC-1993; 93US-00172329.
PR	24-MAY-1995; 95US-00449653.
PR	12-JAN-1998; 98US-00005893.
PA	(AMGE-) AMGEN INC.
XX	
P1	Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX	
DR	WPI; 2001-366062/38.
XX	

PT	mammalian cell in vitro, involves exposing cell that expresses a stem
PT	cell factor receptor to stem cell factor, and introducing polynucleotide
PT	into cell in vitro.
XX	
PS	Example 3; Fig 12C; 210pp; English.
XX	
CC	The present invention describes a method for enhancing (E) the efficiency
CC	of transfer of a polynucleotide (I) into a target mammalian cell (II) in
CC	vitro, comprising exposing (II) that expresses a stem cell factor (SCF)
CC	receptor to a biologically active SCF, its analogue or fragment, which
CC	induces cell proliferation, and introducing (I) to (II) in vitro.
CC	Exposure of SCF to (II) results in increased uptake of (I) into the cell.
CC	The method is useful for enhancing the efficiency of the transfer of a
CC	polynucleotide into a target mammalian cell in vitro. The method is
CC	useful in gene therapy techniques. AAH41301 to AAH41364 and AA98351 to
CC	AA98390 represent sequences used in the exemplification of the present
CC	invention
XX	
SQ	Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX	
Query Match	0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity	95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Oy	4465 TTTT TTTTTTTTTTTTTTG 4484 1 TTTT TTTTTTTTTTTTTCG 20
Dd	
RESULT 748	
AA504112	
ID	AA504112 standard; DNA; 20 BP.
XX	
AC	AA504112;
XX	
DT	29-AUG-2001 (first entry)
XX	
DE	Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
XX	
KW	Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW	blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW	anemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW	PCR primer; ss.
XX	
OS	Homo sapiens.
XX	
PV	US6207417-B1.
XX	
PD	27-MAR-2001.
XX	
PF	07-JUN-1995; 95US-00482918.
XX	
PR	16-OCT-1989; 89US-00422383.
PR	11-JUN-1980; 90US-00537198.
PR	24-AUG-1990; 90US-00573616.
PR	01-OCT-1990; 90US-00589701.
PR	21-DEC-1993; 93US-00172329.
XX	
PA	(ZSEB/) ZSEBO K M.
PA	(BOSS/) BOSSELMAN R A.
PA	(SUGS/) SUGGS S V.
PA	(MART/) MARTIN F H.
XX	
PI	Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
DR	WPI; 2001-298941/31.
XX	
PT	Novel nucleic acids encoding stem cell factor useful for treating
PT	disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's
XX	disease, Kala azar, anemia and septicemia.
XX	
PS	Example 3; Fig 12C; 209pp; English.
XX	

CC cells which are capable of maturing to erythroid, megakaryocyte,
CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
CC SCF is useful for treating haematopoietic disorders. The method is useful
CC for expanding early haematopoietic progenitors in syngeneic, allogeneic
CC or autologous bone marrow transplant. SCF is useful for enhancing the
CC efficiency of gene therapy based on transfecting haematopoietic stem
CC cells. SCF is also useful for combating the myelosuppressive effects of
CC anti-HIV drugs such as AZT and for enhancing haematopoietic recovery
CC after acute blood loss and as a boost to the immune system for fighting
CC neoplasia (cancer). The present sequence represents a universal
CC oligonucleotide which is used in an example from the present invention
XX

SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4465 TTTT TTTT TTTT TTTT TTTT TTTT G 4484
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT CG 20

RESULT 742
AAAS5806/C
ID AAAS5806 standard; DNA; 20 BP.

AC AAAS5806;

DT 01-SEP-2000 (first entry)

DE Human histone deacetylase HD2 antisense oligonucleotide SEQ ID NO:51.

XX Human; DNA methyltransferase; DNA Methylase; antisense oligonucleotide;
XX modulation; inhibition; gene expression; combination therapy; p16;
XX histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
XX methylation; gene therapy; tumour; cytostatic; antitastmatic;
XX antiinflammatory; inflammation; asthma; ss.

OS Homo sapiens.

XX MO200023112-A1.

XX 27-APR-2000.

XX 19-OCT-1999; 99WO-US024278.

XX 19-OCT-1998; 98US-0104804P.

XX (METH-) METHYLGENE INC.

XX Besterman JM, Macleod AR, Siders WM;

XX WPI; 2000-339532/29.

PT Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
PT with a synergistic amount of antisense oligonucleotide and protein
PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
PT of e.g. tumors.
XX

PS Disclosure; Page 29; 99pp; English.

XX The present invention describes a method for inhibiting the expression of
XX a gene in a cell comprising contacting the cell with an effective
XX synergistic amount of an antisense oligonucleotide which inhibits
XX expression of the gene, and an effective synergistic amount of a protein
XX effector of a product of the gene. Also described are: (1) a method for
XX treating a disease responsive to inhibition of a gene in a mammal; (2) a
XX method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
XX comprising an antisense oligonucleotide which inhibits expression of the
XX gene in operable association with a protein effector of a gene product;
XX and (4) a pharmaceutical composition comprising the inhibitor of (3). The

CC methods and compositions are useful as analytical tools for transgenic
CC studies and as therapeutic tools e.g. as gene therapy tools for human
CC diseases including benign and malignant tumors, inflammation or asthma.
CC The methods, inhibitors and compositions of the invention that inhibit
CC expression or activity of a gene or gene product may be used to treat
CC patients having, or predisposed to developing, a disease responsive to
CC inhibition of the gene. These may also be used to activate silenced genes
CC to provide missing gene functions and improve a given condition.
CC Furthermore, the methods and compositions are useful as probes of the
CC physiological function of a gene product in an experimental cell culture
CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AAAS5758 to AAAS5842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX

SQ Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7413 CAGCAGCAGCAGCAGCAGCA 7432
DB 20 CGCAGCAGCAGCAGCAGCA 1

RESULT 743
AAH43116/C
ID AAH43116 standard; DNA; 20 BP.

AC AAH43116;

DT 19-SEP-2001 (first entry)

DE Antisense oligo, target HDAC-2 121-141.

XX Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
XX cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
XX fungal infections; ss.

OS Synthetic.

XX WO200138322-A1.

XX 31-MAY-2001.

XX 22-NOV-2000; 2000WO-IB001881.

XX 23-NOV-1999; 99US-0167035P.

XX (METH-) METHYLGENE INC.

XX Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;

XX WPI; 2001-432601/46.

PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
XX

PS Disclosure; Page 40; 147pp; English.

XX The sequences given in AAH43115-21 are oligonucleotides which are
XX antisense to the histone deacetylase gene, HDAC-2. These oligonucleotides
XX may be used in combination with an inhibitor of histone deacetylase
XX enzyme function, to give an improved inhibitory effect, thereby reducing
XX the amount of inhibitor required to obtain a given inhibitory effect.
XX Compounds containing these oligonucleotides may be used to treat cell
XX proliferation conditions such as cancer, restenosis or psoriasis. They
XX can also be used to treat protozoal and fungal infections
XX

SQ Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 20;

XX WPI, 1995-018287/03.

DR Analysis of cDNA and gene expression - by amplification of mRNA followed

XX PT by digestion with restriction enzymes.

PT Disclosure; Page 5; 11pp; Japanese.

PS

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX

SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Cy Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Db 1 TTTTCTTTTTTTTTTCG 20

RESULT 738
AA04916
ID AA04916 standard; cDNA; 20 BP.
AC AA04916;
XX
DT 25-MAR-2003 (revised)
DT 15-MAY-1996 (first entry)
DE Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-7.
XX
XX Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KM thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
transplant; neoplasia; myelosuppression; bone marrow; ss.
OS Synthetic.
XX
PN EP676470-AI.
XX
PD 11-OCT--1995.
XX
PF 04-OCT-1990; 9SEP-00105391.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 28-SEP-1990; 90WO-US005548.
PR 01-OCT-1990; 90US-00589701.
PA (AMGE-) AMGEN INC.
XX
FI Zeebo KM, Suggs SV, Bosselman RA, Martin FH;
DR WPI, 1995-146090/45.
XX
XX New stem cell factor polypeptide(s) - for stimulating the growth of
PT primitive progenitor cells, esp. for treating disorders involving blood
PT cells.
XX
XX Example 3; Fig 12C; 127pp; English.
XX
XX AA04915-T04922 are oligonucleotide primers and probes used for the
CC amplification and sequencing of mammalian stem cell factor (SCF). Non-
CC naturally occurring SCF and C-terminally truncated polypeptides, having
CC amino acid sequences sufficiently duplicative of naturally occurring SCF,

[illegible]

CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

SO Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 5.2e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4467 TTTTGTCTGTC 4486
 1 TTTTGTCTGTC 20

Db 1 TTTTGTCTGTC 20

RESULT 735
 AAQ75583
 ID AAQ75583 standard; DNA; 20 BP.

XX AC AAQ75583;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KM Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 5; 11pp; Japanese.
 XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

SO Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 5.2e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4465 TTTTGTCTGTC 4484
 1 TTTTGTCTGTC 20

Db 1 TTTTGTCTGTC 20

RESULT 736
 AAQ75602
 ID AAQ75602 standard; DNA; 20 BP.

XX AC AAQ75602;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KM Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 5; 11pp; Japanese.
 XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

SO Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 5.2e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4467 TTTTGTCTGTC 4486
 1 TTTTGTCTGTC 20

Db 1 TTTTGTCTGTC 20

RESULT 737
 AAQ75599
 ID AAQ75599 standard; DNA; 20 BP.

XX AC AAQ75599;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KM Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.


```

ID AAQ75586 standard; DNA; 20 BP.
XX
XX AAQ75586;
AC
XX
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX
SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4467 TTTT TTTT TTTT TTTT TTTT GTC 4486
DB 1 TTTT TTTT TTTT TTTT TTTT ATC 20
RESULT 730
AAQ75577
ID AAQ75577 standard; DNA; 20 BP.
XX
XX AAQ75577;
AC
XX
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX

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PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4466 TTTT TTTT TTTT TTTT TTTT GTC 4485
DB 1 TTTT TTTT TTTT TTTT TTTT AGT 20
RESULT 731
AAQ75593
ID AAQ75593 standard; DNA; 20 BP.
XX
XX AAQ75593;
AC
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 0.2%; Score 18.4; DB 1; Length 20;

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XX Synthetic.
OS JP06303997-A.
PN 01-NOV-1994.
PD 16-APR-1993; 93JP-00112515.
PR 16-APR-1993; 93JP-00112515.
PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
DR Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 5; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4467 TTTT TTTT TTTT TTTT TTTT GTC 4486
DB 1 TTTT TTTT TTTT TTTT TTTT GAC 20
RESULT 727
AAQ75574
ID AAQ75574 standard; DNA; 20 BP.
AC AAQ75574;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
DE Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
OS JP06303997-A.
PN 01-NOV-1994.
PD 16-APR-1993; 93JP-00112515.
PR 16-APR-1993; 93JP-00112515.
PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
DR Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 5; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC
```

```
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4467 TTTT TTTT TTTT TTTT TTTT GTC 4486
DB 1 TTTT TTTT TTTT TTTT TTTT GCC 20
RESULT 728
AAQ75585
ID AAQ75585 standard; DNA; 20 BP.
AC AAQ75585;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
DE Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
OS JP06303997-A.
PN 01-NOV-1994.
PD 16-APR-1993; 93JP-00112515.
PR 16-APR-1993; 93JP-00112515.
PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 5; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT 20
RESULT 729
AAQ75586
```


CC resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
 CC and hormone dependence
 XX
 SQ Sequence 27 BP; 0 A; 0 C; 23 G; 4 T; 0 U; 0 Other;
 Query Match 0.2%; Score 18.6; DB 1; Length 27;
 Best Local Similarity 84.0%; Pred. No. 7.3e+02;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3622 GGGGTGGGGTGGAGAGAGGTAG 3646
 DB 2 GGGGTGGGGTGGGGTGGGGTGG 26
 RESULT 722
 AAL43225
 ID AAL43225 standard; DNA; 27 BP.
 XX
 AC AAL43225;
 XX
 DT 16-AUG-2002 (first entry)
 XX
 DE 187-2 protein PCR primer 3.
 XX
 KM 187-2 protein; heart muscle; myocardial infarction; heart disease; ss;
 XX PCR; primer.
 XX
 OS Mammalia.
 XX
 PN WO200236763-A1.
 XX
 PD 10-MAY-2002.
 XX
 PF 29-OCT-2001; 2001WO-JP009478.
 XX
 PR 30-OCT-2000; 2000JP-00331401.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Koyama N, Tanida S, Watanabe T;
 XX
 DR WPI; 2002-417276/44.
 XX
 PT Gene overexpressed in heart muscle after myocardial infarction and its
 PT protein expression product, useful for screening potential drugs for
 PT treatment of heart disease.
 XX
 PS Example 1; Page 93; 107pp; Japanese.
 XX
 CC The invention comprises the amino acid and coding sequences of human and
 CC rat 187-2 proteins. The 187-2 gene is overexpressed in heart muscle after
 CC myocardial infarction. The 187-2 DNA and protein sequences are useful for
 CC the treatment and prevention of heart disease (i.e. myocardial
 CC infarction). The present DNA sequence represents a 187-2 protein-specific
 CC PCR primer
 CC
 SQ Sequence 27 BP; 11 A; 1 C; 9 G; 6 T; 0 U; 0 Other;
 Query Match 0.2%; Score 18.6; DB 1; Length 27;
 Best Local Similarity 84.0%; Pred. No. 7.3e+02;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2919 TATAGAGTGTCTAAGAGTGGGA 2943
 DB 2 TATAGAGAGTATTAAGAGTGGCA 26
 RESULT 723
 ADE84748/C
 ID ADE84748 standard; DNA; 27 BP.
 XX
 AC ADE84748;
 XX

DT 29-JAN-2004 (first entry)
 XX
 DE Ebola virus glycoprotein PCR primer SEQ ID NO:35.
 XX
 KM chimeric Ebola envelope protein; Ebola glycoprotein binding domain;
 KM Ebola virus; immune response; virucide; antibacterial; antiparasitic;
 KM cytostatic; vaccine; cancer; tumour; PCR primer; ss.
 XX
 OS Synthetic.
 OS
 OS Ebola virus.
 XX
 PN WO2003092582-A2.
 XX
 PD 13-NOV-2003.
 XX
 PF 28-APR-2003; 2003WO-US011494.
 XX
 PR 30-APR-2002; 2002US-0376480P.
 PR 04-JUN-2002; 2002US-0395704P.
 PR 20-NOV-2002; 2002US-0427752P.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Wilson JM, Medina MFC, Kobinger G;
 XX
 DR WPI; 2004-011795/01.
 XX
 PT New chimeric Ebola envelope protein comprising a functional Ebola
 PT glycoprotein binding domain fused to a heterologous amino acid sequence,
 PT useful for inducing an immune response against Ebola virus, bacteria, or
 PT fungi.
 XX
 XX Example 1; SEQ ID NO 35; 107pp; English.
 PS
 CC The present invention describes a chimeric Ebola envelope protein (1)
 CC comprising a functional Ebola glycoprotein binding domain fused to a
 CC heterologous amino acid sequence. Also described: (1) a nucleic acid
 CC molecule encoding (1); (2) a host cell comprising the chimeric Ebola
 CC protein or nucleic acid molecule encoding the protein; (3) a method of
 CC inducing an immune response against Ebola by delivering a composition
 CC comprising the chimeric Ebola protein or nucleic acid molecule encoding
 CC the protein; (4) a recombinant virus having a chimeric Ebola envelope
 CC protein and a minigen; (5) a host cell containing the recombinant virus;
 CC (6) a method of treating a patient with a selected molecule by
 CC transducing the cells of the patient with the recombinant virus above;
 CC (7) a method of delivering a molecule to the apical cells of the lung by
 CC administering a recombinant virus above intratracheally; (8) an
 CC immunogenic composition comprising a DNA molecule encoding a chimeric
 CC Ebola envelope protein above under the control of sequences which direct
 CC its expression in a host cell, and a carrier; and (9) an immunogenic
 CC composition comprising an Ebola envelope protein defined above, and a
 CC carrier. (1) has virucide, antibacterial, antiparasitic and cytostatic
 CC activities, and can be used in vaccines. The recombinant virus can be
 CC used in preparing a medicament. The chimeric Ebola envelope protein is
 CC useful as an antigen for inducing an immune response against Ebola virus,
 CC and for generating a chimeric Ebola-pseudotyped virus, which delivers a
 CC selected molecule to a target cell. The proteins may be used to provide
 CC heterologous envelope to any vector derived from a viral source, which
 CC naturally contain an envelope. The protein may further be used to
 CC immunise a (non-)human animal against other pathogens including bacteria,
 CC fungi, parasitic microorganisms or multicellular parasites, which infect
 CC human and non-human vertebrates, or from a cancer or tumour cell. The
 CC present sequence is used in the exemplification of the present invention.
 CC
 SQ Sequence 27 BP; 8 A; 11 C; 2 G; 6 T; 0 U; 0 Other;
 Query Match 0.2%; Score 18.6; DB 1; Length 27;
 Best Local Similarity 84.0%; Pred. No. 7.3e+02;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4364 GTGACAGGCTGGGGAATTTGCTG 4388
 DB 25 GTGACAGGATGGAGCTTTTGATG 1

PT	Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
PT	
XX	
PS	Claim 9; Page 156; 218pp; English.
XX	
CC	
CC	The present invention describes nucleic acid molecules which modulate the receptors, expression and/or stability of a mRNA encoding 1 or more
CC	receptors of vascular endothelial growth factor (VEGF). A patient
CC	(preferably human) having a condition associated with the level of the
CC	fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC	receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC	angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC	treated by administering the nucleic acid molecule or the expression
CC	vector to the patient. AAX67275 to AAX75752 represent specific examples
CC	of nucleic acid molecules from the present invention
XX	
SQ	Sequence 27 BP; 5 A; 8 C; 5 G; 0 T; 8 U; 1 Other;
XX	
Query Match	0.2%; Score 18.6; DR 1; Length 27;
Best Local Similarity	53.8%; Pred. No. 7,3e+02;
Matches 14; Conservative 7; Mismatches 5; Indels 0; Gaps 0;	
Qy	5813 TGCCATGTGATGATGAATCTCTGC 5838
Db	2 UGCCUGUCUGANGANGAANUCCUCC 27
XX	
RESULT 720	
AAH46019	
ID	AAH46019 standard; DNA; 27 BP.
XX	
AC	AAH46019;
XX	
DT	12-SEP-2001 (first entry)
XX	
DE	Synthetic oligonucleotide 19.
XX	
KM	Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;
KW	cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
KW	tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
XX	lymphoma; ss.
XX	
OS	Synthetic.
XX	
PN	WO200144465-A2.
XX	
PF	12-DEC-2000; 2000WO-CA001467.
XX	
PR	13-DEC-1999; 99US-0170325P.
PR	29-AUG-2000; 2000US-0228925P.
XX	
XX	(BION-) BIONICHE LIFE SCI INC.
XX	
P1	Phillips NC, Filion MC;
XX	
DR	WPI; 2001-398150/42.
PT	
PT	Composition comprising synthetic oligonucleotides which comprise multiple
PT	repeats of dinucleotides such as GT, TG useful for treating cancer by
PT	inducing cell cycle arrest, inhibiting proliferation, activating
PT	caseases.
XX	
PS	Disclosure; Page 74; 77pp; English.
XX	
CC	The present sequence is that of a synthetic oligonucleotide useful to the
CC	invention. The invention relates to a composition, comprising a 2 to 20
CC	base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple
CC	repeats of dinucleotides such as GT, TG, etc., according to specific
CC	formula and having cytostatic activity. The oligonucleotide compositions
CC	are useful for inducing cell cycle arrest, inhibition of proliferation,

CC	activation of caspases and induction of apoptosis or production of
CC	cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour
CC	necrosis factor (TNF)-alpha by immune system cells, in an animal having
CC	cancer such as primary carcinoma, secondary carcinoma, primary sarcoma
CC	and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,
CC	colorectal, ovarian or bone cancer. The compositions induce apoptosis
CC	independent of Fas, p53/p21, p21/waf-1/cip, p15(ink4B), p16(ink4), drug
CC	resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
CC	and hormone dependence
SQ	Sequence 27 BP; 0 A; 0 C; 23 G; 4 T; 0 U; 0 Other;
XX	
Query March	0.2%; Score 18.6; DB 1; Length 27;
Best Local Similarity	84.0%; Pred. No. 7.3e+02;
Matches 21; Conservative	0; Mismatches 4; Indels 0; Gaps 0
Oy	3622 GGCGTGCGGTCGGAGCGAGGTAG 3646
Dd	 2 GGCGTGCGGTCGGCGTGGCGGTGG 26
RESULT 721	
ID AAH46003	standard; DNA; 27 BP.
AAH46003;	
AC	
XX	
DT	12-SEP-2001 (first entry)
XX	
DE	Synthetic oligonucleotide 3.
KM	Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;
KM	cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
KM	tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
KM	lymphoma; ss.
XX	
OS	Synthetic.
XX	
PN	WO200144465-A2.
PD	
XX	
PF	12-DEC-2000; 200MO-CA001467.
PR	13-DEC-1999; 99US-0170325P.
PR	29-AUG-2000; 2000US-0226925P.
XX	
PA	(BION-) BIONICHE LIFE SCI INC.
PT	Phillips NC, Filion MC;
XX	
DR	WPI; 2001-398150/42.
XX	
PT	Composition comprising synthetic oligonucleotides which comprise multiple
PT	repeats of dinucleotides such as GT, TG useful for treating cancer by
PT	inducing cell cycle arrest, inhibiting proliferation, activating
PT	caspases.
XX	
PS	Example 4; Page 16; 77pp; English.
XX	
CC	The present sequence is that of a synthetic oligonucleotide useful to treat
CC	invention. The invention relates to a composition, comprising a 2 to 20
CC	base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple
CC	repeats of dinucleotides such as GT, TG, etc., according to specific
CC	formula and having cytostatic activity. The oligonucleotide compositions
CC	are useful for inducing cell cycle arrest, inhibition of proliferation,
CC	activation of caspases and induction of apoptosis or production of
CC	cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour
CC	necrosis factor (TNF)-alpha by immune system cells, in an animal having
CC	cancer such as primary carcinoma, secondary carcinoma, primary sarcoma
CC	and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,
CC	colorectal, ovarian or bone cancer. The compositions induce apoptosis
CC	independent of Fas, p53/p21, p21/waf-1/cip, p15(ink4B), p16(ink4), drug
CC	resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
CC	and hormone dependence

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XX C-myc; cancer; HIV-1; AIDS; collagenase; Alzheimers disease; EGF;
KW epidermal growth factor; GSTP1; HMGCoA; thalassemia;
KW Herpes simplex virus; nerve growth factor receptor; globin; ss.
XX Synthetic.
XX EP375408-A.
XX 27-JUN-1990.
XX 20-DEC-1989; 89BP-00313391.
XX 20-DEC-1988; 88US-00287359.
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX (HOGA/) HOGAN M E.
XX Hogan ME, Kessler DJ;
XX WPI, 1990-195509/26.
XX Synthetic oligo-nucleotide(s) which bind target duplex DNA - forming co-
XX linear triplex to control transcription process in gene-specific fashion.
XX Claim 47; Page 31; 40pp; English.
XX
XX Sequence forms triplex with the double stranded target sequence with G
XX binding to G-C and T to A-T. The strand runs 3' to 5' in an antiparallel
XX orientation and when targeted to a specific sequence will deactivate it.
XX This allows for growth inhibition in cancerous cells; manipulation of
XX cellular structural protein content; inhibition of IL-2 chain receptor;
XX disrupting plaque formation in Alzheimer's disease; inhibiting EGF gene;
XX modulating cholesterol synthesis through the HMGCoA gene; suppressing NGF
XX gene expression; arresting HSV-1 replication and suppressing Beta- globin
XX expression in thalassemia and sickle cell anaemia patients. (Updated on
XX 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA
XX field.)
XX
XX Sequence 27 BP; 0 A; 0 C; 6 G; 21 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 18.6; DB 1; Length 27;
XX Best Local Similarity 84.0%; Pred. No. 7.3e+02;
XX Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4459 TCGACTTTTTTTTTTTTTTTTTT 4483
DB 2 TGGGTGTTTTTTTTTGTGTTTTTTT 26
XX
XX RESULT 718
XX ID AAQ36361 standard; DNA; 27 BP.
XX AAQ36361;
XX AAQ36361;
XX 25-MAR-2003 (revised)
XX 07-JUN-1993 (first entry)
XX
XX GL6par, targeted to human beta globin sequence.
XX
XX Hemoglobin; beta thalassemia; sickle cell anaemia; delta protein;
XX triplex; target; duplex; promoter; coding domain; 3'-5'; ss.
XX Synthetic.
XX US5176996-A.
XX 05-JAN-1993.
XX 22-DEC-1989; 89US-00453532.
XX 20-DEC-1988; 88US-00287359.

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XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX Hogan ME, Kessler DJ;
XX WPI, 1993-035718/04.
XX Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -
XX which bind to target sequence in duplex DNA forming colinear triplex by
XX binding to major groove.
XX Example 13; Col 35; 29pp; English.
XX
XX The beta globin gene encodes on of the proteins comprising human adult
XX haemoglobin. Mutation in this gene is responsible for beta thalassemia
XX and sickle cell anaemia. Expression of the gene may be prevented by the
XX formation of a triplex between the duplex target DNA sequence and an anti
XX parallel or parallel synthetic oligonucleotide. The triplex
XX oligonucleotides are designed to inhibit the beta globin gene in
XX thalassemics and in patients with sickle cell anaemia, to be replaced by
XX the naturally occurring delta protein. Two classes of triplex
XX oligonucleotides may be used, targeted against the 5' enhancer or the
XX promoter/coding domain, in this case from base 874 to 900 (numbering is
XX relative to the principal mRNA start site). A suitable parallel
XX oligonucleotide is GL6par (3'-5'). See also AAQ36219-362. (Updated on 25-
XX MAR-2003 to correct PF field.)
XX
XX Sequence 27 BP; 0 A; 0 C; 6 G; 21 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 18.6; DB 1; Length 27;
XX Best Local Similarity 84.0%; Pred. No. 7.3e+02;
XX Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4459 TCGACTTTTTTTTTTTTTTTTTT 4483
DB 2 TGGGTGTTTTTTTTTGTGTTTTTTT 26
XX
XX RESULT 719
XX ID AAX73563 standard; RNA; 27 BP.
XX AAX73563;
XX AAX73563;
XX 28-JUL-1999 (first entry)
XX
XX Mouse flt-1 VEGF receptor hammerhead ribozyme #35.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; ocular disease;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX Synthetic.
XX Mus sp.
XX W09715662-A2.
XX 01-MAY-1997.
XX 25-OCT-1996; 96WO-US017480.
XX 26-OCT-1995; 95US-0005974P.
XX 11-JAN-1996; 96US-00584040.
XX (RIBO-) RIBOZYME PHARM INC.
XX (CHIR ) CHIRON CORP.
XX Pavco P, Mcswigen J, Stinchcomb D, Escobedo J;
XX WPI, 1997-259017/23.

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DR WPI; 2001-432601/46.
XX
XX New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer.
PT reticulos or fungal infections.
XX
XX
PS Disclosure; Page 40; 147pp; English.
XX
XX The sequences given in AAH43115-21 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-2. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to give an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, reticulos or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
SQ Sequence 26 BP; 6 A; 5 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.6; DB 1; Length 26;
Best Local Similarity 84.0%; Pred. No. 6.9e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5574 CAGCAAGCTTTGGCTCATGTGATT 5598
DB 1 CAGCAAGTTATGGTCAATGCGGATT 25
|||||

RESULT 715
AAC89535
ID AAC89535 standard; DNA; 26 BP.
XX
XX AAC89535;
XX
DT 08-MAR-2001 (first entry)
XX
XX Human HDAC-1/HDAC-2 PCR primer SEQ ID NO: 5.
DE
XX
XX Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
KM HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
KW gene therapy; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200071703-A2.
PN
XX
PD 30-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-IB001252.
PF
XX
XX 03-MAY-1999; 99US-0132287P.
PR
XX
XX (METH-) METHYLENE INC.
PA
XX
XX Macleod AR, Li Z, Besterman JM;
PI
XX
XX WPI; 2001-016407/02.
DR
XX
XX Antisense oligonucleotide that inhibits expression of a histone
PT deacetylase, useful for treating and/or alleviating the symptoms of
PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
XX
XX
PS Example 2; Page 12; 125pp; English.
XX
XX The present invention provides inhibitors of histone deacetylase enzymes
CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
CC inhibitors may be antisense strands or they may be compounds identified
CC by contacting the enzyme with the compound and measuring the resulting
CC enzyme activity. These inhibitors are useful for treating cancers and for
CC identifying which histone deacetylase is involved in a neoplasia
XX
SQ Sequence 26 BP; 6 A; 5 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.6; DB 1; Length 26;
Best Local Similarity 84.0%; Pred. No. 6.9e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5574 CAGCAAGCTTTGGCTCATGTGATT 5598
DB 1 CAGCAAGTTATGGTCAATGCGGATT 25
|||||

RESULT 716
AAC89544
ID AAC89544 standard; DNA; 26 BP.
XX
XX AAC89544;
XX
AC
XX
DT 08-MAR-2001 (first entry)
XX
XX Human HDAC-1/HDAC-2 antisense sequence SEQ ID NO: 14.
DE
XX
XX Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
KM HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
KW gene therapy; PCR primer; ss.
XX
XX
XX Homo sapiens.
OS
XX
XX WO200071703-A2.
PN
XX
PD 30-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-IB001252.
PF
XX
XX 03-MAY-1999; 99US-0132287P.
PR
XX
XX (METH-) METHYLENE INC.
PA
XX
XX Macleod AR, Li Z, Besterman JM;
PI
XX
XX WPI; 2001-016407/02.
DR
XX
XX Antisense oligonucleotide that inhibits expression of a histone
PT deacetylase, useful for treating and/or alleviating the symptoms of
PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
XX
XX
XX Example 1; Page 23; 125pp; English.
PS
XX
XX The present invention provides inhibitors of histone deacetylase enzymes
CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
CC inhibitors may be antisense strands or they may be compounds identified
CC by contacting the enzyme with the compound and measuring the resulting
CC enzyme activity. These inhibitors are useful for treating cancers and for
CC identifying which histone deacetylase is involved in a neoplasia
XX
SQ Sequence 26 BP; 6 A; 5 C; 8 G; 5 T; 2 U; 0 Other;

Query Match 0.2%; Score 18.6; DB 1; Length 26;
Best Local Similarity 76.0%; Pred. No. 6.9e+02;
Matches 19; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5574 CAGCAAGCTTTGGCTCATGTGATT 5598
DB 1 CAGCAAGTTATGGTCAATGCGGATT 25
|||||

RESULT 717
AAQ05023
ID AAQ05023 standard; DNA; 27 BP.
XX
XX AAQ05023;
XX
AC
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-1990 (first entry)
XX
XX
DE Sequence binding to and inhibiting the Beta-globin gene.

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XX OS Homo sapiens.
XX PN WO200023112-A1.
XX PD 27-APR-2000.
XX PF 19-OCT-1999; 99WO-US024278.
XX PR 19-OCT-1998; 98US-0104804P.
XX (METH-) METHYLGENE INC.
XX PA Besterman JM, Macleod AR, Siders WM;
XX PI WPI; 2000-339532/29.
XX DR
XX PT Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
XX PR with a synergistic amount of antisense oligonucleotide and protein
XX PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
XX PT of e.g. tumors.
XX PS Example 9; Page 29; 99pp; English.
XX CC The present invention describes a method for inhibiting the expression of
XX CC a gene in a cell comprising contacting the cell with an effective
XX CC synergistic amount of an antisense oligonucleotide which inhibits
XX CC expression of the gene, and an effective synergistic amount of a protein
XX CC effector of a product of the gene. Also described are: (1) a method for
XX CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
XX CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
XX CC comprising an antisense oligonucleotide which inhibits expression of the
XX CC gene in operable association with a protein effector of a gene product;
XX CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
XX CC methods and compositions are useful as analytical tools for transgenic
XX CC studies and as therapeutic tools, e.g. as gene therapy tools for human
XX CC diseases including benign and malignant tumours, inflammation or asthma.
XX CC The methods, inhibitors and compositions of the invention that inhibit
XX CC expression or activity of a gene or gene product may be used to treat
XX CC patients having, or predisposed to developing, a disease responsive to
XX CC inhibition of the gene. These may also be used to activate silenced genes
XX CC to provide missing gene functions and improve a given condition.
XX CC Furthermore, the methods and compositions are useful as probes of the
XX CC physiological function of a gene product in an experimental cell culture
XX CC or animal system; and to evaluate the effect of inhibiting gene activity
XX CC or expression. AA55758 to AA55842 represent oligonucleotide sequences
XX CC which are used in the exemplification of the present invention
XX SQ Sequence 26 BP; 6 A; 5 C; 8 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 18.6; DB 1; Length 26;
XX Best Local Similarity 84.0%; Pred. No. 6.9e+02;
XX Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 5574 CAGCAAGCTTGGCTCATGTGATT 5598
XX ||||| ||||| ||||| |||||
XX 1 CAGCAAGTTATGGCTATCGGATT 25
XX
XX RESULT 713
XX AAF74913/C
XX ID AAF74913 standard; DNA; 26 BP.
XX XX
XX AC AAF74913;
XX XX
XX DT 23-MAY-2001 (first entry)
XX XX
XX DE CD40L poly-A tract sequence SEQ ID NO:10.
XX XX
XX KM Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
XX KM diagnosis; antiarthritic; antirheumatic; immunosuppressive;
XX KM antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX XX

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OS OS Homo sapiens.
XX XX PN WO200119844-A1.
XX XX PD 22-MAR-2001.
XX XX PF 13-SEP-2000; 2000WO-US024966.
XX XX PR 13-SEP-1999; 99US-0153625P.
XX XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX XX PA Crow MK, Li Y;
XX XX PI WPI; 2001-244776/25.
XX XX DR
XX XX PT New altered CD40L promoter for use in the study, diagnosis and treatment
XX XX PR of a variety of inflammatory disorders and autoimmune diseases, such as
XX XX PT rheumatoid arthritis.
XX PS Example 1; Fig 3; 90pp; English.
XX CC The present invention describes an isolated, purified nucleic acid, which
XX CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
XX CC residues 331-455 of the sequence comprising 455 nucleotides given in
XX CC AAF74905 where A in the wild type sequence at position 331 (corresponding
XX CC to position -125) is replaced with C. (I) has antiarthritic, and can
XX CC be used in gene therapy. (I) is useful in the study, diagnosis and
XX CC treatment of inflammatory and autoimmune diseases, as well as diseases in
XX CC which elevated expression of CD40L is a factor, e.g., rheumatoid
XX CC arthritis. The present sequence represents a CD40L poly-A tract sequence
XX CC which is used in an example from the present invention
XX SQ Sequence 26 BP; 20 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 18.6; DB 1; Length 26;
XX Best Local Similarity 84.0%; Pred. No. 6.9e+02;
XX Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 4458 ATGACCTTTTCTTTTCTTTTCTTTT 4482
XX ||||| ||||| ||||| |||||
XX 25 AAGGTTTCTTTCTTTTCTTTTCTTTT 1
XX
XX RESULT 714
XX AAH43120
XX ID AAH43120 standard; DNA; 26 BP.
XX XX
XX AC AAH43120;
XX XX
XX DT 19-SEP-2001 (first entry)
XX XX
XX DE Antisense oligo, target HDAC-2 211-236.
XX XX
XX KM Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
XX KM cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
XX KM fungal infections; ss.
XX XX
XX OS Synthetic.
XX OS
XX OS WO200138322-A1.
XX PN
XX PD 31-MAY-2001.
XX XX
XX PF 22-NOV-2000; 2000WO-IB001881.
XX XX
XX PR 23-NOV-1999; 99US-0167035P.
XX XX
XX PA (METH-) METHYLGENE INC.
XX XX
XX PI Delorme D, Ruel R, Lavole R, Thibault C, Abou-Khalil E;
XX XX

```

CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC particular

XX Sequence 25 BP; 2 A; 3 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.6; DB 1; Length 25;

Best Local Similarity 84.0%; Pred. No. 6.5e+02;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4469 TTTTGTGCTGAGAC 4493

DB 1 TTTTGTGCTGAGAC 25

RESULT 710

ACC96235 standard; DNA; 25 BP.

XX AAC96235;

AC AAC96235;

XX 26-FEB-2001 (first entry)

XX 16S rRNA gene PCR primer #202.

XX DNA sequence analysis; sequencing; protein structure;

XX gene typing; organ donation; bacteria identification; 16S rRNA; HLA;

XX human leukocyte antigen; PCR primer; ss.

XX Homo sapiens.

XX WC200065088-A2.

XX 02-NOV-2000.

XX 20-APR-2000; 2000WC-EP003636.

XX 26-APR-1999; 99EP-00303215.

XX (AMSH) AMERSHAM PHARMACIA BIOTECH AB.

XX ulfendahl P, Wong K;

XX WPI; 2000-679677/66.

XX Identifying extendible primers for use in identification, or

XX classification of a nucleic acid of an organism, allele or gene such as

XX PT class 1/2 HLA comprises identifying all possible nucleotide sequences of

XX specific length.

XX Claim 14; Page 47; 66pp; English.

XX The present invention provides a method for identifying a set of

XX extendible primers which can be used in the identification, typing and

XX classification of genes. This can then be used to predict protein

XX sequence and structure, in organ donation to match the organ with the

XX receiver, and to identify bacteria in a sample. The method can be used to

XX type the human leukocyte antigen genes (HLA) and 16S rRNA genes in

XX particular

XX Sequence 25 BP; 3 A; 4 C; 3 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.6; DB 1; Length 25;

Best Local Similarity 84.0%; Pred. No. 6.5e+02;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4470 TTTTGTGCTGAGAC 4494

DB 1 TTTTGTGCTGAGAC 25

RESULT 711

AAQ47177

ID AAQ47177 standard; DNA; 26 BP.

XX AAQ47177;

AC 25-MAR-2003 (revised)

XX 25-JAN-1994 (first entry)

XX MHC DR A intron binding oligomer T81.

XX MHC, major histocompatibility complex; class II; control oligomers; DR A;

XX transplacental; antigen; autoimmune disease; ss.

XX Synthetic.

XX WO9314769-A1.

XX 05-AUG-1993.

XX 29-JAN-1993; 93WO-US000797.

XX 31-JUN-1992; 92US-00830427.

XX 14-SEP-1992; 92US-00944868.

XX (REGC) UNIV CALIFORNIA.

XX Weiss TL, Garovoy MR, Hunt A, Huey B, Tam S;

XX WPI; 1993-258367/32.

XX Depletion of transplantation antigens in donor cells - using anti-sense

XX or triplex-forming oligonucleotide(s), used for treating auto-immune

XX disease and in transplants.

XX Example; Page 22; 71pp; English.

XX The sequences given in AAQ47176-77 represent triplex forming oligo-

XX nucleotides which bind to the mRNA sequence of the MHC class II locus DR

XX A structural gene at positions 851-876. The sequences given in AAQ47178-

XX 80 represent control oligomers which contain base compositions similar to

XX that around this DR A region but not containing the correct sequences. DR

XX A is a transplantation antigen. Binding of this sequence to the DR A gene

XX inhibits antigen production. This method may be used for treating

XX individuals with autoimmune disease, characterised by dysfunctional

XX expression of a transplantation antigen. It may also be used to produce

XX cells which are more easily transplanted into a recipient. (Updated on 25

XX -MAR-2003 to correct PN field.)

XX Sequence 26 BP; 0 A; 0 C; 22 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.6; DB 1; Length 26;

Best Local Similarity 84.0%; Pred. No. 6.9e+02;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3622 GGGGTGGGCTGGAGAGAGCTAG 3646

DB 2 GGGGTGGGCTGGAGAGAGCTAG 26

RESULT 712

AAA55810 standard; DNA; 26 BP.

XX AAA55810;

AC 01-SEP-2000 (first entry)

XX Human histone deacetylase HD2 antisense oligonucleotide SEQ ID NO:55.

XX Human, DNA methyltransferase; DNA Methylase; antisense oligonucleotide;

XX modulation; inhibition; gene expression; combination therapy; p16;

XX histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;

XX methylation; gene therapy; tumour; cyclostatic; antiasthmatic;

XX antiinflammatory; inflammation; asthma; ss.

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XX 16S rRNA gene PCR primer #196.
DE DNA sequence analysis; sequencing; protein structure;
XX gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
KW human leukocyte antigen; PCR primer; 88.
XX Homo sapiens.
XX WO200065088-A2.
XX 02-NOV-2000.
XX 20-APR-2000; 2000WO-EP003636.
XX 26-APR-1999; 99EP-00303215.
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX Ulfendahl P, Wong K;
XX WPI; 2000-679677/66.
XX Identifying extendible primers for use in identification, or
XX classification of a nucleic acid of an organism, allele or gene such as
XX class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX specific length.
XX Claim 14; Page 47; 66pp; English.
XX The present invention provides a method for identifying a set of
XX extendible primers which can be used in the identification, typing and
XX classification of genes. This can then be used to predict protein
XX sequence and structure, in organ donation to match the organ with the
XX receiver, and to identify bacteria in a sample. The method can be used to
XX type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
XX particular
XX Sequence 25 BP; 3 A; 5 C; 3 G; 14 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 6.5e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4472 TTTTGTCTTGCTGACATG 4496
DB 1 TTTTGTCTTGCTGACATG 25
RESULT 708
AAC96296
ID AAC96296 standard; DNA; 25 BP.
XX AAC96296;
AC 26-FEB-2001 (first entry)
XX 26-FEB-2001 (first entry)
DE HLA DPB1 gene PCR primer #28.
XX DNA sequence analysis; sequencing; protein structure;
KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
KW human leukocyte antigen; PCR primer; 88.
XX Homo sapiens.
XX WO200065088-A2.
XX 02-NOV-2000.
XX 20-APR-2000; 2000WO-EP003636.
XX 26-APR-1999; 99EP-00303215.
XX

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PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX Ulfendahl P, Wong K;
XX WPI; 2000-679677/66.
XX Identifying extendible primers for use in identification, or
XX classification of a nucleic acid of an organism, allele or gene such as
XX class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX specific length.
XX Claim 14; Page 49; 66pp; English.
XX The present invention provides a method for identifying a set of
XX extendible primers which can be used in the identification, typing and
XX classification of genes. This can then be used to predict protein
XX sequence and structure, in organ donation to match the organ with the
XX receiver, and to identify bacteria in a sample. The method can be used to
XX type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
XX particular
XX Sequence 25 BP; 2 A; 2 C; 3 G; 18 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 6.5e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4468 TTTTGTCTTGCTGACA 4492
DB 1 TTTTGTCTTGCTGACA 25
RESULT 709
AAC96462
ID AAC96462 standard; DNA; 25 BP.
XX AAC96462;
AC 26-FEB-2001 (first entry)
XX 26-FEB-2001 (first entry)
DE HLA DOB1 gene PCR primer #14.
XX DNA sequence analysis; sequencing; protein structure;
KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
KW human leukocyte antigen; PCR primer; 88.
XX Homo sapiens.
XX WO200065088-A2.
XX 02-NOV-2000.
XX 20-APR-2000; 2000WO-EP003636.
XX 26-APR-1999; 99EP-00303215.
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX Ulfendahl P, Wong K;
XX WPI; 2000-679677/66.
XX Identifying extendible primers for use in identification, or
XX classification of a nucleic acid of an organism, allele or gene such as
XX class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX specific length.
XX Claim 14; Page 51; 66pp; English.
XX The present invention provides a method for identifying a set of
XX extendible primers which can be used in the identification, typing and
XX classification of genes. This can then be used to predict protein
XX sequence and structure, in organ donation to match the organ with the

```

CC correlated with an alteration in the activity or expression of a
 CC polypeptide encoded by the ESE-3 gene, by administering to the individual
 CC an agent that interferes with the function or expression of ESE-3; and
 CC identifying an agent that interferes with the function or expression of
 CC ESE-3 in an individual having a polymorphism in the ESE-3 gene, which is
 CC correlated with an alteration in the activity or expression of a
 CC polypeptide encoded by the ESE-3 gene, comprising: contacting the ESE-3
 CC gene with the agent to be tested; assessing the level of function or
 CC expression of the ESE-3 gene; and comparing the level of function or
 CC expression with the level of function or expression of the ESE-3 gene in
 CC the absence of the agent. Preferred Method: In detecting a polymorphism
 CC in the ESE-3 gene, the polymorphism is selected from a single nucleotide
 CC polymorphism (SNP) at position -40 and a SNP at position -4458. In
 CC particular, the polymorphism comprises: a SNP at position -140, where the
 CC SNP is a guanine (G) nucleotide in comparison to an adenine (A)
 CC nucleotide in the wild type ESE-3 gene; and a SNP at position -4458,
 CC where the SNP is a thymine (T) nucleotide in comparison to a cytosine (C)
 CC nucleotide in the wild type ESE-3 gene. In detecting a polymorphism in
 CC the ESE-1 gene, the polymorphism is selected from a SNP at position -
 CC 2034, a SNP at position +171, a SNP at position +949, a SNP at position
 CC +1275, a SNP at position +1639, a SNP at position +1744, or a SNP at
 CC position +2836. In particular, the polymorphism comprises: a SNP at
 CC position -2034, where the SNP is a cytosine (C) nucleotide in comparison
 CC to an adenine (A) nucleotide in the wild type ESE-1 gene; a SNP at
 CC position +171, where the SNP is a cytosine (C) nucleotide in comparison
 CC to a thymine (T) nucleotide in the wild type ESE-1 gene; a SNP at
 CC position +949, where the SNP is a thymine (T) nucleotide in comparison to
 CC a guanine (G) nucleotide in the wild type ESE-1 gene; a SNP at position
 CC +1275, where the SNP is an adenine (A) nucleotide in comparison to a
 CC cytosine (C) nucleotide in the wild type ESE-1 gene; a SNP at position
 CC +1639, where the SNP is an adenine (A) nucleotide in comparison to a
 CC guanine (G) nucleotide in the wild type ESE-1 gene; or a SNP at position
 CC +1744, where the SNP is an adenine (A) nucleotide in comparison to a
 CC guanine (G) nucleotide in the wild type ESE-1 gene. In detecting the ESE-
 CC 2 gene, the polymorphism is a SNP at position -151, where the SNP is a
 CC cytosine (C) nucleotide in comparison to a guanine (G) nucleotide in the
 CC wild type ESE-2 gene. In method (1), treating an autoimmune disease in an
 CC individual comprises: screening an individual for a genetic
 CC predisposition to autoimmune disease by detecting the presence of a
 CC polymorphism in the ESE-3, ESE-1 or ESE-2 gene, which is correlated with
 CC an alteration in the activity or expression of a polypeptide encoded by
 CC the ESE-3, ESE-1 or ESE-2 gene; and if such a predisposition is
 CC identified, treating the individual to prevent or reduce autoimmune
 CC disease or to delay the onset of autoimmune disease. Treating or
 CC preventing autoimmune disease or inflammation in an individual having the
 CC polymorphism in the ESE-3 gene also comprises administering to the
 CC individual an agent that interferes with the function or expression of
 CC ESE-3. This agent blocks the function or expression of ESE-3. In method
 CC (2), assaying a sample for the presence of a polymorphism in the ESE-3
 CC gene comprises contacting the sample with an antibody that specifically
 CC binds to the encoded polypeptide. The method also comprises: contacting
 CC the sample with a nucleic acid comprising a contiguous nucleotide
 CC sequence which is at least partially complementary to the ESE-3 gene
 CC under conditions appropriate for hybridization; and assessing whether
 CC hybridization has occurred between an ESE-3 gene and the nucleic acid
 CC comprising a contiguous nucleotide sequence which is at least partially
 CC complementary to the ESE-3 gene. Preferably, the nucleic acid comprising
 CC a contiguous nucleotide sequence is completely complementary to the ESE-3
 CC gene nucleic acid. The method further comprises amplification of the ESE-
 CC 3 gene nucleic acid, immunosuppressive; Antidiabetic; Neuroprotective;
 CC Antiinflammatory; Dermatological; Antipsoriatic; Anticanceric; No
 CC biological data given. ESE-3 Modulator; ESE-2 Modulator; ESE-1 Modulator.
 CC The method is useful for diagnosing the presence, predisposition to, or
 CC susceptibility to an autoimmune disease, e.g. diabetes (e.g. Type I
 CC diabetes or Type II diabetes), multiple sclerosis, rheumatoid arthritis,
 CC lupus, psoriasis, asthma, myasthenia gravis, Sjogren's syndrome,
 CC Hashimoto's thyroiditis, pemphigus vulgaris, or inflammation (e.g.
 CC atherosclerosis, rheumatoid arthritis, or inflammation associated with
 CC restenosis). The method is also useful for preventing or treating any of
 CC these diseases (all claimed).

Query Match 0.3%; Score 18.8; DB 1; Length 28;
 Best Local Similarity 90.9%; Pred. No. 7.1e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7414 AGCAGCAGCAGCAGCAGCAGCA 7435
 Db 23 AGCAGCAGCAGCAGCAGCAGCCCA 2
 RESULT 706
 AAC96303 standard; DNA; 25 BP.
 XX AAC96303:
 AC AAC96303:
 DT 26-FEB-2001 (first entry)
 XX
 DE HLA DPB1 gene PCR primer #35.
 XX
 KM DNA sequence analysis; sequencing; protein sequence; protein structure;
 KM gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
 KM human leukocyte antigen; PCR primer; ss.
 XX Homo sapiens.
 OS
 PN WO200065088-A2.
 XX
 PD 02-NOV-2000.
 XX
 XX 20-APR-2000; 2000WO-EP003636.
 PF
 XX 26-APR-1999; 99EP-00303215.
 PR
 XX (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 PA
 XX Ulfendahl P, Wong K;
 PI
 XX WPI; 2000-679677/66.
 DR
 XX
 PT Identifying extendible primers for use in identification, or
 PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 PT
 XX
 PS Claim 14; Page 49; 66pp; English.
 XX
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
 CC particular
 CC
 XX
 SQ Sequence 25 BP; 2 A; 3 C; 17 T; 0 U; 0 Other;
 QY
 Db 1 TTTT TTTT TTTT TTTT GCTGAGAC 4493
 1 TTTT TTTT TTTT TTTT GCTGAGAC 25
 Query Match 0.2%; Score 18.6; DB 1; Length 25;
 Best Local Similarity 84.0%; Pred. No. 6.5e+02;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4469 TTTT TTTT TTTT TTTT GCTGAGAC 4493
 Db 1 TTTT TTTT TTTT TTTT GCTGAGAC 25
 RESULT 707
 AAC96229
 ID AAC96229 standard; DNA; 25 BP.
 XX AAC96229:
 AC AAC96229:
 XX
 DT 26-FEB-2001 (first entry)
 XX

PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
 XX Lee J, Kim Y, Kang H, Pyun K, Choi I;
 XI WPI; 2001-146043/15.
 XX
 XX PT Treatment of hepatocirrhosis comprises administering an extract of the
 PT of Stephania tetrandra in an amount effective to inhibit production
 PT of interleukin-6.
 XX
 XX PS Example 4; Col 9; 27pp; English.
 XX
 CC The present sequence was used in an example to illustrate a method for
 CC treating hepatocirrhosis. The method comprises administering an extract
 CC of the root of Stephania tetrandra in an amount effective to inhibit
 CC production of interleukin-6 (IL-6). Hepatocirrhosis is often associated
 CC with chronic hepatitis or chronic alcoholism
 XX
 SQ Sequence 26 BP; 0 A; 4 C; 4 G; 18 T; 0 U; 0 Other;
 Query Match 0.3%; Score 18.8; DB 1; Length 26;
 Best Local Similarity 90.9%; Pred. No. 6.4e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 4460 GGACCTTTTCTTTTCTTTTCTTTT 4481
 Db 5 GGCCTTTTCTTTTCTTTTCTTTT 26
 RESULT 704
 AB080985
 ID AB080985 standard; DNA; 27 BP.
 AC AB080985;
 XX
 DT 07-JAN-2003 (first entry)
 XX
 DE Human prostacyclin synthetase PCR primer #4.
 XX
 KW Human; prostacyclin synthetase; diagnosis; myocardial infarction;
 KW polymorphism; Variable Number of Tandem Repeat; PCR; primer;
 XX Single Nucleotide Polymorphism; SNP; ss.
 OS Homo sapiens.
 XX
 JP2002136291-A.
 PN
 XX
 PD 14-MAY-2002.
 XX
 PF 02-NOV-2000; 2000JP-00336676.
 XX
 PR 02-NOV-2000; 2000JP-00336676.
 XX
 PA (UYN1-) UNIV NIPPON.
 XX
 DR WPI; 2003-002979/01.
 XX
 XX PT An oligonucleotide used for determination of genetic factor of myocardial
 PT infarction by analysis of polymorphism of human prostacyclin synthetase
 PT gene.
 XX
 XX PS Example 2; Page 6; 9pp; Japanese.
 XX
 CC The present invention relates to a method for genetic diagnosis of
 CC myocardial infarction. The method involves analysis of human prostacyclin
 CC synthetase gene polymorphisms, specifically, determination of repetitive
 CC number of Variable Number of Tandem Repeat polymorphisms having a
 CC repetitive unit of CCGCCGACC, and determination of a Single Nucleotide
 CC Polymorphism (SNP) at position 182 (either A or C). The present sequence
 CC is a PCR primer for human prostacyclin synthetase gene, used in the
 CC method of the invention
 XX
 SQ Sequence 27 BP; 8 A; 8 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.3%; Score 18.8; DB 1; Length 27;
 Best Local Similarity 90.9%; Pred. No. 6.7e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 7412 TCAGCAGCAGCAGCAGCAGCAG 7433
 Db 5 TCAGTACGACGACGACGACGACG 26
 RESULT 705
 ADE50831/C
 ID ADE50831 standard; DNA; 28 BP.
 AC ADE50831;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE TGF-beta1 gene SNP #1.
 XX
 KW ss; single nucleotide polymorphism; immunosuppressive; antidiabetic;
 KW neuroprotective; antirheumatic; antiarthritic; thyrometric;
 KW antiarteriosclerotic; antiinflammatory; dermatological; antipsoriatic;
 KW antiashtmatic; diagnosis; autoimmune disease; ESE-3; ESE-2; ESE-1;
 KW diabetes; multiple sclerosis; rheumatoid arthritis; lupus; psoriasis;
 KW asthma; myasthenia gravis; Sjogren's syndrome; Hashimoto's thyroiditis;
 KW pemphigus vulgaris; atherosclerosis; rheumatoid arthritis; restenosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Variation replace(14,T)
 FT /*tag= a
 XX
 XX WO2003034896-A2.
 XX
 PD 01-MAY-2003.
 XX
 PF 15-OCT-2002; 2002WO-US032116.
 XX
 PR 12-OCT-2001; 2001US-0329158P.
 XX
 PR 26-APR-2002; 2002US-0376139P.
 XX
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX
 PI Libermann T, Tautu O, Grall F, Gu X;
 XX
 DR WPI; 2003-441218/41.
 XX
 PT Diagnosing the presence, predisposition or susceptibility to an
 PT autoimmune disease e.g. diabetes or multiple sclerosis, comprises
 PT detecting a polymorphism in the ESE-3, ESE-1 or ESE-1 genes.
 XX
 XX PS Disclosure; Fig 1B; 96pp; English.
 XX
 CC Diagnosing an autoimmune disease, a predisposition or a susceptibility to
 CC the disease, comprises detecting a polymorphism in the ESE-3, ESE-2 or
 CC ESE-1 genes, which is correlated with an alteration in the activity or
 CC expression of a polypeptide encoded by these genes. Detection of the
 CC polymorphism is indicative of the occurrence, predisposition or
 CC susceptibility to autoimmune disease. INDEPENDENT CLAIMS are included for
 CC the following: Treating autoimmune diseases in an individual; Assaying a
 CC sample for the presence of a polymorphism in the ESE-3 gene; Reagent kits
 CC for assaying a sample for the presence of a polymorphism in the ESE-3
 CC gene, which is correlated with an alteration in the activity or
 CC expression of a polypeptide that is encoded by the ESE-3 gene,
 CC comprising: in separate containers: one or more labeled antibodies which
 CC specifically binds to the polypeptide; and reagents for detecting the
 CC label; or in separate containers: one or more labeled nucleic acids
 CC comprising a contiguous nucleic acid sequence that is at least partially
 CC complementary to a part of the ESE-3 nucleotide sequence; and reagents
 CC for detecting the label; interfering with the function or expression of
 CC ESE-3 in an individual having a polymorphism in the ESE-3 gene, which is

Db 5 TGCAGTTTTTTTTTTTTTTT 26

RESULT 701

AAK04087 AAX04087 standard; DNA; 26 BP.

XX AAX04087;

XX 12-APR-1999 (first entry)

XX PUR-alpha RACE reaction primer PDT-01.

XX PUR element; PUR-alpha; hyperproliferative disease; cancer; human;

XX monoclonal antibody; identification; characterisation; RACE primer; ss.

XX Synthetic.

XX Homo sapiens.

XX US5869622-A.

XX 09-FEB-1999.

XX 07-JUN-1995; 95US-00486809.

XX 28-AUG-1992; 92US-00938189.

XX 02-FEB-1993; 93US-00014943.

XX 06-JUN-1995; 95US-00470911.

XX (MOUN) MOUNT SINAI SCHOOL MEDICINE.

XX Bergemann AD, Johnson EM;

XX WPI; 1999-152881/13.

XX Monoclonal antibody specific for PUR protein - useful for treating

XX cancer.

XX Example; Col 9; 64pp; English.

XX The present invention describes a monoclonal antibody that specifically

XX binds to an epitope of the PUR protein. Antibodies that bind to the PUR

XX protein and neutralise PUR activity may be used to treat

XX hyperproliferative diseases such as cancer. PUR antibodies may be used

XX diagnostically to detect aberrant expression of the PUR protein and/or

XX mutations in the PUR gene. The present sequence represents a PUR-alpha

XX RACE primer which is used in an example from the present invention

XX Sequence 26 BP; 2 A; 2 C; 2 G; 20 T; 0 U; 0 Other;

XX Query Match 0.3%; Score 18.8; DB 1; Length 26;

XX Best Local Similarity 90.9%; Pred. No. 6.4e+02;

XX Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 4459 TGCAGTTTTTTTTTTTTTTT 4480

XX 5 TGCAGTTTTTTTTTTTTTTT 26

XX RESULT 702

XX AAH91547

XX AAH91547 standard; DNA; 26 BP.

XX AAH91547;

XX 09-OCT-2001 (first entry)

XX Human inflammatory bowel disease associated polymorphic site #622.

XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;

XX single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

XX chromosome 5q31-33; forensic test; gene therapy; ds.

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX FT misc_feature

XX FT 11

XX FT /*tag= a

XX FT /note= "SNP, optionally T or A at this position"

XX WO200142511-A2.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US033632.

XX 10-DEC-1999; 99US-0170257P.

XX 10-APR-2000; 2000US-0196046P.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.

XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;

XX WPI; 2001-367874/38.

XX Testing for the presence of polymorphisms associated with inflammatory

XX bowel disease, using a hybridization assay.

XX Claim 1; Page 65; 463pp; English.

XX The present invention describes a method for detecting the presence of

XX CC polymorphisms associated with inflammatory bowel diseases such as

XX CC ulcerative colitis and Crohn's disease. The methods can be used to detect

XX CC the presence of genetic polymorphisms associated with inflammatory bowel

XX CC disease and correlating their occurrence with disease states. They may be

XX CC used in this way for phenotypic correlations, forensics, paternity

XX CC testing, medicine and genetic analysis. The present sequence is a

XX CC polymorphic site described in the exemplification of the invention

XX Sequence 26 BP; 5 A; 1 C; 3 G; 16 T; 0 U; 1 Other;

XX Query Match 0.3%; Score 18.8; DB 1; Length 26;

XX Best Local Similarity 87.0%; Pred. No. 6.4e+02;

XX Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX 4456 GCATGACTTTTTTTTTTTTTT 4478

XX 4 GCAAGAAATTTTTTTTTTTTTT 26

XX RESULT 703

XX AAC93128

XX AAC93128 standard; DNA; 26 BP.

XX AAC93128;

XX 21-MAR-2001 (first entry)

XX Stephanian tetrandra S. moore RNA reverse transcriptase primer Noci-dT.

XX Stephanian tetrandra S. moore; IL-6; interleukin-6; hepatocarcinoma;

XX antiinflammatory; hepatocirrhosis; hepatitis; alcoholism; primer; ss.

XX Unidentified.

XX US6162437-A.

XX 19-DEC-2000.

XX 25-NOV-1997; 97US-00978321.

XX 05-JUN-1995; 95MO-KR000073.

XX 06-DEC-1996; 96US-00750462.

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XX PI Bergemann AD, Johnson EM;
XX DR WPI; 1997-488859/45.
XX PT Assays for PUR protein ligands or modulators - using immobilised PUR
XX protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.
XX PS Disclosure; Col 9; 64pp; English.
XX CC The primers AAT9265-T99269 were used to PCR amplify and isolate the
XX complete sequence of the human PUR-alpha gene (AAT9264). The PUR
XX sequence can be used to identify chemical or biological compounds that
XX bind to PUR or binding fragments of PUR. Inhibitors of PUR activity may
XX be used to treat hyperproliferative diseases such as cancer.
XX SQ Sequence 26 BP; 2 A; 2 C; 2 G; 20 T; 0 U; 0 Other;

Query Match          0.3%; Score 18.8; DB 1; Length 26;
Best Local Similarity 90.9%; Pred. No. 6.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4459 TCGACTTTTGTGTTT 4480
DB 5 TCGACTTTTGTGTTT 26

RESULT 699
AAT93819
ID AAT93819 standard; DNA; 26 BP.
XX AC AAT93819;
XX DT 25-MAR-2003 (revised)
XX DT 24-FEB-1998 (first entry)
XX DE Antitumoural phosphodiester oligonucleotide 9 with cytotoxic activity.
XX KW Phosphodiester; selective binding; cell viability; growth;
XX KW tumoural cell line; cytotoxic activity; tumour cell; lymphoma;
XX KW lymphoblastic tumour; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..26 a
XX FT /tag= a
XX FT /note= "phosphodiester oligonucleotide"
XX PN WO9720924-A1.
XX PD 12-JUN-1997.
XX PF 04-DEC-1996; 96WO-EP005388.
XX PR 04-DEC-1995; 95IT-MI002539.
XX PA (SAIC-) SAICOM SRL.
XX PI Scagliante B, Quadrifoglio F;
XX DR WPI; 1997-319771/29.
XX PT New phosphodiester oligonucleotide(s) - which exert a specific and
XX selective cytotoxic effect on tumour cells, for treating both solid and
XX liquid tumours.
XX PS Claim 10; Page 5; 38pp; English.
XX CC Novel phosphodiester oligonucleotides AAT93811-27 are based on the
XX genetic formula, in the 3'-5' or 5'-3' direction: (Gata')a''-(Gbtb')b''-
XX (Gctc')c''-(Gdtd')d''-(Gete')e''-(Gftr')f''-(G-grg')g''-N', where: N and
XX N' = T or G, equal or different from each other; x = 0-8, equal or

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CC different from each other; a, b, c, d, e, f, and g = 0-10, equal or
CC different from each other; a', b', c', d', e', f', and g' = 0-30, equal
CC or different from each other; a'', b'', c'', d'', e'', f'', and g'' = 1-
CC 16, equal or different from each other; The oligonucleotides are believed
CC to selectively bind and sequester some proteins which are essential to
CC the viability and growth of tumoural cell line. They have specific and
CC selective cytotoxic activity against tumour cells, and can be used for
CC treating tumours of the liquid type, in particular of lymphoblastic
CC origin, and of solid type, in particular lymphomas. The present
CC phosphodiester oligonucleotide, at a concentration of 15 micromolar,
CC reduced growth of CCRF-CEM tumoural cells by 76%, which is detectable 48
XX hours after administration. (Updated on 25-MAR-2003 to correct PR field.)
XX SQ Sequence 26 BP; 0 A; 0 C; 2 G; 24 T; 0 U; 0 Other;

Query Match          0.3%; Score 18.8; DB 1; Length 26;
Best Local Similarity 90.9%; Pred. No. 6.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4467 TTTTGTGTTTGTGTTT 4488
DB 1 TTTTGTGTTTGTGTTT 22

RESULT 700
AAV31721
ID AAV31721 standard; DNA; 26 BP.
XX AC AAV31721;
XX DT 24-SEP-1998 (first entry)
XX DE Nucleotide sequence of the PUR specific PCR primer.
XX KW PUR-alpha gene; inhibition; viral infection; cancer; PCR; primer;
XX KW hyperproliferative disease; amplification; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN US5756684-A.
XX PD 26-MAY-1998.
XX PF 06-JUN-1995; 95US-00470911.
XX PR 28-AUG-1992; 92US-00938189.
XX PR 02-FEB-1993; 93US-00014943.
XX PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX PI Bergemann AD, Johnson EM;
XX DR WPI; 1998-321632/28.
XX PT PUR protein and its fragments - that inhibit PUR protein binding to PUR
XX element or other proteins.
XX PS Disclosure; Col 9; 63pp; English.
XX CC This is the nucleotide sequence of the PUR pssific PCR primer used for
XX amplification in the method of the invention, involving the use of the
XX PUR protein and its fragments, which inhibit PUR protein binding to PUR
XX element or other proteins. Inhibitors of PUR activity may be useful for
XX treating viral infections and hyperproliferative diseases such as cancer
XX SQ Sequence 26 BP; 2 A; 2 C; 2 G; 20 T; 0 U; 0 Other;

Query Match          0.3%; Score 18.8; DB 1; Length 26;
Best Local Similarity 90.9%; Pred. No. 6.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4459 TCGACTTTTGTGTTT 4480

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CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstructed as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL4257 to ABL4532 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL4532 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention

XX
SQ Sequence 25 BP; 18 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 0.3%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 6.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4463 CTTTCTTTCTTTCTTTCTTTG 4484
DB 22 CTTTCTTTCTTTCTTTCTTTG 1

RESULT 692
ADB04569
ID ADB04569 standard; DNA; 25 BP.
XX
AC ADB04569;
XX
DT 20-NOV-2003 (first entry)
DE Human MD27 scanning oligonucleotide SEQ ID 5555.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
XX Homo sapiens.
OS
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
PI WP1; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5553; 103pp; English.

XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as

CC vaccines. The present sequence was used to illustrate the invention.

XX
SQ Sequence 25 BP; 3 A; 1 C; 3 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 6.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4460 GGACTTTTCTTTCTTTCTTTT 4481
DB 2 GGACTTTTCTTTCTTTCTTTT 23

RESULT 693
ADB04567
ID ADB04567 standard; DNA; 25 BP.
XX
AC ADB04567;
XX
DT 20-NOV-2003 (first entry)
DE Human MD27 scanning oligonucleotide SEQ ID 5553.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
XX Homo sapiens.
OS
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
PI WP1; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5553; 103pp; English.

XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.

XX
SQ Sequence 25 BP; 2 A; 1 C; 4 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 6.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

PD	16-JAN-2002.
XX	
PF	28-JUN-2000; 2000CN-00116823.
XX	
PR	28-JUN-2000; 2000CN-00116823.
XX	
PA	(BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX	
PI	Mao Y, Xie Y;
XX	
DR	WPI; 2002-305482/35.
XX	
PT	Polypeptide-human cyclophilin-40-12.54 and polynucleotide for coding it.
XX	
PS	Example 2; Page 17 (Disclosure); 33pp; Chinese.
XX	
CC	The present invention provides the protein and coding sequences of human
CC	cyclophilin-40-12.54. The sequences can be used in the treatment of
CC	immunity and cancer. The present sequence is a PCR primer for the
CC	coding sequence of the invention
XX	
SQ	Sequence 24 BP; 2 A; 1 C; 2 G; 19 T; 0 U; 0 Other;
Qy	Query Match 0.3%; Score 18.8; DB 1; Length 24;
	Best Local Similarity 90.9%; Pred. No. 5.7e+02;
Db	Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0
	4464 TTTTTTTTTTTTTTTTTTTTGT 4485
	1 TTTTTTTCTTTTTTTTTTTAGT 22
RESULT 690	
AAT27193/C	
ID	AAT27193 standard; DNA; 25 BP.
XX	
AC	AAT27193;
XX	
DT	20-NOV-1996 (first entry)
XX	
DE	Stem loop oligonucleotide targeted to p53 chromosomal binding site.
XX	
KW	Stem loop; target; secondary structure; parallel binding domain;
KW	antiparallel; replication inhibitor; cell growth inhibitor; p53;
KW	detection; stable; strong affinity; nuclease resistant;
KW	Watson-Crick bonding; Hoogsteen bonding; ss.
XX	
OS	Synthetic.
XX	
Key	Location/Qualifiers
FT	1..25
FT	/tag= a
FT	/note= "loop without stem structure"
FT	3..10
FT	/tag= b
FT	/note= "target binding area"
FT	16..23
FT	/tag= c
FT	/note= "target binding area"
XX	
PN	US5514546-A.
XX	
PD	07-MAY-1996.
XX	
PE	01-SEP-1993; 93US-00115497.
XX	
PR	01-SEP-1993; 93CA-02105364.
XX	
PA	(RESE) RESEARCH CORP TECHNOLOGIES INC.
XX	
PI	Kool ET;
XX	
DR	WPI; 1995-162088/22.

Stem-loop oligo:nucleotide(s) contain parallel and antiparallel binding domains - for binding target nucleic acids, to regulate biosynthesis of nucleic acid or protein in a cell, for treating e.g. cancer.

Example 1; Col 30; 34pp; English.

AAT727193-727198 and AAT727200 are stem loop oligonucleotides directed towards chromosomal sites normally bound by p53 (see AAT75519). The stem loop oligonucleotides bind with strong affinity and high selectivity to their target nucleic acids, they are also nuclease resistant. They are used to inhibit cell growth and DNA replication and other processes involving a nucleic acid template. In addition to this the oligonucleotides may be used for the detection and isolation of target nucleic acids and for cell type-specific drug delivery. The stem loops bind to their target via a system of co-operative Watson-Crick bonding and Hoogsteen bonding

Sequence 25 BP; 0 A; 7 C; 0 G; 18 T; 0 U; 0 Other;

	Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
	0.3%;	Score 18.8; DB 1;	Length 25;	90.9%;	Pred. No. 6.1e+02;		
				0;		0;	0

OY 4017 GAGAAAAAAGAGACAAACA 4038
|||
24 GAAAAAAAAAGAGAAAAAAAAA 3

Db

RESULT 691
ABL45245/C
ID ABL45245 standard; DNA; 25 BP.
XX
XX AC ABL45245;
XX DT 11-APR-2002 (first entry)
DE Human chromosome 1p36-35 PCR primer SEQ ID NO:2289.
XX
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KM PCR primer; ss.
XX Homo sapiens.
OS JP2001321190-A.
PN 20-NOV-2001.
PD 12-MAR-2001; 2001JP-00068285.
PF 10-MAR-2000; 2000JP-0006716.
PR (RIKA) RIKAGAKU KENKYUSHO.
PA (GENO-) GENOTEX YG.
XX WPI; 2002-144136/19.
DR
XX
XX Arraying genome clones.
PT
XX Claim 4; Page 49; 528bp; Japanese.
PS
XX
XX The present invention describes a method of arraying genome clones. The CC method comprises: (a) clones of the genomic libraries contained in CC multiwell plates numbered for discrimination are mixed in each of the CC multiwell plates; (b) a primer designed based on the chromosome marker CC sequence is added to the mixture to carry out an amplification reaction; CC (c) a signal corresponding to the marker is detected from the resultant CC amplified product to specify the discrimination Nos. of the multiwell CC plates containing the clones having said marker sequence; (d) the order CC of the markers is changed so that the same discrimination Nos. succeed to CC the maximum in the specified discrimination Nos. to array the multiwell CC plates; (e) the clones in the multiwell plates of the specified CC discrimination Nos. are mixed respectively in each wells of longitudinal

QY 4459 TGGACCTTTTCTTTTCTTTT 4480
 DB 2 TCGAGTTTCTTTTCTTTTCTTT 23

RESULT 687
 ID AAH24266 standard; DNA; 24 BP.
 XX
 AC AAH24266;
 XX

DT 11-SEP-2001 (first entry)

XX Human phosphatase 79 RT-PCR primer, SEQ ID NO:4.

XX
 DE Phosphatase 79; human; BAC clone CTB-54D4-encoded protein homologue;
 XX recombinant production; malignant tumour; cancer; blood disease;
 KM HIV infection; human immunodeficiency virus; immune disorder;
 KM inflammatory condition; cytostatic; anti-HIV; antiinflammatory;
 KM immunomodulator; reverse transcription-PCR; RT-PCR primer; ss.

XX Homo sapiens.

XX WO200138385-A1.

XX 31-MAY-2001.

XX 20-NOV-2000; 2000MO-CN000459.

XX 22-NOV-1999; 99CN-00124059.

XX (BIOR-) BIORAD GENE DEV LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2001-355903/37.

XX Human phosphatase 79 and encoded polynucleotide, applicable in diagnosis
 PT and treatment of malignant tumor, hemopathy, HIV infection, immunological
 PT diseases and various inflammation.

XX Example 3; Page 12; 38pp; Chinese.

XX The invention relates to human phosphatase 79 (AAH23700), nucleic acids
 CC encoding it (AAH24264), and a method for the recombinant production of
 CC human phosphatase 79. The present invention additionally discloses an
 CC agonist of phosphatase 79 for therapeutic use, and an antibody which
 CC specifically binds to human phosphatase 79. Human phosphatase 79, and
 CC nucleotides which encode it may be used for treating a variety of
 CC diseases, such as malignant tumours, blood diseases, HIV (human
 CC immunodeficiency virus) infection, immune disorders and inflammatory
 CC conditions. The protein may also be used to screen for modulators of its
 CC activity or for peptide fingerprinting identification. The polynucleotide
 CC can be used as a primer for nucleic acid amplification reaction or as a
 CC probe for hybridisation reactions, or in producing gene chips or
 CC microarrays. Sequences AAH24265-AAH24266 represent reverse transcription-
 CC PCR (RT-PCR) primers used in an exemplification of the invention to
 CC isolate human phosphatase 79 cDNA

XX SQ Sequence 24 BP; 2 A; 0 C; 0 G; 22 T; 0 U; 0 Other;

Query Match 0.3%; Score 18.8; DB 1; Length 24;
 Best Local Similarity 90.9%; Pred. No. 5.7e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4462 ACTTTTCTTTTCTTTTCTTTT 4483
 DB 3 ATTATTTTCTTTTCTTTTCTTT 24

RESULT 688
 ABK13715
 ID ABK13715 standard; DNA; 24 BP.

XX
 AC ABK13715;
 XX
 DT 23-APR-2002 (first entry)

XX RT-PCR primer #2 for human transcriptional activation subunit 14 cDNA.

XX Human; transcriptional activation subunit 14; malignant neoplasm;
 KM haematopathy; cytostatic; HIV infection; human immunodeficiency virus;
 KM immunological disease; inflammation; virocid; immunomodulatory;
 KM antiinflammatory; reverse transcriptase-PCR; RT-PCR; primer; ss.

XX Homo sapiens.

XX WO200194403-A1.

XX 13-DEC-2001.

XX 14-MAY-2001; 2001MO-CN000753.

XX 16-MAY-2000; 2000CN-00115720.

XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX Mao Y, Xie Y;

XX WPI; 2002-090139/12.

XX Human transcriptional activation subunit 14 and encoding polynucleotide,
 PT used in diagnosis and treatment of malignant tumors, hemopathy, human
 PT immunodeficiency virus infection, immunological diseases and
 PT inflammation.

XX Example 2; Page 17; 36pp; Chinese.

XX The present invention relates to the isolation of human transcriptional
 CC activation subunit 14, and the polynucleotide encoding it. Also described
 CC is the process for preparing the protein by DNA recombination and the
 CC application of the polypeptide and polynucleotide in treating various
 CC diseases such as malignant neoplasms, haematopathy, human
 CC immunodeficiency virus (HIV) infection, immunological diseases, and
 CC various inflammations. Antagonists against the polypeptide can also be
 CC used in treating such diseases. The present sequence for reverse
 CC transcriptase (RT)-PCR primer #2 is used with RT-PCR primer #1 (ABK13714)
 CC for isolating cDNA encoding human transcriptional activation subunit 14

XX SQ Sequence 24 BP; 0 A; 2 C; 2 G; 20 T; 0 U; 0 Other;

Query Match 0.3%; Score 18.8; DB 1; Length 24;
 Best Local Similarity 90.9%; Pred. No. 5.7e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4463 CTTTCTTTTCTTTTCTTTTCT 4484
 DB 3 CTTTCTTTTCTTTTCTTTTCTTG 24

RESULT 689
 AAL47515
 ID AAL47515 standard; DNA; 24 BP.

XX AAL47515;

XX 13-SEP-2002 (first entry)

XX Human cyclophilin-40-12-54 coding sequence PCR primer #2.

XX Human; cyclophilin-40-12.54; immunopathy; cancer; PCR; primer; ss.

XX Homo sapiens.

XX CN1331162-A.

XX

XX Novel maize cytochrome P450 monooxygenase cDNA used to confer herbicide
PT resistance to plants.
XX
XX Example 1c; Fig 5; 85pp; English.
XX
CC The invention relates to maize cytochrome P450 monooxygenase CYP71C3V2
CC (AA177222) and nucleotides which encode it. CYP71C3V2 cDNA was generated
CC via reverse transcriptase-PCR (RT-PCR) from poly (A)+ mRNA isolated from
CC naphthalic anhydride and herbicide (trifluralin)-treated maize
CC seedlings. This was used to construct a cDNA library, which was screened
CC using previously generated cDNA as hybridisation probes. The CYP71C3V2
CC cDNA clone was extended via 5' RACE (rapid amplification of cDNA ends)
CC and cloned into plasmid. Genomic DNA was also screened for clones
CC encoding CYP71C3V2 - this was found to contain 2 introns (AA287321-
CC 287322). Cytochrome P450 monooxygenase CYP71C3V2 reductively cleaves
CC molecular dioxygen to produce functionalised organic substrates.
CC Nucleotides encoding cytochrome P450 monooxygenase CYP71C3V2 are used to
CC produce transgenic plants with increased resistance to herbicides, such
CC as trifluralin. When such transgenic plants are grown, undesired
CC vegetation such as pigweed, velvet leaf, lambs quarters, Chenopodium
CC album and quack grass, can easily be controlled. The methods may also be
CC used to identify those compounds with herbicidal activity. Sequences
CC AA287323-287335 represent PCR primers used to isolate, clone and study
CC maize CYP71C3V2 nucleotide sequences in the exemplifications and the
CC disclosure of the present invention
XX
SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4460 GGACTTTTCTTTTCTTTTCTTTT 4481
DB 2 GGAACTCTTTTCTTTTCTTTTCTTTT 23

RESULT 686
AA250028
ID AA250028 standard; DNA; 23 BP.
XX
AC AA250028;
XX
DT 25-APR-2000 (first entry)
XX
DE Oligo dT primer 3'PC-1, for RNA extraction from maize seedling.
XX
XX Cytochrome P450 monooxygenase; CYP71C3V2; maize; chromosome 4p; weed;
KM P450 gene; molecular dioxygen; herbicidal; pigweed; transgenic organism;
KM herbicide resistant; trifluralin; quack grass; velvet leaf; PCR primer;
KM labs quarter; Chenopodium album; naphthalic anhydride; ss.
XX
XX Zea mays.
OS
XX
XX MO200000502-A1.
PN
XX
PD 06-JAN-2000.
XX
PF 23-JUN-1999; 99MO-US014117.
XX
PR 26-JUN-1998; 98US-0090759P.
XX
PA (UNIT) UNIV ILLINOIS FOUND.
XX
PI Schuler MA, Persans MW;
XX
DR MPI; 2000-170902/15.
XX
XX Novel maize cytochrome P450 monooxygenase polypeptides and
PT polynucleotides, used to confer trifluralin herbicide resistance to
XX plants.

PS Example 1c; Page 52; 77pp; English.
XX
XX The present sequence is the oligo (dT) non-degenerate RT-PCR primer, 3'PC
CC -1, complementary to the poly(A) tract of the CYP71C3V2 mRNA. It is used
CC to extract and amplify mRNA isolated from naphthalic anhydride-treated
CC maize seedlings. The CYP71C3V2 gene is mapped to a single locus on the
CC short arm of maize chromosome 4 (4p). CYP71C3V2 reductively cleaves
CC molecular dioxygen to produce functionalised organic substrates. It has
CC herbicidal activity. CYP71C3V2 polynucleotides are used to produce
CC transgenic organisms, such as yeast, plants and bacteria that are
CC resistant to herbicides, such as trifluralin. Undesired vegetation,
CC e.g. weed, pigweed, velvet leaf, labs quarters, Chenopodium album and
CC quack grass, can easily be controlled when such transgenic plants are
CC grown. Transformed organisms can also be used to identify compounds with
CC herbicidal activity
XX
SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4460 GGACTTTTCTTTTCTTTTCTTTT 4481
DB 2 GGAACTCTTTTCTTTTCTTTTCTTTT 23

RESULT 686
ABA97431
ID ABA97431 standard; DNA; 23 BP.
XX
AC ABA97431;
XX
DT 21-MAR-2002 (first entry)
XX
DE Glycosyltransferase genes PCR primer #2.
XX
XX Glycosyltransferase; anthocyanin; flower colour; enzyme; PCR primer; ss.
KM
XX
XX Unidentified.
OS
XX
XX MO200192509-A1.
PN
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-JP004675.
XX
PR 02-JUN-2000; 2000JP-00170436.
XX
PA (ITFL-) INT FLOWER DEV PTY LTD.
XX
PI Mizutani M, Sakakibara K, Tanaka Y, Kusumi T, Ono E;
XX
XX MPI; 2002-114345/15.
DR
XX
XX New gene encoding protein that transfers a sugar to the 3' position of
PT anthocyanin for changing flower color.
XX
XX Example 3; Page 13; 50pp; Japanese.
PS
XX
CC The present invention provides the genes and proteins of
CC glycosyltransferases from Gentiana triflora, Senecio cruentus and
CC Clitoria ternatea. The protein transfers a sugar to the 3' position of
CC anthocyanin, and can be used for changing the colour of flowers. The
CC present sequence is a PCR primer used to isolate glycosyltransferase
CC coding sequences of the invention
XX
SQ Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 0.3%; Score 19; DB 1; Length 35;
 Best Local Similarity 71.4%; Pred. No. 8.8e+02;
 Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3278 AAGAGAAAAATGAAACCGACCGATCAATATT 3312
 1 AAAAAAAAAAAAAAAAAATCCTTATCAATATT 35

RESULT 680

AA161662
 ID AA161662 standard; DNA; 35 BP.

AC AA161662;

DT 22-SBP-2003 (first entry)

DE Oligonucleotide #22 used in the nucleic acid detection method.

KW Nucleic acid detection; fabrication; ss.

OS Unidentified.

PN WO2003035829-A2.

PD 01-MAY-2003.

PF 08-OCT-2002; 2002WO-US032088.

PR 09-OCT-2001; 2001US-0327864P.

PR 07-DEC-2001; 2001US-00008978.

PA (NANO-) NANOSPHERE INC.

PI Park S, Taton TA, Mirkin CA;

DR WPI; 2003-430409/40.

PT Detecting nucleic acid having two portions, by providing nanoparticles having oligonucleotides attached to it, contacting nucleic acid and nanoparticles to allow hybridization, and observing detectable change.

PS Example 25; Fig 45; 467pp; English.

XX The invention relates to a method of detecting a nucleic acid having two portions. The method involves providing nanoparticles having oligonucleotides attached to it which has a sequence complementary to sequence of two portions of nucleic acid, contacting nucleic acid and nanoparticles to allow hybridization of oligonucleotides with two or more portions of nucleic acid and observing a detectable change brought about by hybridization. The method and aggregate probes are useful for detecting two or more nucleic acids (from a biological source) having at least two portions such as viral RNA, bacterial or fungal DNA, a gene associated with a disease, synthetic or structurally modified natural or synthetic RNA or DNA, or a product of a polymerase chain reaction amplification. The invention is useful for preparing a nanoprobe conjugate for detecting an analyte and for detecting a nucleic acid bound to an electrode surface. It is also useful for fabrication and for separating a selected nucleic acid having two portions from other nucleic acid. The present sequence is an oligo used to illustrate the method of the invention

XX Sequence 35 BP; 25 A; 3 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 0.3%; Score 19; DB 1; Length 35;

Best Local Similarity 71.4%; Pred. No. 8.8e+02;
 Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3278 AAGAGAAAAATGAAACCGACCGATCAATATT 3312
 1 AAAAAAAAAAAAAAAAAATCCTTATCAATATT 35

RESULT 681
 ABK8725/C
 ID ABK8725 standard; DNA; 22 BP.

AC ABK8725;

DT 07-OCT-2002 (first entry)

DE Human Pur alpha anti-sense strand, phosphorothioate oligonucleotide #4.

KW Human; apoptotic cell death; proteinaceous transcription factor;

KW translation of gene transcription; apoptosis; p53; CD95; TRA;

KW transcriptional regulator of apoptosis; Y-box family; YB-1; cancer;

KW tumour cell; embryonic cell; nervous system; intracellular pathogens;

KW DNA-damaging agent; retroviral infection; neurodegenerative disorder;

KW immune system dysfunction; anti-tumour; cytostatic; Pur alpha;

KW phosphorothioate; ss.

OS Homo sapiens.

FN Key Location/Qualifiers

FT modified_base 1..22

FT /*tag= a

FT /mod_base= OTHER

FT /note= "Phosphorothioate internucleotide linkages"

PN WO200244363-A1.

PD 06-JUN-2002.

PF 28-NOV-2001; 2001WO-NZ000287.

PR 28-NOV-2000; 2000US-00724809.

PA (GENE-) GENESIS RES & DEV CORP LTD.

PI Lasham A, Watson JD;

DR WPI; 2002-557540/59.

PT Modulating p53-mediated apoptotic cell death in a population of cells, by modulating the amount of a transcriptional regulator of apoptosis available to bind to a target polynucleotide in the cells.

PS Example 2; Page 57; 62pp; English.

XX The present invention relates to methods for modulating apoptotic cell death using proteinaceous transcription factors that regulate the transcription of genes encoding proteins involved in apoptosis (e.g. CD95 and p53). The methods involve modulating the amount of a transcriptional regulator of apoptosis (TRA) available to bind to a target polynucleotide in the cells, where TRA is a member of the Y-box nucleic acid binding family of polypeptides (e.g. YB-1). The methods of the invention are useful for modulating apoptotic cell death in a population of cells, where the cells are selected from tumour cells, cells of the immune system, embryonic cells, cells of the nervous system, or cells infected with intracellular pathogens. The methods are also useful for increasing the sensitivity of tumour cells to a DNA-damaging agent, and for increasing sensitivity to apoptosis in a population of cells harbouring intracellular pathogens. The methods are useful for screening an apoptosis modulatory agent that modulates the binding of TRA. The methods for regulating apoptosis can be used therapeutically and prophylactically for various disorders such as cancer, viral and retroviral infections, CC neurodegenerative disorders, and immune system dysfunction. The present sequence represents a phosphorothioate oligonucleotide to the anti-sense strand of human Pur alpha

XX Sequence 22 BP; 0 A; 5 C; 9 G; 8 T; 0 U; 0 Other;

Query Match 0.3%; Score 18.8; DB 1; Length 22;

Best Local Similarity 90.9%; Pred. No. 5.1e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX	Sequence	35 BP; 25 A; 3 C; 0 G; 7 T; 0 U; 0 Other;
5Q	Query Match	0.3%; Score 19; DB 1; Length 35;
	Best Local Similarity	71.4%; Pred. No. 8.8e+02;
	Matches 25; Conservative	0; Mismatches 10; Indels 0; Gaps
QY	3278 AAGAGAGAAAATGAAACCAAGCCCAAGTCAATATT	3312
DB	1 AAAAAAAAAAAAAAAAAAATCCTTATCAATATT	35
RESULT 678		
ABS64690	ABS64690 standard; DNA; 35 BP.	
ID	ABS64690 standard; DNA; 35 BP.	
XX	ABS64690;	
AC		
XX	15-NOV-2002 (first entry)	
DT		
XX	Nucleic acid detection method associated polynucleotide #2.	
DE		
XX	Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;	
KW	nanoparticle; viral RNA detection; bacterial DNA detection;	
KM	fungal DNA detection; nanoprobe conjugate; ss.	
XX		
OS	Synthetic.	
XX		
PN	WO200246472-A2.	
XX		
PD	13-JUN-2002.	
XX		
PF	07-DEC-2001; 2001WO-US046418.	
XX		
PR	08-DEC-2000; 2000US-0254392P.	
PR	08-DEC-2000; 2000US-0254418P.	
PR	11-DEC-2000; 2000US-0255235P.	
PR	11-DEC-2000; 2000US-0255236P.	
PR	12-JAN-2001; 2001US-00760500.	
PR	28-MAR-2001; 2001US-00820279.	
PR	09-APR-2001; 2001US-0282640P.	
PR	10-AUG-2001; 2001US-00927777.	
XX		
PA	(NANO-) NANOSPHERE INC.	
XX		
PI	Mitkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghamian R;	
PI	Taeon TA, Garimella V, Li Z, Park S;	
XX		
DR	WPI; 2002-608256/65.	
XX		
PT	Detecting nucleic acid having two portions, by providing nanoparticles	
PT	having oligonucleotides attached to it, contacting nucleic acid and	
PT	nanoparticles to allow hybridization, and observing detectable change.	
XX		
XX	Example 25; Fig 45; 442bp; English.	
XX		
CC	The invention describes a method of detecting (M1) a nucleic acid having	
CC	two portions, involving providing nanoparticles having oligonucleotides	
CC	attached to it, which has a sequence complementary to sequence of two	
CC	portions of nucleic acid, contacting nucleic acid and nanoparticles, to	
CC	allow hybridisation of oligonucleotides with two or more portions of	
CC	nucleic acid, and observing a detectable change brought about by	
CC	hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide	
CC	conjugates (II) and the aggregate probe are useful for detecting two or	
CC	more nucleic acids (from a biological source) having at least two	
CC	portions, such as viral RNA, bacterial or fungal DNA, a gene associated	
CC	with a disease, synthetic, or structurally-modified natural or synthetic	
CC	RNA or DNA, or a product of a polymerase chain reaction amplification.	
CC	(II) is useful for preparing a nanoprobe conjugate for detecting an	
CC	analyte, and for detecting a nucleic acid bound to an electrode surface.	
CC	(I) and (II) are useful for fabrication, and for separating a selected	
CC	nucleic acid having two portions from other nucleic acids. (I), (II) and	
CC	the aggregate probe are useful for detecting an analyte (especially	

CC polyvalent analyte) in a sample. This sequence represents a
CC polynucleotide used to demonstrate the method of the invention
XX

SQ Sequence 35 BP; 25 A; 3 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 0.3%; Score 19; DB 1; Length 35;
Best Local Similarity 71.4%; Pred. No. 8.86+02;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3278 AAGAGAAAAATGAACCGAGCCGAGTCAATT 3312
DB 1 AAAAAAAAAAAAAAAAAAATCCTTCATCATATT 35

RESULT 679
AAL61667
ID AAL61667 standard; DNA; 35 BP.
XX
AC AAL61667;
XX
DT 22-SEP-2003 (first entry)
XX
DE Oligonucleotide #26 used in the nucleic acid detection method.
XX
KW Nucleic acid detection; fabrication; ss.
XX
OS unidentified.
XX
FH Key Location/Qualifiers
FT 35
FT misc_feature /*tag= a
FT /note= "Linked to steriod disulphide"
FT
PN WO2003035829-A2.
XX
PD 01-MAY-2003.
XX
PF 08-OCT-2002; 2002WO-US032088.
XX
PR 09-OCT-2001; 2001US-0327864P.
PR 07-DEC-2001; 2001US-00008978.
PA (NANO-) NANOSPHERE INC.
PI Park S, Taton TA, Mirkin CA;
PI
XX
DR WPI, 2003-430409/40.

PT Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PS nanoparticles to allow hybridization, and observing detectable change.

Disclousure; Page 58; 467pp; English.

XX The invention relates to a method of detecting a nucleic acid having two
CC portions. The method involves providing nanoparticles having
CC oligonucleotides attached to it which has a sequence complementary to
CC sequence of two portions of nucleic acid, contacting nucleic acid and
CC nanoparticles to allow hybridisation of oligonucleotides with two or more
CC portions of nucleic acid and observing a detectable change brought about
CC by hybridisation. The method and aggregate probes are useful for
CC detecting two or more nucleic acids (from a biological source) having at
CC least two portions such as viral RNA, bacterial or fungal DNA, a gene
CC associated with a disease, synthetic or structurally modified natural or
CC synthetic RNA or DNA, or a product of a polymerase chain reaction
CC amplification. The invention is useful for preparing a nanoprobe
CC conjugate for detecting an analyte and for detecting a nucleic acid bound
CC to an electrode surface. It is also useful for fabrication and for
CC separating a selected nucleic acid having two portions from other nucleic
CC acids. The present sequence is an oligo used to illustrate the method of
CC the invention
XX

SQ Sequence 35 BP; 25 A; 3 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 0.3%; Score 19; DB 1; Length 35;
Best Local Similarity 71.4%; Pred. No. 8.8e+02;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
3278 AAGAGAAAAATGAACAGACCCAGATCAATATT 3312
1 AAAAAAAAAAAAAAAAAATCCTTATCAATATT 35

RESULT 676
ABK65052
ID ABK65052 standard; DNA; 35 BP.
XX
AC ABK65052;
XX
DT 02-JUL-2002 (first entry)
XX
DE Nanoparticle-oligonucleotide #72.
XX
KW Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
KM ss.
XX
OS Synthetic.
XX
PN WO200218643-A2.
XX
PD 07-MAR-2002.
XX
PF 10-AUG-2001; 2001WO-US025237.
XX
PR 11-AUG-2000; 2000US-0224631P.
XX
PR 08-DEC-2000; 2000US-0254392P.
XX
PR 11-DEC-2000; 2000US-0255235P.
XX
PR 12-JAN-2001; 2001US-00760500.
XX
PR 28-MAR-2001; 2001US-00820279.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z, Park S;
XX
DR WPI; 2002-258024/30.
XX
PT Detecting nucleic acid, useful for diagnosis of genetic, viral or
PT bacterial disease, comprises hybridizing nanoparticles with attached
PT oligonucleotides to nucleic acid and detecting change brought about by
PT hybridization.
XX
XX
XX Example 25; Fig 45; 412pp; English.
XX
CC The invention relates to a method of detecting a nucleic acid (NA) having
CC at least 2 portions comprising: (a) providing nanoparticles (NP) with
CC attached oligonucleotides (OGN), where OGN has a sequence complementary
CC to the sequence of NA; (b) contacting NA and NP under conditions
CC effective to allow hybridisation of OGN with NA; and (c) observing a
CC detectable change brought about by hybridisation of OGN with NA. The
CC method is useful for detecting a nucleic acid, separating a selected
CC nucleic acid from others and methods of nanofabrication. Detecting
CC analytes such as nucleic acids and proteins are useful for the diagnosis
CC of genetic, bacterial and viral diseases. The OGN-NP conjugates that use
CC cyclic disulphide linkers improve the sensitivity of diagnostic assays.
CC In particular assays using OGN-NP conjugates prepared using linkers
CC comprising a steroidal residue attached to a cyclic disulphide have been
CC found to be approximately 10 times more sensitive than assays employing
CC conjugates prepared using alkanethiols or acyclic disulphides as the
CC linker. The OGN-NP conjugates are stable allowing them to be used
CC directly in PCR solutions. Therefore conjugates added as probes to a DNA
CC target to be PCR amplified can be carried through the 30 or 40 heating
CC cooling cycles of the PCR and are still able to detect the amplicons
CC without opening the tubes and causing contamination. ABK64981-ABK65055
CC represent nanoparticle-oligonucleotides of the invention
XX
SQ Sequence 35 BP; 25 A; 3 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 0.3%; Score 19; DB 1; Length 35;
Best Local Similarity 71.4%; Pred. No. 8.8e+02;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
3278 AAGAGAAAAATGAACAGACCCAGATCAATATT 3312
1 AAAAAAAAAAAAAAAAAATCCTTATCAATATT 35

RESULT 677
ABK64695
ID ABK64695 standard; DNA; 35 BP.
XX
AC ABK64695;
XX
DT 15-NOV-2002 (first entry)
XX
DE Nucleic acid detection method associated polymnucleotide #77.
XX
KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KW nanoparticle; viral RNA detection; bacterial DNA detection;
KM fungal DNA detection; nanoprobe conjugate; ss.
XX
OS Synthetic.
XX
PN WO200246472-A2.
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046418.
XX
PR 08-DEC-2000; 2000US-0254392P.
XX
PR 08-DEC-2000; 2000US-0254418P.
XX
PR 11-DEC-2000; 2000US-0255235P.
XX
PR 11-DEC-2000; 2000US-0255236P.
XX
PR 12-JAN-2001; 2001US-00760500.
XX
PR 28-MAR-2001; 2001US-00820279.
XX
PR 09-APR-2001; 2001US-0282640P.
XX
PR 10-AUG-2001; 2001US-00927777.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z, Park S;
XX
DR WPI; 2002-608256/65.
XX
PT Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change.
XX
XX
XX Disclosure; Page 56; 442pp; English.
XX
CC The invention describes a method of detecting (M1) a nucleic acid having
CC two portions, involving providing nanoparticles having oligonucleotides
CC attached to it, which has a sequence complementary to sequence of two
CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to
CC allow hybridisation of oligonucleotides with two or more portions of
CC nucleic acid, and observing a detectable change brought about by
CC hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
CC conjugates (II) and the aggregate probe are useful for detecting two or
CC more nucleic acids (from a biological source) having at least two
CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated
CC with a disease, synthetic, or structurally-modified natural or synthetic
CC RNA or DNA, or a product of a polymerase chain reaction amplification.
CC (II) is useful for preparing a nanoprobe conjugate for detecting an
CC analyte, and for detecting a nucleic acid bound to an electrode surface.
CC (I) and (II) are useful for fabrication, and for separating a selected
CC nucleic acid having two portions from other nucleic acids. (I), (II) and
CC the aggregate probe are useful for detecting an analyte (especially
CC polyvalent analyte) in a sample. This sequence represents a
CC polymnucleotide used to demonstrate the method of the invention

DR WPI; 2002-147445/19.
XX Detecting minority genomes in viral quasi-species, useful for identifying
PT mutants responsible for drug resistance and to individualize therapy.
XX
PS Example 2; Page 55; 107pp; Spanish.
XX
CC The present invention relates to a new method for detecting minority
CC genomes, present at less than 50%, in a population of nucleic acids of a
CC viral quasi-species and having at least one mutation with respect to the
CC majority genome. The invention can be used for genetic diagnosis of viral
CC infections, especially human immune deficiency virus and hepatitis B or
CC C, particularly to detect memory minority genomes that are implicated in
CC failure of antiviral therapy, so the method may make possible design of
CC therapies customised for individual patients. The present nucleic acid
CC sequence represents the VH-WT-12 DNA sequence that was used in the
CC methods of the invention
XX
SQ Sequence 28 BP; 3 A; 1 C; 4 G; 19 T; 0 U; 1 Other;
XX
Query Match 0.3%; Score 19; DB 1; Length 28;
Best Local Similarity 81.5%; Pred. No. 6.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 4467 TTTT TTTT TTTT TTTT TTTT GCTTGAGAC 4493
Db 2 TTTT TTTT TTTT TTTT TTTT TTTT GTGTGTAAGTC 28
RESULT 670
ABK52625
ID ABK52625 standard; DNA; 28 BP.
XX
AC ABK52625;
XX
DT 27-AUG-2002 (first entry)
XX
DE Minority genome method VIH-WT-12 DNA sequence.
XX
KM Minority genome method; viral quasi-species; majority genome;
KM genetic diagnosis; viral infection; human immune deficiency virus;
KM hepatitis B; hepatitis C; antiviral therapy; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_difference 1 /*tag= a
FT /*label= unknown
FT /*note= "C6 amino linker sequence"
XX
PN WO200183815-A1.
XX
PD 08-NOV-2001.
XX
PF 27-APR-2001; 2001WO-ES000165.
XX
PR 27-APR-2000; 2000ES-00001068.
XX
PA (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
XX
PI Arias Esteban A, Baranowski E, Briones Llorente C;
PI Domingo Solans B, Escarnis Homs C, Gomez Castilla U;
PI Martin Ruiz-Jarabo C, Parro Garcia V;
XX
DR WPI; 2002-147445/19.
XX
XX Detecting minority genomes in viral quasi-species, useful for identifying
PT mutants responsible for drug resistance and to individualize therapy.
XX
PS Example 2; Page 55; 107pp; Spanish.
XX
CC The present invention relates to a new method for detecting minority

CC genomes, present at less than 50%, in a population of nucleic acids of a
CC viral quasi-species and having at least one mutation with respect to the
CC majority genome. The invention can be used for genetic diagnosis of viral
CC infections, especially human immune deficiency virus and hepatitis B or
CC C, particularly to detect memory minority genomes that are implicated in
CC failure of antiviral therapy, so the method may make possible design of
CC therapies customised for individual patients. The present nucleic acid
CC sequence represents the VH-WT-12 DNA sequence that was used in the
CC methods of the invention
XX
SQ Sequence 28 BP; 2 A; 1 C; 5 G; 19 T; 0 U; 1 Other;
XX
Query Match 0.3%; Score 19; DB 1; Length 28;
Best Local Similarity 81.5%; Pred. No. 6.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 4467 TTTT TTTT TTTT TTTT TTTT GCTTGAGAC 4493
Db 2 TTTT TTTT TTTT TTTT TTTT TTTT GTGTGTAAGTC 28
RESULT 671
AAL45359/c
ID AAL45359 standard; RNA; 28 BP.
XX
AC AAL45359;
XX
DT 06-JUN-2002 (first entry)
XX
DE Puromycin linker DNA sequence.
XX
KM Peptide cleavage; chemical active ingredient targeted release; diagnosis;
KM antiasthmatic; osteopathic; cytostatic; asthma; osteoporosis; cancer;
KM stroke; neuronal disease; arthritis; pancreatitis; hypertension;
KM thrombosis; infection; schistosomiasis; herbicide; insecticide;
KM fungicide; cerebroprotective; neurological; antiallergic; pancreatic;
KM hypotensive; antithrombotic; virucide; protozoacide; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*mod_base= OTHER
FT /*note= "modified by psoralen and 2'-O-methyl"
FT modified_base 28 /*tag= b
FT /*mod_base= OTHER
FT /*note= "modified by (PEG) 2 CC (Puromycin linker)"
XX
PN WO200216574-A2.
XX
PD 28-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-EP009102.
XX
PR 22-AUG-2000; 2000DE-01041238.
XX
PA (XZIL-) XZILLION GMBH & CO KG.
XX
PI Reinholz R, Ploeger F;
XX
DR WPI; 2002-269356/31.
XX
XX Identifying specifically cleavable peptide, useful for targeted drug
PT delivery and developing protease inhibitors, by incubating test compound
PT with peptide-nucleic acid fusion.
XX
PS Example 1; Page 19; 38pp; German.
XX
CC The present invention relates to the identification of specific
CC proteolytically cleavable peptides by incubating a library of fusion
CC molecules, comprising a peptide and nucleic acid encoding said peptide,


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XX JP2001204472-A.
XX
XX 31-JUL-2001.
PD
XX 21-JAN-2000; 2000JP-00012535.
PF
XX 21-JAN-2000; 2000JP-00012535.
PR
XX (SUMI ) SUMITOMO ELECTRIC IND CO.
PA
XX WPI; 2001-609513/70.
XX
XX New polynucleotide for the amplification of a one-side single-stranded
PT DNA and the production of a double-stranded cDNA comprises a single-
PT stranded DNA primer.
XX
XX Disclosure; Page 11; 13pp; Japanese.
XX
XX The present invention describes a single-stranded DNA primer comprising a
CC single-stranded DNA having a dtn sequence, which hybridises with the
CC polyA site of an mRNA at the 3'-terminal, and has a blocking group at the
CC 5'-terminal in which the other part constitutes an adapter double-
CC stranded DNA connected to the double-stranded cDNA. The terminal of the
CC side of the DNA is not connected to the double-stranded cDNA, which
CC consists of a base sequence having full homology to the single-stranded
CC cDNA corresponding to the 5'-terminal. A method is also described for the
CC preparation of a double-stranded cDNA in which the above single-stranded
CC DNA primer is hybridised with the polyA site of an mRNA and said single-
CC stranded DNA primer is used as the primer to reverse-transcribe said mRNA
CC and further it is converted to a double-stranded cDNA by a DNA
CC polymerase. The primer is used for the uniform amplification of DNAs. The
CC present sequence represents a PCR primer which is given in the
XX exemplification of the present invention
XX
SQ Sequence 28 BP; 3 A; 3 C; 2 G; 20 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 19; DB 1; Length 28;
Best Local Similarity 100.0%; Pred.No. 6.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 4463 CTTTCTTTTTTTTTTTTTTT 4481
Db 10 CTTTTTTTTTTTTTTTTT 28
XX
RESULT 668
AAF60450/C
ID AAF60450 standard; DNA; 28 BP.
XX
XX AAF60450;
XX
XX 27-APR-2001 (first entry)
DT
XX RNA oligonucleotide #7.
DE
XX Protein-RNA fusion; ss.
KM
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "C6-psoralen-2-Ome-U"
FT modified_base 28 /*tag= b
FT /mod_base= OTHER
FT /note= "A-TGG2"
PN WO200107657-A1.
XX
XX 01-FEB-2001.

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XX 19-JUL-2000; 2000WO-US019653.
XX
XX 27-JUL-1999; 99US-0145834P.
XX
XX (PHYL-) PHYLUS INC.
XX
XX Kurz M, Lohse P, Wagner R;
XX
XX WPI; 2001-182803/18.
XX
XX Affixing a peptide acceptor to an RNA molecule useful for producing
XX fusion proteins for isolating proteins or nucleic acids with desired
XX properties through attachment of a peptide acceptor to the 3' end of an
XX RNA molecule.
XX
XX Example 6; Page 29; 56pp; English.
XX
XX The present invention relates to a method for affixing a peptide acceptor
XX to an RNA molecule through the formation of a covalent bond, noncovalent
XX bond, or by chemical ligation. The method is useful for producing RNA-
XX protein fusions which can be used for the isolation of proteins or
XX nucleic acids with desired properties from large pools of partially or
XX completely random amino acid or nucleic acid sequences. The present
XX sequence is an RNA oligonucleotide used in the present invention
XX
XX Sequence 28 BP; 20 A; 2 C; 4 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 0.3%; Score 19; DB 1; Length 28;
XX Best Local Similarity 100.0%; Pred. NO. 6.6e+02; Mismatches 0; Gaps 0
XX Matches 19; Conservative 0; Indels 0;
XX
XX 4466 TTTTTTTTTTTTTTTTGG 4484
XX |||||||
XX 28 TTTTTTTTTTTTTTTTGG 10
XX
XX RESULT 669
XX ABRK52626
XX ID ABRK52626 standard; DNA; 28 BP.
XX
XX ABRK52626;
XX
XX 27-AUG-2002 (first entry)
XX
XX Minority genome method VIH-MUT-12 DNA sequence.
XX
XX Minority genome method; viral quasi-species; majority genome;
XX genetic diagnosis; viral infection; human immune deficiency virus;
XX hepatitis B; hepatitis C; antiviral therapy; ss.
XX
XX unidentified.
XX
XX Key Location/Qualifiers
XX misc_difference 1
XX FT /*tag= a
XX FT //label= unknown
XX FT //note= "C6 amino linker sequence"
XX
XX WO200183815-A1.
XX
XX 08-NOV-2001.
XX
XX 27-APR-2001; 2001WO-ES000165.
XX
XX 27-APR-2000; 2000ES-00001068.
XX
XX (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
XX
XX Arias Esteban A, Baranowski E, Briones Llorente C;
XX Domingo Solana E, Escarimis Homs C, Gomez Castilla J;
XX Martin Ruiz-Jarabo C, Parro Garcia V;
XX

```


FT /tag= b
FT /note= "this base represents an unspecified number of
bases"
XX
XX WO200295071-A2.
XX
XX 28-NOV-2002.
XX
XX 22-MAY-2002; 2002WO-NL000322.
XX
XX 22-MAY-2001; 2001EP-00201936.
XX
XX (NEVA-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.
XX (TIS/) TISTSTERMAN M.
XX
XX plaetserk RHA, Tjsterman M;
XX
XX WPI; 2003-129440/12.
XX
XX Determining whether a product of a gene is involved in preventing a
PT replication error in a cell comprises providing a specific inhibitor for
PT the product and determining the level of expression of a marker gene.
XX
XX Example 1; Fig 3; 47pp; English.
XX
XX The specification describes a method for determining whether a product of
CC a gene is involved in preventing a replication error in a cell. The
CC method comprises providing the cell with a specific inhibitor for the
CC product and determining the level of functional expression of a marker
CC gene in the cell, where the level of expression of the marker gene is
CC dependent on the occurrence of the replication error. The method is used
CC for determining whether a product of a gene is involved in preventing a
CC replication error in a cell. The identified genes are useful for
CC developing diagnostic tools, or as targets for drug development to
CC manipulate cells on the basis of the presence or absence of function of
CC the gene. AB22535-36 represents fragments of plasmids used to detect
CC somatic instability, in the course of the invention
XX
XX Sequence 24 BP; 20 A; 0 C; 1 G; 1 T; 0 U; 2 Other;
SQ
Query Match 0.3%; Score 19; DB 1; Length 24;
Best Local Similarity 95.0%; Pred. No. 5.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
DB 24 TTTT TTTT TTTT TTTT TTTT TTTT 5
RESULT 663
ADCT5073
ID ADCT5073 standard; DNA; 24 BP.
XX
XX AC ADCT5073;
XX
XX DT 01-JAN-2004 (first entry)
XX
XX DE Biosensor related oligonucleotide of the invention SEQ ID NO.1.
XX
XX KW ss; biosensor; hybridisation.
XX
XX OS Synthetic.
XX
XX JP2003172737-A.
XX
XX PD 20-JUN-2003.
XX
XX PF 07-DEC-2001; 2001JP-00374764.
XX
XX PR 07-DEC-2001; 2001JP-00374764.
XX
XX (TOJO) TOYO KOHAN CO LTD.
XX
XX

DR WPI; 2003-819164/77.
XX
XX Solid support body comprising crystal resonator on which a surface
PT treatment layer is formed, and a substrate whose surface treatment layer
PT is chemically modified, useful as biosensor.
XX
XX
XX Disclosure; SEQ ID NO 1; 7pp; Japanese.
XX
XX The invention relates to a novel solid support body comprising a crystal
CC resonator on which a surface treatment layer is formed. The biosensor is
CC useful for analysing biological samples e.g., gene, a protein, and a
CC peptide, and for analysing bioactive substances. Preferably, the
CC biosensor is useful for analysing base sequences by carrying out
CC hybridisation. The present sequence is used in the exemplification of the
CC invention.
XX
XX SQ Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;
SQ
Query Match 0.3%; Score 19; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4466 TTTT TTTT TTTT TTTT TTTT TTTT 4484
DB 6 TTTT TTTT TTTT TTTT TTTT TTTT 24
RESULT 664
AA172268
ID AA172268 standard; DNA; 25 BP.
XX
XX AA172268;
XX
XX 15-APR-2002 (first entry)
XX
XX DT
XX
XX P4 primer used in differential display s-AFP analysis.
XX
XX DE
XX
XX Lung; cancer; metastasis; solid tumour; blood; bone marrow; syndecan 1;
KW collagen 1 alpha 2; 7013; 7018; amplification; mammary; human; dog; cat;
KW bile duct; colon; breast; uterus; oesophagus; larynx; liver; brain; PCR;
KW remission; relapse; polymerase chain reaction; amplify; primer; ss.
XX
XX OS Synthetic.
XX
XX PN WO200196539-A2.
XX
XX PD 27-DEC-2001.
XX
XX PF 21-JUN-2001; 2001WO-US019980.
XX
XX PR 21-JUN-2000; 2000US-0215727P.
XX
XX PR 27-OCT-2000; 2000US-0243976P.
XX
XX PA (HITB) HITACHI CHEM CO LTD.
XX (HITB) HITACHI CHEM RES CENT INC.
XX (HITA) HITACHI LTD.
XX
XX PI Mitsuhashi M, Kambara H, Matsunaga H, Kawamura M;
XX
XX DR WPI; 2002-098233/13.
XX
XX PT Identifying lung cancer/metastasis of solid tumor in patient by isolating
PT blood or non-lung tissue, or bone marrow from patient and identifying
PT presence of marker e.g. syndecan 1, collagen 1 alpha 2, 7013, or 7018.
XX
XX PS Example 1; Page 6; 29pp; English.
XX
XX The sequences given in AA172265-69 are oligonucleotides which were used
CC in the method of the invention for identifying lung cancer or metastasis
CC of a solid tumour. The method comprises isolating blood (or non-lung
CC tissue in the case of identifying lung cancer, or bone marrow in case of
CC identifying metastasis) from a patient, and identifying the presence of
CC at least one marker (M) such as syndecan 1, collagen 1 alpha 2, 7013, or

QY	4466	TTTTTTTTTTTTTTTTTTG	4484
Db	6	TTTTTTTTTTTTTTTTTTG	24

1

OS Synthetic.
 XX JP2001333800-A.
 XX
 XX PD 04-DEC-2001.
 XX
 XX PF 30-MAY-2000; 2000JP-00160324.
 XX
 XX PR 30-MAY-2000; 2000JP-00160324.
 XX
 XX PA (UNIT-) UNITECH CO LTD.
 XX
 XX MPI; 2002-135950/18.
 XX
 XX Comparative detection of the amounts of RNA and DNA.
 XX
 XX PS Disclosure; Page 9; 9pp; Japanese.
 XX
 XX CC The present invention describes a method for the comparative detection of
 CC the amount of an RNA. The method comprises: (a) cDNAs obtained by
 CC transcribing respectively from at least two tissue RNAs are respectively
 CC fragmented by using a same restriction enzyme; (b) each different adaptor
 CC and a common adaptor are added to each of the cDNA fragments derived from
 CC the same or different tissues by the step (a); (c) the resultant adaptor-
 CC added cDNAs are mixed together; (d) an adaptor primer having the common
 CC sequence to said different adaptor and a gene-specific adaptor are used
 CC to amplify said adaptor-added cDNAs containing no region derived from
 CC polyadenylic acid of the mRNA before the addition of the adaptor among
 CC the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the
 CC cDNA amounts are measured between the tissues; (f) the RNA is detected
 CC from the measured result; (g) each different adaptor and a common adaptor
 CC are added to each of the genomic DNA fragments derived from a same or
 CC different individuals; (h) the resultant adaptor-added genomic DNAs are
 CC mixed together; (i) the adaptor-added genomic DNAs are amplified by using
 CC an adaptor primer having the common sequence to the different adaptor and
 CC a sequence-specific adaptor; and (j) the ratios of the amplified amounts
 CC of the genomic DNAs are measured between the individuals. The method is
 CC used for the detection of the amounts of RNA and DNA. The present
 CC sequence represents an oligonucleotide which is used in the
 CC exemplification of the present invention
 CC
 CC SQ Sequence 22 BP; 19 A; 1 C; 1 G; 1 T; 0 U; 0 Other;
 CC
 CC Query Match 0.3%; Score 19; DB 1; Length 22;
 CC Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 CC Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 4466 TTTTTTTTTTTTTTTTG 4484
 CC |||||
 CC DB 22 TTTTTTTTTTTTTTTTG 4
 CC
 CC RESULT 658
 CC AAQ75028/c
 CC ID AAQ75028 standard; DNA; 23 BP.
 CC
 CC AC AAQ75028;
 CC
 CC XX 25-MAR-2003 (revised)
 CC DT 03-AUG-1995 (first entry)
 CC
 CC XX LCR oligo 2.
 CC
 CC DE Synthetic oligo; solid phase immunoassay; ss.
 CC
 CC KM Synthetic.
 CC OS
 CC XX MO9426932-A1.
 CC PN
 CC XX 24-NOV-1994.
 CC PD
 CC XX 13-MAY-1994; 94WO-US005407.
 CC PF
 CC XX

PR 13-MAY-1993; 93US-00061694.
 XX
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX PI Fields HA, Khudyakov YE;
 XX
 XX DR MPI; 1995-006819/01.
 XX
 XX PT Solid phase immunoassay using oligo:nucleotide as label - also new
 XX conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
 XX diagnosing hepatitis C or E virus infection.
 XX
 XX PS Example; Page 13; 34pp; English.
 XX
 XX CC AAQ62941 and AAQ62942 are examples of synthetic immunoreactive peptides.
 CC They are used in a method for detecting an antigen in a subject. The
 CC method involves binding the antigen to a solid support and then reacting
 CC it with an immunoreactive ligand (L) bound to an oligo; removing any
 CC unreacted L, and then detecting the presence of the oligo. A similar
 CC method can be used to detect Abs, in which case the ligand is an oligo-
 CC labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
 CC to be detected at very low levels. An exemplary oligo is AAQ75024 which
 CC can be covalently attached by the 5'-terminus to the N- or C-terminal of
 CC a synthetic peptide. For LCR using oligo AAQ75024, oligos 1-4 (see
 CC AAQ75027-Q75030) can be used. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 CC
 CC SQ Sequence 23 BP; 19 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
 CC
 CC Query Match 0.3%; Score 19; DB 1; Length 23;
 CC Best Local Similarity 100.0%; Pred. No. 5e+02;
 CC Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 4466 TTTTTTTTTTTTTTTTG 4484
 CC |||||
 CC DB 23 TTTTTTTTTTTTTTTTG 5
 CC
 CC RESULT 659
 CC AAQ75029
 CC ID AAQ75029 standard; RNA; 23 BP.
 CC
 CC AC AAQ75029;
 CC
 CC XX 25-MAR-2003 (revised)
 CC DT 03-AUG-1995 (first entry)
 CC
 CC XX LCR oligo 3.
 CC
 CC DE Synthetic oligo; solid phase immunoassay; ss.
 CC
 CC KM Synthetic.
 CC OS
 CC XX MO9426932-A1.
 CC PN
 CC XX 24-NOV-1994.
 CC PD
 CC XX 13-MAY-1994; 94WO-US005407.
 CC PF
 CC XX 13-MAY-1993; 93US-00061694.
 CC PR
 CC XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 CC
 CC PI Fields HA, Khudyakov YE;
 CC
 CC DR MPI; 1995-006819/01.
 CC
 CC PT Solid phase immunoassay using oligo:nucleotide as label - also new
 CC conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
 CC diagnosing hepatitis C or E virus infection.
 CC
 CC PS Example; Page 13; 34pp; English.
 CC
 CC XX


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RESULT 652
AA075642
ID AA075642 standard; DNA; 21 BP.
XX
AC AA075642;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI, 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AA075547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4467 TTTTTTTTTTTTTTTTGT 4485
DB 1 TTTTTTTTTTTTTTTTGT 19

RESULT 653
AA075640
ID AA075640 standard; DNA; 21 BP.
XX
AC AA075640;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX

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PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI, 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AA075547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4467 TTTTTTTTTTTTTTTTGT 4485
DB 1 TTTTTTTTTTTTTTTTGT 19

RESULT 654
AA075644
ID AA075644 standard; DNA; 21 BP.
XX
AC AA075644;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI, 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AA075547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

```

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KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX OS
XX JP06303997-A.
XX PN
XX 01-NOV-1994.
XX PD
XX 16-APR-1993; 93JP-00112515.
XX PF
XX 16-APR-1993; 93JP-00112515.
XX PR
XX 16-APR-1993; 93JP-00112515.
XX PS
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX PA
XX WPI; 1995-018287/03.
XX DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PT
XX Disclosure; Page 6, 11pp; Japanese.
XX PS
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENSEQ files AAQ75547-075798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX CC
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 0.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 4,4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4467 TTTTTTTTTTTTTTTTGT 4485
Db 1 TTTTTTTTTTTTTTTGT 19
RESULT 650
AAQ75646
ID AAQ75646 standard; DNA; 21 BP.
XX
XX AAQ75646;
XX AC
XX 04-AUG-1995 (first entry)
XX DT
XX Reverse transcription primer used in cDNA analysis technique.
XX DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX KW
XX Synthetic.
XX OS
XX JP06303997-A.
XX PN
XX 01-NOV-1994.
XX PD
XX 16-APR-1993; 93JP-00112515.
XX PF
XX 16-APR-1993; 93JP-00112515.
XX PR
XX 16-APR-1993; 93JP-00112515.
XX PS
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX PA
XX WPI; 1995-018287/03.
XX DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PT
XX Disclosure; Page 6, 11pp; Japanese.
XX PS

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XX      A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC      labelled reverse transcription primers (GENBSEQ files AAQ75547-075798)
CC      and using the aggregate of mRNAs as the template for each reverse
CC      transcription primer; (b) digesting each of the prepared aggregates of
CC      the double-stranded cDNAs with restriction enzyme and; (c)
CC      electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC      method can be used to analyse gene expression rapidly and easily
XX
SQ      Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match      0.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
OY      4467 TTTTTCCTTTTTCCTTTCCT 4485
      |||||
      1 TTTTTCCTTTTTCCTTTCCT 19
XX
RESULT 651
AAQ75650
ID      AAQ75650 standard; DNA; 21 BP.
XX
AC      AAQ75650;
XX
DT      04-AUG-1995 (first entry)
XX
DE      Reverse transcription primer used in cDNA analysis technique.
XX
KM      Analysis; gene expression; reverse transcription; primer; cDNA;
XX      aggregate; restriction enzyme; ss.
XX
OS      Synthetic.
XX
PN      JP06303997-A.
XX
PD      01-NOV-1994.
XX
PF      16-APR-1993; 93JP-00112515.
XX
PR      16-APR-1993; 93JP-00112515.
XX
PA      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
WP; 1995-018287/03.
XX
DR      Analysis of cDNA and gene expression - by amplification of mRNA followed
XX      by digestion with restriction enzymes.
XX
PS      Disclosure; Page 6; 11pp; Japanese.
XX
CC      A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC      labelled reverse transcription primers (GENBSEQ files AAQ75547-075798)
CC      and using the aggregate of mRNAs as the template for each reverse
CC      transcription primer; (b) digesting each of the prepared aggregates of
CC      the double-stranded cDNAs with restriction enzyme and; (c)
CC      electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC      method can be used to analyse gene expression rapidly and easily
XX
SQ      Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;
XX
Query Match      0.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
OY      4467 TTTTTCCTTTTTCCTTTCCT 4485
      |||||
      1 TTTTTCCTTTTTCCTTTCCT 19
XX
DB      1 TTTTTCCTTTTTCCTTTCCT 19

```


immune deficiency, also related nucleic acid and antibodies.

Disclosure; SEQ ID NO 32; 217bp; English.

The invention relates to stem cell factor (SCF) polypeptides with haematopoietic activity and the polynucleotides encoding them. The polypeptides are used for treating infertility, intestinal damage, myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia, for improving engraftment of bone marrow transplants, for enhancing bone marrow recovery after radiotherapy or chemotherapy and in treatment of immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are also used to expand haematopoietic progenitor cells for transplantation and to prepare such cells for transfection with a gene. The SCF polynucleotides can be used for recombinant expression of the polypeptides and also as probes for mapping of the SCF gene, for identifying SCF-related diseases and as a marker for neighbouring genes. Antibodies raised against the polypeptides are useful in diagnosis and to remove SCF from blood. This sequence represents SCF related DNA of the invention.

Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

	Query Match	0.3%;	Score 19;	DB 1;	Length 20;
	Best Local Similarity	100.0%;	Pred. No. 4.1e+02;		
	Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Oy 4466 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 647
AAQ75648
ID AAQ75648 standard; DNA; 21 BP.
XX
AC AAQ75648;
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
KM Analysis; gene expression; reverse transcription; primer; cDNA;
aggregate; restriction enzyme; ss.
OS Synthetic.
PN JP06303997-A.
XX 01-NOV-1994.
PF 16-APR-1993; 93JP-00112515.
PR 16-APR-1993; 93JP-00112515.
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
DX WPI; 1995-018287/03.
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
by digestion with restriction enzymes.
PS Disclosure; Page 6; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
and using the aggregate of mRNAs as the template for each reverse
transcription primer; (b) digesting each of the prepared aggregates of
the double-stranded cDNAs with restriction enzyme and; (c)
electrophoresing the digested aggregate of cDNAs in separate lanes. The
method can be used to analyse gene expression rapidly and easily

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00 Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
^ Query Match 0.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. NO. 4.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4467 TTTTTTTTTTTTTTTTGGT 4485
|||||
1 TTTTTTTTTTTTTTTTGGT 19
DB 1 TTTTTTTTTTTTTTTTGGT 19

RESULT 648
AAQ75639
AAQ75639 standard; DNA; 21 BP.
XX
XX AAQ75639;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENBSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX
XX Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;
SQ
Query Match 0.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4467 TTTTTTTTTTTTTTTTGGT 4485
|||||
1 TTTTTTTTTTTTTTTTGGT 19
DB 1 TTTTTTTTTTTTTTTTGGT 19

RESULT 649
AAQ75643
AAQ75643 standard; DNA; 21 BP.
XX
XX AAQ75643;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX

```


CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cyostatic activity. The composition may have a
CC use in antiense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
CC XX
SQ Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4464 TTTT TTTT TTTT TTTT TTTT 4482
Db 20 TTTT TTTT TTTT TTTT TTTT 2
RESULT 641
ABZ89179/c
ID ABZ89179 standard; DNA; 20 BP.
XX
AC ABZ89179;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antiense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cyostatic; gene therapy;
KW antiense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; de.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPL; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antiense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4421; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antiense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cyostatic activity. The composition may have a
CC use in antiense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
CC XX
SQ Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4464 TTTT TTTT TTTT TTTT TTTT 4482
Db 20 TTTT TTTT TTTT TTTT TTTT 2
RESULT 642
ABZ99050
ID ABZ99050 standard; DNA; 20 BP.
XX
AC ABZ99050;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human PDB4C oligonucleotide sequence.
XX
KW Human; antiense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cyostatic; gene therapy;
KW antiense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; de.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPL; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antiense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 14292; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antiense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,


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PT Analyzing target nucleic acid sequences, useful for population genetics,
PT drug development and diagnosing cancer, comprises hybridizing triple
PT forming oligonucleotide and probe to target sequence.
XX
PS Example 2; Page 66; 141pp; English.
XX
CC The sequence is a second reverse phase triplex forming oligonucleotide,
CC RP-TFO (3' to the SNP) used to analyse Factor V Leiden SNP using the
CC method of the invention. The invention relates to analysing target
CC nucleic acid sequences comprising restricting isolated DNA, hybridising
CC at least one triplex forming oligonucleotide (TFO), adding a 3' to 5'
CC exonuclease to form a protected nucleic acid sequence (PNAS) tail
CC structure, hybridising the captured structure with a single nucleotide
CC polymorphisms (SNP) identification probe and determining the SNP score.
CC The methods can be used for analysing target nucleic acid sequences,
CC especially genomic DNA sequences, to determine if they contain SNPs or
CC short tandem repeats (STRs). The methods can be used to detect SNPs for
CC use in population genetics, drug development, forensics, cancer, genetic
CC disease research, genomic analysis, diagnostics and therapeutics in
CC humans, plants and animals
CC
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 1 Other;
OY Query Match 0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 4;le+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 1 TTTTTTTTTTTTTTTTTTTT 4483
OY 4464 TTTTTTTTTTTTTTTTTTTT 4483
1 TTTTTTTTTTTTTTTTTTTT 20
RESULT 635
AAH23889
ID AAH23889 standard; DNA; 20 BP.
AC AAH23889;
XX
DT 07-AUG-2001 (first entry)
XX
DE Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
XX
KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW anaemia; Kala azar; septicæmia; malaria; hypopigmentation disorder;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6204363-B1.
XX
PD 20-MAR-2001.
XX
PF 25-NOV-1992; 92US-00982255.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 10-APR-1991; 91US-00684535.
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
DR WPI, 2001-256683/26.
XX
PT New stem cell factor polypeptides and their analogs which stimulate
PT growth of early hematopoietic progenitors, useful for treating aplastic
PT anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
PT disease.
XX
PS Example 3; Fig 12C; 16pp; English.

```

CC	XX	The present sequence for universal PCR primer 220-3 is 1 of 8 universal
CC	XX	oligonucleotides (AAH2388-AAH2395) used in the isolation of the human
CC	XX	SCF (stem cell factor) cDNA sequence. The present invention relates to
CC	XX	novel stem cell factors (AAH73561-AAH73568, AAH73571-AAH73576) and the
CC	XX	polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC	XX	including early haematopoietic progenitor cells. The invention also
CC	XX	describes SCF peptides (AAH73578-AAH73597) and the oligonucleotides
CC	XX	(AAH23859-AAH23887) used in the isolation of human and rat SCF sequences.
CC	XX	The polynucleotide encoding SCF is useful for producing SCF and useful in
CC	XX	gene therapy. It is useful for treating disorders involving blood cells
CC	XX	such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC	XX	myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC	XX	congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC	XX	disseminated fungus disease, Fulminating septicemia, malaria, vitamin
CC	XX	B12 and folic acid deficiency, pyridoxine deficiency, and
CC	XX	hypopigmentation disorders such as prebaldism and vitiligo
CC	XX	
CC	XX	Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
CC	XX	
CC	XX	Query Match 0.3%; Score 19; DB 1; Length 20;
CC	XX	Best Local Similarity 100.0%; Pred. No. 4.1e+02;
CC	XX	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC	XX	
CC	XX	4466 TTTT TTTT TTTT TTTT TTTT G 4484
CC	XX	
CC	XX	1 TTTT TTTT TTTT TTTT TTTT G 19
CC	XX	
CC	XX	RESULT 636
CC	XX	AA504212
CC	XX	ID AA504212 standard; DNA; 20 BP.
CC	XX	AC
CC	XX	AA504212;
CC	XX	
CC	XX	29-AUG-2001 (first entry)
CC	XX	
CC	XX	Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
CC	XX	
CC	XX	Human; stem cell factor; SCF; early haematopoietic progenitor cell;
CC	XX	blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
CC	XX	anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
CC	XX	PCR primer; se.
CC	XX	
CC	XX	Homo sapiens.
CC	XX	
CC	XX	US6218148-B1.
CC	XX	
CC	XX	17-APR-2001.
CC	XX	
CC	XX	21-DEC-1993; 93US-00172329.
CC	XX	
CC	XX	16-OCT-1989; 89US-00422383.
CC	XX	PR 11-JUN-1990; 90US-00537198.
CC	XX	PR 24-AUG-1990; 90US-00573616.
CC	XX	PR 01-OCT-1990; 90US-00589701.
CC	XX	25-NOV-1992; 92US-00982255.
CC	XX	
CC	XX	(AMGE-) AMGEN INC.
CC	XX	
CC	XX	Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
CC	XX	WPI; 2001-281051/29.
CC	XX	
CC	XX	Isolated DNA sequence, encoding polypeptide product useful for
CC	XX	stimulating growth of early hematopoietic progenitor cells.
CC	XX	
CC	XX	Example 3; Fig 12C; 167bp; English.
CC	XX	
CC	XX	The present sequence for universal PCR primer 220-3 is 1 of 8 universal
CC	XX	oligonucleotides (AA504211-AA504218) used in the isolation of the human
CC	XX	SCF (stem cell factor) cDNA sequence. The present invention relates to
CC	XX	novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)

transplantation or for bone marrow recovery after chemotherapy or radiation-induced bone marrow aplasia or myelosuppression. They can also be used for treating neoplasia, nerve damage, infertility, intestinal damage or myeloproliferative disorders. Antibodies may be raised against the peptides for use in detection or neutralisation of SCF in serum. SCF may be useful for the treatment of AIDS and severe combined immunodeficiency (SCID) states alone or in combination with other factors such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4466 TTTT TTTT TTTT TTTT TTTT G 4484
1 TTTT TTTT TTTT TTTT TTTT G 19

RESULT 627

AAV07752 standard; DNA; 20 BP.

AAV07752;

07-DEC-1998 (first entry)

Phosphorothioate oligonucleotide.

phosphorothioate; sulphurisation; heterocycle; automated synthesis;

antisense; EDITR; Beaucage reagent; ss.

Synthetic.

Key misc_feature Location/Qualifiers

1..20 /tag= a

/notes="phosphorothioate internucleotide linkages"

WO9741130-A2.

06-NOV-1997.

29-APR-1997; 97WO-US007118.

30-APR-1996; 96US-00641920.

(MINU) UNIV MINNESOTA.

(LOUV) UNIV LOUISIANA STATE & AGRIC.

Barany G, Mustier-Forsyth K, Xu Q, Chen L, Hammer RP;

WPI; 1997-549671/50.

Sulphurisation of phosphorus-containing compounds, e.g. oligo-nucleotide(s) - by contacting the compound with a di-sulphide-containing five-membered heterocycle.

Example 7; Page 30; 51pp; English.

The present invention provides a method for sulphurising phosphorus-containing compounds. It comprises contacting the phosphorus-containing compound with a 1,2,4-dithiazolidine-2,5-dione compound or a 3-substituted-1,2,4-dithiazolin-5-one compound. The method is especially useful for incorporation of phosphorothioate linkages into biologically important molecules such as DNA, RNA and phosphopeptides. Molecules containing such linkages are useful e.g. as antisense compounds for inhibiting gene expression, as reagents for studying DNA-protein or RNA-protein interactions, or as catalytic RNA. The present sequence represents an oligonucleotide with phosphorothioate linkages prepared by the method of the invention

Sequence 20 BP; 1 A; 0 C; 0 G; 0 T; 19 U; 0 Other;

Query Match 0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 0.0%; Pred. No. 4.1e+02;
Matches 0; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

4464 TTTT TTTT TTTT TTTT TTTT T 4482
1 UUUUUUUUUUUUUUUUUUU 19

RESULT 628

AAV68373/C standard; DNA; 20 BP.

AAV68373;

10-MAR-1999 (first entry)

Adapter primer oligonucleotide #12 for CAG repeat analysis.

CAG repeat; human; genome analysis; adapter primer; medical diagnostic;

nucleic acid analysis; variation assessment; neurological disease;

Huntington's chorea; PCR suppression; ss.

Synthetic.

WO9849345-A1.

05-NOV-1998.

29-APR-1998; 98WO-US008616.

29-APR-1997; 97US-0045078P.

(UYBO-) UNIV BOSTON.

Smith CL;

WPI; 1998-594983/50.

Analysing nucleic acid samples - using amplification primers which contain CAG or CTG trinucleotide repeats for differential display of samples from different sources.

Example; Page 31; 44pp; English.

This sequence represents an adapter primer oligonucleotide. It was used to isolate CAG repeat containing sequences from the human genome to test the method of the invention. The method is for analysing nucleic acids in a sample, and comprises: (a) providing a sample containing nucleic acid, a first oligonucleotide primer comprising a CTG repeat, a second oligonucleotide primer comprising a CAG repeat and a polymerase and PCR reagents; (b) preparing said nucleic acid so that it is amplifiable; (c) amplifying the nucleic acid with the first and second primers; and (d) detecting the amplified product. The method is used to distinguish between the expression of genes in two or more biological samples, e.g. body fluids, cells, solid tissue or solid and liquid foods. It can be used in medical diagnostics, e.g. to differentiate between normal and diseased tissue or to assess the variation within monozygotic twin pairs. The method allows the isolation and analysis of genome subsets containing CAG repeats which are known to be important in a number of neurological diseases including Huntington's chorea. The method uses PCR suppression, in which only fragments which contain a target repeat are efficiently amplified. This allows accurate identification of differentially expressed genes in various cell types. Genome complexity is reduced by the new method which targets genomic subsets containing CAG repeats

Sequence 20 BP; 1 A; 7 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX	DE	Reverse transcription primer used in cDNA analysis technique.
XX	KM	Analysis; gene expression; reverse transcription; primer; cDNA;
XX	KM	aggregate; restriction enzyme; ss.
XX	OS	Synthetic.
XX	PN	JP06303997-A.
XX	PD	01-NOV-1994.
XX	PF	16-APR-1993; 93JP-00112515.
XX	PR	16-APR-1993; 93JP-00112515.
XX	PA	(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX	DR	WPI, 1995-018287/03.
XX	PT	Analysis of cDNA and gene expression - by amplification of mRNA followed
XX	PS	by digestion with restriction enzymes.
XX	PS	Disclosure; Page 5; 11pp; Japanese.
XX	CC	A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX	CC	double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX	CC	labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
XX	CC	and using the aggregate of mRNAs as the template for each reverse
XX	CC	transcription primer; (b) digesting each of the prepared aggregates of
XX	CC	the double-stranded cDNAs with restriction enzyme and; (c)
XX	CC	electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX	CC	method can be used to analyse gene expression rapidly and easily
XX	SQ	Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
QY		Query Match 0.3%; Score 19; DB 1; Length 20;
Db		Best Local Similarity 100.0%; Pred. No. 4.1e+02;
		Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY	4467	TTTTTTTTTTTTTTTTTGT 4485
	1	TTTTTTTTTTTTTTTGT 19
RESULT 625		
AAQ75567		
ID	AAQ75567	standard; DNA; 20 BP.
XX	AC	AAQ75567;
XX	DT	04-AUG-1995 (first entry)
XX	DE	Reverse transcription primer used in cDNA analysis technique.
KM	Analysis;	gene expression; reverse transcription; primer; cDNA;
KM	aggregate;	restriction enzyme; ss.
XX	OS	Synthetic.
XX	PN	JP06303997-A.
XX	PD	01-NOV-1994.
XX	PF	16-APR-1993; 93JP-00112515.
XX	PR	16-APR-1993; 93JP-00112515.
XX	PA	(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX	DR	WPI, 1995-018287/03.
XX	PT	Analysis of cDNA and gene expression - by amplification of mRNA followed

[illegible]

SO	Sequence	19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
	Query Match	0.3%; Score 19; DB 1; Length 19; '
	Best Local Similarity	100.0%; Pred.No. 3.8e+02;
	Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Oy	4464	TTTTTTTTTTTTTTTTTTT 4482 1 TTTTTTTTTTTTTTTTTT 19
Db	1	TTTTTTTTTTTTTTTTTTT 19
RESULT 622		
ABZ58336		
ID	ABZ58336	standard; DNA; 19 BP.
XX AC	ABZ58336;	
XX XX	28-APR-2003	(first entry)
DT		
DE	Oligonucleotide with 2'-O-(2-(methylthio)ethyl)-5-methyluridine.	
XX XX	Oligonucleotide; 2'-O-(2-(methylthio)ethyl)-5-methyluridine; antisense;	
KW	DNA-RNA hybrid; ss.	
XX	Synthetic.	
OS		
FH XX	Key	Location/Qualifiers
FT FT	modified_base	16 /tag= a /mod_base= OTHER /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
FT FT	modified_base	17 /tag= b /mod_base= OTHER /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
FT FT	modified_base	18 /tag= c /mod_base= OTHER /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
FT FT	modified_base	19 /tag= d /mod_base= OTHER /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
PM	WO2003004603-A2.	
PD	16-JAN-2003.	
XX		
PP	01-JUL-2002; 2002WO-US020940.	
XX		
PR	03-JUL-2001; 2001US-0302683P.	
PR	28-JAN-2002; 2002US-00058740.	
XX		
PA	(ISIS-) ISIS PHARM INC.	
Pi	Prakash TP, Manoharan M;	
XX	WPI; 2003-239204/23.	
DR		
XX		
PT	Increasing binding of oligomeric compound to proteins useful in preparation of antisense therapeutics, involves use of modified oligomeric compound having oligonucleotide group.	
PT		
XX		
PS	Example 27; Page 72; 122pp; English.	
XX		
CC	The present sequence is an example of an oligonucleotide of the invention containing 2'-O-(2-(methylthio)ethyl)-5-methyluridine (2'-O-MTE)-5-methyluridine modifications. In examples of the invention, 2'-O-MTE was incorporated into oligonucleotides and evaluated for antisense properties in comparison with the known 2'-O-(2-methoxyethyl) (2'-O-MOE) modification. The 2'-O-MTE modified oligonucleotides exhibited similar binding affinity to target RNA as their 2'-O-MOE equivalent while binding to human serum albumin was improved. The modification can be used to	
CC		

```
CC      modulate the pharmacokinetics of oligonucleotides, e.g. in antisense  
CC      therapy  
XX:  
SQ      Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 Other;  
  
Query Match          0.3%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 3.8e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
  
OY      4464 TTTTTTTTTTTTTTTT 4482  
        |||||  
        |:::  
DB      1 TTTTTTTTTTTTTTUUUU 19  
  
RESULT 623  
AAQ75569  
ID      AAQ75569 standard; DNA; 20 BP.  
AC  
XX      AAQ75569;  
AC  
DT      04-AUG-1995 (first entry)  
DE      Reverse transcription primer used in cDNA analysis technique.  
XX  
KM      Analysis; gene expression; reverse transcription; primer; cDNA;  
KW      aggregate; restriction enzyme; ss.  
XX  
OS      Synthetic.  
XX  
PN      JP06303997-A.  
XX  
PD      01-NOV-1994.  
XX  
PF      16-APR-1993; 93JP-00112515.  
XX  
PR      16-APR-1993; 93JP-00112515.  
XX  
PA      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR      WPI, 1995-018287/03.  
XX  
PT      Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT      by digestion with restriction enzymes.  
XX  
PS      Disclosure; Page 5; 11pp; Japanese.  
XX  
CC      A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC      labelled reverse transcriptase primers (GENESSEQ files AAQ75547-Q75798)  
CC      and using the aggregate of mRNAs as the template for each reverse  
CC      transcription primer; (b) digesting each of the prepared aggregates of  
CC      the double-stranded cDNAs with restriction enzyme and; (c)  
CC      electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC      method can be used to analyse gene expression rapidly and easily  
CC  
CQ      Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;  
SQ  
  
Query Match          0.3%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY      4467 TTTTTTTTTTTTTTTGT 4485  
        |||||  
        |:::  
DB      1 TTTTTTTTTTTTTTTGCT 19  
  
RESULT 624  
AAQ75568  
ID      AAQ75568 standard; DNA; 20 BP.  
AC  
XX      AAQ75568;  
AC  
DT      04-AUG-1995 (first entry)
```

PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 31; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT 19
XX
RESULT 620
AADA1999
ID AADA1999 standard; DNA; 19 BP.
XX
AC AADA1999;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #2 used to illustrate the method of the invention.
XX
KM Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KM nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 15..18 /*tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-dimethylaminoxyethoxy (2'-DMAOE)
FT residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawaasaki AM, Frazer AS, Manoharan M, Cook PD, Prakash TP;
XX
DR WPI; 2002-546338/58.
XX
PT Alkylating 2' position of 2', 3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 31; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.

CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT 19
XX
RESULT 621
AADA2009
ID AADA2009 standard; DNA; 19 BP.
XX
AC AADA2009;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #12 used to illustrate the method of the invention.
XX
KM Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KM nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 15..18 /*tag= a
FT /mod_base= OTHER
FT /note= "2'-dimethylaminoxyethyl thymidine (T'-2'-DMAOE)"
FT residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawaasaki AM, Frazer AS, Manoharan M, Cook PD, Prakash TP;
XX
DR WPI; 2002-546338/58.
XX
PT Alkylating 2' position of 2', 3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 35; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX

```

FT      /mod_base= OTHER
XX      /note= "5-methyl, 2'-methoxyethyl residues"
XX
XX      US6403779-B1.
XX
XX      PD      11-JUN-2002.
XX
XX      PF      08-JAN-1999;    99US-00227782.
XX
XX      PR      08-JAN-1999;    99US-00227782.
XX
XX      PA      (ISIS-) ISIS PHARM INC.
XX
XX      PI      Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP,
XX
XX      DR      WPI, 2002-546338/58.
XX
XX      PT      Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
XX      for preparation of 2'-O-alkylated compounds comprises dissolving
XX      nucleoside in aprotic solvent, cooling, treating with base, warming,
XX      cooling and reacting with ester.
XX
XX      PS      Example 46; Col 33; 24pp; English.
XX
XX      CC      The present invention relates to a novel method of selective alkylation
XX      of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX      The method involves dissolving the nucleoside in at least one aprotic
XX      solvent, cooling, treating with base, warming, cooling and reacting with
XX      a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX      nucleotides, nucleosides and nucleoside surrogates used for preparation
XX      of oligomeric compounds having improved hybridisation affinity and
XX      nuclear resistance, which are useful as therapeutics, diagnostics and
XX      research reagents. The present sequence is a modified oligonucleotide
XX      used to illustrate the method of the invention
XX
SQ      Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX      Query Match          0.3%; Score 19; DB 1; Length 19;
XX      Best Local Similarity 100.0%; Pred.No. 3.Be+02;
XX      Matches   19; Conservative   0; Mismatches   0; Indels   0; Gaps   0
XX
XX      QY      4464 TTTT TTTTTTTTTTTTTTTTTT 4482
XX           ||||| ||||||| ||||||| |||||
XX      DB      1 TTTT TTTTTTTTTTTTTTTTTT 19
XX
XX      RESULT 618
XX      AAD42003
XX      ID      AAD42003 standard; DNA; 19 BP.
XX
XX      AC      AAD42003;
XX
XX      DT      04-NOV-2002 (first entry)
XX
XX      XX      Oligonucleotide #6 used to illustrate the method of the invention.
DE
XX
XX      KW      Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX      nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
XX      OS      unidentified.
XX
XX      FH      Key                      Location/Qualifiers
XX      FT      modified_base         16..19
XX      FT      /tag=a
XX      FT      /mod_base= OTHER
XX      PN      /note= "5-methyl, 2'-O-propyl residues"
XX
XX      PD      US6403779-B1.
XX
XX      PF      11-JUN-2002.
XX
XX      PR      08-JAN-1999;    99US-00227782.
XX

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PR	08-JAN-1999;	99US-00227782.
XX	(ISIS-) ISIS PHARM INC.	
XX	Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;	
PI	WPI, 2002-546338/58.	
DR		
XX		
XX	Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used	
PT	for preparation of 2'-O-alkylated compounds comprises dissolving	
PT	nucleoside in aprotic solvent, cooling, treating with base, warming,	
PT	cooling and reacting with ester.	
XX		
PS	Example 46; Col 33; 24pp; English.	
XX		
CC	The present invention relates to a novel method of selective alkylation	
CC	of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.	
CC	The method involves dissolving the nucleoside in at least one aprotic	
CC	solvent, cooling, treating with base, warming, cooling and reacting with	
CC	a reactive ester. The method is useful for the preparation of 2'-O-alkyl	
CC	nucleosides, nucleosides and nucleoside surrogates used for preparation	
CC	of oligomeric compounds having improved hybridisation affinity and	
CC	nuclear resistance, which are useful as therapeutics, diagnostics and	
CC	research reagents. The present sequence is a modified oligonucleotide	
CC	used to illustrate the method of the invention	
XX		
SQ	Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;	
Query Match	0.3%; Score 19; DB 1; Length 19;	
Best Local Similarity	100.0%; Pred. No. 3.8e+02;	
Matches 19; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
OY	4464 TTTTTTTTTTTTTTTT 4482	
Db	1 TTTTTTTTTTTTTTTT 19	
RESULT 619		
AAD41998		
ID	AAD41998 standard; DNA; 19 BP.	
XX		
AC	AAD41998;	
XX		
DT	04-NOV-2002 (first entry)	
XX		
DE	Oligonucleotide #1 used to illustrate the method of the invention.	
XX		
XX	Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;	
KW	nuclear resistance; alkylation; therapeutic; diagnostic; ss.	
XX		
OS	Unidentified.	
XX		
FH	Key Location/Qualifiers	
FT	modified_base 15..18	
FT	/tag= a	
FT	/mod_base= OTHER	
FT	/note= "5-methyl, 2'-aminoxyethoxy (2'-AOE) residues"	
XX		
FN	US6403779-B1.	
XX		
PD	11-JUN-2002.	
XX		
PF	08-JAN-1999; 99US-00227782.	
XX		
PR	08-JAN-1999; 99US-00227782.	
XX		
PA	(ISIS-) ISIS PHARM INC.	
XX		
PI	Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;	
XX		
XX	WPI, 2002-546338/58.	
XX		
PT	Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used	

CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4482
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 613
AAD42010
ID AAD42010 standard; DNA; 19 BP.
XX
AC AAD42010;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #13 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 16..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-dimethylaminooxyethyl thymidine (T-2-DMAOE)"
FT modified_base 18..19
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX
DR WPI; 2002-546338/58.
XX
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 35; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2',3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleosides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4482
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 614
AAD42020
ID AAD42020 standard; DNA; 19 BP.
XX
AC AAD42020;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #23 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 15..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methylaminooxyethyl thymidine"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX
DR WPI; 2002-546338/58.
XX
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 41; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2',3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleosides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4482
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19

```

XX DR WPI; 2002-546338/58.
XX
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 31; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
CC
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4482
DB 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 611
AADD2002
ID AAD42002 standard; DNA; 19 BP.
XX
AC AAD42002;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #5 used to illustrate the method of the invention.
XX
KM Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KM nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FH modified_base 16..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-methoxyethyl residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Frazer AS, Manoharan M, Cook PD, Prakash TP;
XX
XX WPI; 2002-546338/58.
XX
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 33; 24pp; English.

```

```

XX CC The present invention relates to a novel method of selective alkylation
XX CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX CC The method involves dissolving the nucleoside in at least one aprotic
XX CC solvent, cooling, treating with base, warming, cooling and reacting with
XX CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX CC nucleotides, nucleosides and nucleoside surrogates used for preparation
XX CC of oligomeric compounds having improved hybridisation affinity and
XX CC nuclear resistance, which are useful as therapeutics, diagnostics and
XX CC research reagents. The present sequence is a modified oligonucleotide
XX CC used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4482
DB 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 612
AADD2004
ID AAD42004 standard; DNA; 19 BP.
XX
AC AAD42004;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #7 used to illustrate the method of the invention.
XX
KM Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KM nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FH modified_base 18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-dimethylaminoxyethyl residue"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Frazer AS, Manoharan M, Cook PD, Prakash TP;
XX
XX WPI; 2002-546338/58.
XX
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 33; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
XX CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX CC The method involves dissolving the nucleoside in at least one aprotic
XX CC solvent, cooling, treating with base, warming, cooling and reacting with
XX CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX CC nucleotides, nucleosides and nucleoside surrogates used for preparation
XX CC of oligomeric compounds having improved hybridisation affinity and
XX CC nuclear resistance, which are useful as therapeutics, diagnostics and

```

DR MPI; 2002-235143/29.

XX Alkylation of alcohols, amines, or thiols, useful for preparing
 PT nucleosides that are precursors for preparation of oligomeric compounds
 PT beneficial as therapeutics, involves use of cyclic sulfate intermediates.
 XX
 PS Example 15; Col 35; 45pp; English.

XX The present sequence is that of a chimeric oligonucleotide having some 2'
 CC -methoxyethoxy modifications. This was compared with oligonucleotides
 CC with methyl thioethyl (see ABA91949) and dimethylaminoethyl (see
 CC ABA91951) modifications for resistance to snake venom phosphodiesterase.
 CC The assay revealed the nuclease resistance of the modified oligomers. The
 CC invention provides methods for the alkylation of alcohols, amines, thiols
 CC and their derivatives by cyclic sulfate intermediates. In particular,
 CC methods for the alkylation of the 2', 3', or 5'-hydroxy position of
 CC nucleosides and their analogues with cyclic sulfates to form the 2', 3'
 CC or 5'-O-alkyl sulfate modified compounds are disclosed. Displacement of
 CC the 2', 3' or 5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-
 CC modified nucleosides and their analogues. The methods are especially
 CC useful for the preparation of 2'-O-alkyl nucleosides, nucleosides and
 CC nucleoside surrogates that are precursors for the preparation of
 CC oligomeric compounds useful as therapeutics, diagnostics and research
 CC reagents

XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.3%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4482
 Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 609
 ABL51520
 ID ABL51520 standard; DNA; 19 BP.
 AC ABL51520;
 DT 01-JUL-2002 (first entry)

XX Tailing reaction related exemplary primer biotin-dT18U SEQ ID NO:1.
 XX
 DE Tailing reaction; tailed primer; primer; probe; identification;
 KW detection; linear amplification scheme; chain extending enzyme;
 KW telomerase; ss.
 XX
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Biotinylated"
 FT misc_RNA
 FT 19
 FT /*tag= b

XX
 PN US2002031776-A1.
 PD 14-MAR-2002.
 PF 26-JUL-2001; 2001US-00917138.
 XX
 PR 28-MAY-1999; 99US-0136545P.
 PR 25-MAY-2000; 2000US-00580358.
 XX
 PA (TULLIS/) TULLIS R H.
 PA (STRE/) STREIFEL J A.
 XX
 PI Tullis RH, Streifel JA;

XX MPI; 2002-361176/39.

XX Identifying and detecting nucleic acids, particularly DNA hybridization
 PT probes, involves employing chain extending enzymes (e.g. telomerase) to
 PT elongate probes to render them readily detectable.
 XX
 PS Example 1; Page 5; 10pp; English.

XX The present invention describes a method for detecting a nucleic acid
 CC probe, which comprises using chain extending enzymes to elongate probes.
 CC The method comprises: (a) treating the sample with a chain terminating
 CC reagent to prevent polynucleotide chain growth from the nucleic acid in
 CC the sample; (b) contacting the sample with the probe containing a
 CC terminus capable of elongation by a chain extending enzyme, where the
 CC probe hybridises to the nucleic acid in the sample; (c) contacting the
 CC sample with a chain extending enzyme and its substrates, which elongates
 CC the probe; and (d) detecting the elongated hybridised probe. Also
 CC described is a method comprising: (a) treating nucleic acid molecules or
 CC modified nucleic acids in a sample with a reagent or reagents that render
 CC the nucleic acid chains unextendable by a non-template-dependent enzyme;
 CC (b) hybridising the treated molecules with a nucleic acid probe that
 CC includes an extendable terminus, under conditions where hybrids form; and
 CC (c) treating any hybrids formed with a non-template dependent chain
 CC elongating enzyme and its substrates, where any hybridised probe is
 CC extended. The method is useful for identifying and detecting nucleic
 CC acids, particularly DNA hybridisation probes. The present sequence
 CC represents a tailing reaction exemplary primer, which is used in an
 CC example from the present invention

XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;

Query Match 0.3%; Score 19; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 3.8e+02;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4482
 Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 610
 AAD42000
 ID AAD42000 standard; DNA; 19 BP.
 AC AAD42000;
 DT 04-NOV-2002 (first entry)

XX Oligonucleotide #3 used to illustrate the method of the invention.
 XX
 DE Dihydroxy sugar moiety; 2'-O-alkyl nucleoside; hybridisation affinity;
 KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
 KW
 XX
 OS Unidentified.

XX
 FH Key Location/Qualifiers
 FT modified_base 15.18
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethoxy (MOE) residues"
 FT .

XX
 PN US6403779-B1.
 PD 11-JUN-2002.
 PF 08-JAN-1999; 99US-00227782.
 XX
 PR 08-JAN-1999; 99US-00227782.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;

CC provides methods for the alkylation of alcohols, amines, thiols and their
CC derivatives by cyclic sulfate intermediates. In particular, methods for
CC the alkylation of the 2', 3' or 5'-hydroxy position of nucleosides and
CC their analogues with cyclic sulfates to form the 2', 3' or 5'-O-alkyl
CC sulfate modified compounds are disclosed. Displacement of the 2', 3' or
CC 5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-modified
CC nucleosides and their analogues. The methods are especially useful for
CC the preparation of 2'-O-alkyl nucleotides, nucleosides and nucleoside
CC surrogates that are precursors for the preparation of oligomeric
CC compounds useful as therapeutics, diagnostics and research reagents
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4482
DB 1 TTTT TTTT TTTT TTTT TTTT 19
RESULT 607
ID ABA91951 standard; DNA; 19 BP.
XX ABA91951:
AC 23-MAY-2002 (first entry)
XX
XX Dimethylaminopropyl modified oligonucleotide.
DE
XX 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.
KM
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 16
FT modified_base /tag= a
FT /mod_base= OTHER
FT /note= "2'-dimethylaminopropyl thymidine"
FT 17
FT modified_base /tag= b
FT /mod_base= OTHER
FT /note= "2'-dimethylaminopropyl thymidine"
FT 18
FT modified_base /tag= c
FT /mod_base= OTHER
FT /note= "2'-dimethylaminopropyl thymidine"
FT 19
FT modified_base /tag= d
FT /mod_base= OTHER
FT /note= "2'-dimethylaminopropyl thymidine"
XX
XX US6277982-B1.
XX
XX 21-AUG-2001.
XX
XX 20-AUG-1999; 99US-00378665.
XX
XX 20-AUG-1999; 99US-00378665.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;
XX
XX WPI; 2002-235143/29.
XX
XX Alkylation of alcohols, amines, or thiols, useful for preparing
XX nucleosides that are precursors for preparation of oligomeric compounds
XX beneficial as therapeutics, involves use of cyclic sulfate intermediates.
XX
XX Example 15; Col 35; 45pp; English.

XX The present sequence is that of a chimeric oligonucleotide having some 2'
CC -dimethylaminopropyl modifications. This was compared with
CC oligonucleotides with methyl thioethyl (see ABA91949) and methoxyethoxy
CC (see ABA91950) modifications for resistance to snake venom
CC phosphodiesterase. The assay revealed the nuclease resistance of the
CC modified oligomers. The invention provides methods for the alkylation of
CC alcohols, amines, thiols and their derivatives by cyclic sulfate
CC intermediates. In particular, methods for the alkylation of the 2', 3' or
CC 5'-hydroxy position of nucleosides and their analogues with cyclic
CC sulfates to form the 2', 3' or 5'-O-alkyl sulfate modified compounds are
CC disclosed. Displacement of the 2', 3' or 5'-O-sulfate with a nucleophile
CC provides 2', 3' or 5'-O-modified nucleosides and their analogues. The
CC methods are especially useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates that are precursors
CC for the preparation of oligomeric compounds useful as therapeutics,
CC diagnostics and research reagents
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4482
DB 1 TTTT TTTT TTTT TTTT TTTT 19
RESULT 608
ID ABA91950 standard; DNA; 19 BP.
XX ABA91950:
AC 23-MAY-2002 (first entry)
XX
XX Methoxyethoxy modified oligonucleotide.
DE
XX 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.
KM
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 16
FT modified_base /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethoxy thymidine"
FT 17
FT modified_base /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethoxy thymidine"
FT 18
FT modified_base /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethoxy thymidine"
FT 19
FT modified_base /tag= d
FT /mod_base= OTHER
FT /note= "2'-methoxyethoxy thymidine"
XX
XX US6277982-B1.
XX
XX 21-AUG-2001.
XX
XX 20-AUG-1999; 99US-00378665.
XX
XX 20-AUG-1999; 99US-00378665.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;
XX
XX

CC quantification of ribonucleic acid and deoxyribonucleic acid or for
CC modulating the activity of an ribonucleic acid or deoxyribonucleic acid
CC molecule. They have a modified nucleoside monomer and are specifically
CC hybridizable with a preselected nucleotide sequence of a single-stranded
CC or double-stranded target deoxyribonucleic acid or ribonucleic acid
CC molecule. The oligomers are further useful in a ras-luciferase fusion
CC system using ras-luciferase transactivation. They are useful in abnormal
CC cell proliferation and tumour formation and modulation of expression of
CC protein kinase C and cell adhesion molecules such as ICAM. They are
CC useful in the modulation of proteins related to multidrug resistance and
CC viral genomic nucleic acids such as HIV, herpes viruses, Epstein-Barr
CC virus, cytomegalovirus, papillomavirus, hepatitis C virus and influenza
CC virus
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4482
DB 1 TTTT TTTT TTTT TTTT TTTT 19
RESULT 605
AAK98526
ID AAK98526 standard; DNA; 19 BP.
XX
AC AAK98526;
XX
DT 16-APR-2002 (first entry)
XX
DE Nucleic acid quantitative analysis related oligonucleotide #1.
XX
XX Target detection; quantitative analysis; probe; medical diagnosis;
KM forensics; bacterial screening; tissue typing; gene expression analysis;
KW genotyping; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "modified by thiol"
XX
XX WO200202810-A2.
XX
XX PN 10-JUN-2002.
PD
XX
XX 02-JUL-2001; 2001WO-EP007575.
XX
XX 01-JUL-2000; 2000DE-01033334.
XX
XX (CLON-) CLONING CHIP TECHNOLOGIES GMBH.
XX
XX Bickel R, Ehrlich R, Ellinger T, Emsentraut E, Kaiser T;
PI Schultz T, Wagner G;
XX
XX WPI; 2002-154760/20.
DR
XX
XX
PT Determining targets by interaction with probe array; useful e.g. for
PT diagnosis, based on detecting formation of precipitate at specific probe
PT sites.
XX
XX
PS Example 5; Page 47; 92pp; German.
XX
CC The present invention relates to a method for the qualitative and
CC quantitative detection of targets in a sample by molecular interaction
CC between the target and probes in an array. The method can be used to
CC detect interactions between nucleic acids, antigens and antibodies or
CC receptor and ligands, particularly in applications such as medical

CC diagnosis, forensic science, bacterial screening, tissue typing for
CC transplantation, monitoring gene expression, and genotyping. The present
CC sequence is a modifying oligonucleotide used in the exemplification of
CC the invention
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4482
DB 1 TTTT TTTT TTTT TTTT TTTT 19
RESULT 606
ABA91949
ID ABA91949 standard; DNA; 19 BP.
XX
AC ABA91949;
XX
DT 23-MAY-2002 (first entry)
XX
DE Methyl thioethyl modified oligonucleotide.
XX
XX 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 16
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methyl thioethyl thymidine"
FT modified_base 17
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methyl thioethyl thymidine"
FT modified_base 18
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methyl thioethyl thymidine"
FT modified_base 19
FT /*tag= d
FT /mod_base= OTHER
FT /note= "2'-methyl thioethyl thymidine"
XX
XX US6277982-B1.
XX
XX PN 21-AUG-2001.
PD
XX
XX 20-AUG-1999; 99US-00378665.
XX
XX 20-AUG-1999; 99US-00378665.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Frazer AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;
PI WPI; 2002-235143/29.
DR
XX
XX
PT Alkylation of alcohols, amines, or thiols, useful for preparing
PT nucleosides that are precursors for preparation of oligomeric compounds
PT beneficial as therapeutics, involves use of cyclic sulfate intermediates.
XX
XX
PS Example 15; Col 35; 45pp; English.
XX
CC The present sequence is that of a chimeric oligonucleotide having some 2'
CC -methyl thioethyl modifications. This was compared with oligonucleotides
CC with methoxyethoxy (see ABA91950) and dimethylaminoethyl (see ABA91951)
CC modifications for resistance to snake venom phosphodiesterase. The assay
CC revealed the nuclease resistance of the modified oligomers. The invention

PF 29-SEP-2000; 2000WO-US026729.
XX
XX 30-SEP-1999; 99US-00409926.
XX
XX (ISIS-) ISIS PHARM INC.
XX
PI Crooke ST, Lima WF, Wu H, Manoharan M;
XX
XX WPI; 2001-343164/36.
XX
PT Chimeric oligonucleotides that can serve as substrates for human RNase
HI, useful for enhancing the effectiveness of antisense gene therapies.
XX
XX Example 54; Page 88; 178bp; English.
XX
CC The present invention provides a number of DNA-RNA oligonucleotides which
CC can act as substrates for human RNase HI (a type II RNase). The sequence
CC consists of two portions, one of which is capable of supporting cleavage
CC of a complementary target RNA and the other of which is incapable of
CC supporting such cleavage. These can be used to enhance the effectiveness
CC of antisense therapies. The present sequence is an RNase H substrate used
CC in the exemplification of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482
Db 1 TTTT TTTT TTTT TTTT TTTT 19
RESULT 603
AAH25738
ID AAH25738 standard; DNA; 19 BP.
XX
XX AAH25738;
AC
XX
DT 14-AUG-2001 (first entry)
XX
XX Human type II RNase H substrate oligonucleotide #5.
DE
XX Human; RNase H type II; RNase HI cleavage substrate; antisense therapy;
KM Gene therapy; primer; phosphorothioate backbone; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..19 /*tag= a
FT /*mod_base= OTHER
FT /*note= "optionally phosphorothioate backbone"
FT modified_base 16..19 /*tag= b
FT /*mod_base= OTHER
FT /*note= "optionally 3'-O⁻-(2-methoxyethyl) or 2'-O⁻-(2-methoxyethyl)"
FT misc_RNA 19 /*tag= c
FT
FT
XX
XX WO200123613-A1.
XX
XX PD 05-APR-2001.
XX
XX PF 29-SEP-2000; 2000WO-US026729.
XX
XX PR 30-SEP-1999; 99US-00409926.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX Crooke ST, Lima WF, Wu H, Manoharan M;

XX
XX WPI; 2001-343164/36.
XX
XX Chimeric oligonucleotides that can serve as substrates for human RNase
PT HI, useful for enhancing the effectiveness of antisense gene therapies.
XX
XX Example 54; Page 88; 178bp; English.
XX
CC The present invention provides a number of DNA-RNA oligonucleotides which
CC can act as substrates for human RNase HI (a type II RNase). The sequence
CC consists of two portions, one of which is capable of supporting cleavage
CC of a complementary target RNA and the other of which is incapable of
CC supporting such cleavage. These can be used to enhance the effectiveness
CC of antisense therapies. The present sequence is an RNase H substrate used
CC in the exemplification of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;
XX
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.8e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482
Db 1 TTTT TTTT TTTT TTTT TTTT 19
RESULT 604
AAC83664
ID AAC83664 standard; DNA; 19 BP.
XX
XX AAC83664;
AC
XX
XX 02-MAR-2001 (first entry)
DT
XX
XX 2'-O-N-[2-(dimethylamino)ethyl]acetamido]-modified oligo ISIS #32335.
DE
XX 2'-O-acetamido; diagnostic; kinase modulator; nuclease resistance;
KM tumour formation; cancer; protein kinase C expression;
KM cell adhesion molecule expression; multidrug resistance; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 16..19 /*tag= a
FT /*mod_base= OTHER
FT /*note= "2'-O-N-[2-(dimethylamino)ethyl]acetamido] 5MeU"
FT
FT
XX
XX US6147200-A.
XX
XX PD 14-NOV-2000.
XX
XX PF 19-AUG-1999; 99US-00378568.
XX
XX PR 19-AUG-1999; 99US-00378568.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Manoharan M, Cook PD, Frazer AS, Prakash TP, Kawasaki AM;
PI
XX WPI; 2001-069824/08.
XX
XX New 2'-O-acetamido modified nucleosides (I) used to produce
PT oligonucleotides which have enhanced nuclease resistance and superior
PT hybridization properties than prior art.
XX
XX Example 12; Col 28; 29pp; English.
XX
CC The present sequence is a modified oligonucleotide. 2'-O-acetamido-
CC modified nucleosides were used to produce oligonucleotides which have
CC enhanced nuclease resistance and superior hybridization properties than
CC prior art. The oligomeric compounds are useful for identification or

```
AAAF31564
XX ID AAAF31564 standard; DNA; 19 BP.
XX AC AAAF31564;
XX PD
XX DT 09-APR-2001 (first entry)
XX DE ISIS sequence 32327.
XX KW DNA/RNA hybrid; oligomer; C3' methylene hydrogen phosphate; AIDS;
XX KM atherosclerosis; ss.
XX OS Synthetic.
XX PN WO200102419-A1.
XX PD 11-JAN-2001.
XX PF 05-JUL-2000; 2000MO-US040304.
XX PR 07-JUL-1999; 99US-00349033.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Cook PD, Manoharan M, Maier M, An H;
XX DR WPI; 2001-138117/14.
XX PT New oligomers for use as research reagent, for treating disease caused by
XX PT undesired production of proteins, and for diagnosing and treating AIDS,
XX PT atherosclerosis.
XX PS Example 46; Page 74; 110pp; English.
XX CC The present invention relates to C3' methylene hydrogen phosphate
XX CC oligomers. The oligomers may be used as research reagents, for treating
XX CC disease caused by undesired production of proteins and for diagnosing and
XX CC treating AIDS and atherosclerosis
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 Other;

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 3.8e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 601
AAH46460
XX ID AAH46460 standard; DNA; 19 BP.
XX AC AAH46460;
XX DT 14-SEP-2001 (first entry)
XX DE Oligonucleotide #8.
XX KM Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.
XX OS Synthetic.
XX PN Key Location/Qualifiers
XX FT modified_base 1..19
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "All bases are phosphorothioate"
XX FT modified_base 1
XX FT /tag= b
XX FT /mod_base= OTHER
XX FT /note= "Modified with 2'-O-methoxyethyl"
```

```
XX PN US6242591-B1.
XX PD 05-JUN-2001.
XX PF 11-JAN-2000; 2000US-00481486.
XX PR 15-OCT-1997; 97US-00950779.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Cole DL, Ravikumar VT, Cheruvallath ZS;
XX DR WPI; 2001-407218/43.
XX PT Preparing sulfurized 2' substituted phosphorothioate oligonucleotides
XX PT useful in biological research, comprises phosphorylating the 5'-hydroxyl
XX PT of a nucleic acid having a nucleoside with a 2' modification.
XX PS Example 12; Col 7; 7pp; English.
XX CC The present invention relates to a method for preparing phosphorothioate
XX CC oligonucleotides having at least one nucleoside with a 2' modification.
XX CC The method comprises phosphorylating the 5'-hydroxyl of a nucleic acid
XX CC group having at least one nucleoside with a 2' modification in an
XX CC acetonitrile. The present sequence was used to illustrate the method of
XX CC the present invention. The method is useful for synthesizing sulphurised
XX CC 2' substituted phosphorothioate oligonucleotides, which may be used in
XX CC molecular biological research, in applications such as anti-viral
XX CC therapy, and for determining the stereochemical pathways of certain
XX CC enzymes which recognise nucleic acids
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 602
AAH25737
XX ID AAH25737 standard; DNA; 19 BP.
XX AC AAH25737;
XX DT 14-AUG-2001 (first entry)
XX DE Human type II RNase H substrate oligonucleotide #4.
XX KM Human; RNase H type II; RNase H1 cleavage substrate; antisense therapy;
XX KM gene therapy; primer; phosphorothioate backbone; ss.
XX OS Synthetic.
XX PN Key Location/Qualifiers
XX FT modified_base 1..19
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "optionally phosphorothioate backbone"
XX FT modified_base 16..19
XX FT /tag= b
XX FT /mod_base= OTHER
XX FT /note= "optionally 3'-O-(2-methoxyethyl) or 2'-O-(2-methoxyethyl)"
XX PN WO200123613-A1.
XX PD 05-APR-2001.
```


[illegible]

```

FT      /mod_base= OTHER
FT      /note= "2'-O-(2-methoxyethyl)uridine"
XX      '
XX      WO200066609-A1.
XX      PD
XX      09-NOV-2000.
XX      PF
XX      03-MAY-2000; 2000WO-US011913.
XX      PR
XX      03-MAY-1999; 99US-00303586.
XX      PA
XX      (ISIS-) ISIS PHARM INC.
XX      Manoharan M, Mohan V;
XX      PI
XX      WPI; 2000-672833/65.
XX      DR
XX      New oligonucleotides containing sequences with A and B geometry, used to
XX      PT treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
XX      PT bacterial infections, bind to single stranded RNA or DNA.
XX      PS
XX      Example 54; Page 69; 132pp; English.
XX      CC
XX      Oligonucleotide ISIS 2211 contains a phosphodiester backbone and has 2'-
XX      CC O-(2-methoxyethyl) chemistry. It was used in experiments to determine the
XX      CC effects of snake venom phosphodiesterase and liver homogenate on the
XX      CC stability of oligonucleotides. Novel oligonucleotides of the invention
XX      CC have both A- and B-form conformational geometry. The A-form geometry
XX      CC modulates the binding affinity and nuclease resistance of the
XX      CC oligonucleotide. The B-form geometry allows the oligonucleotide to serve
XX      CC as substrate for RNase-H when bound to a target nucleic acid strand. The
XX      CC oligonucleotides can be used to treat psoriasis and other inflammatory
XX      CC skin conditions, skin cancers and viral, bacterial and fungal infections,
XX      CC and in various diagnostic applications
XX      SQ
XX      Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX      Query Match 0.3%; Score 19; DB 1; Length 19;
XX      Best Local Similarity 100.0%; Pred. No. 3.8e+02;
XX      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY      4464 TTTTTTTTTTTTTTTTTT 4482
DB      1 TTTTTTTTTTTTTTTTTT 19
RESULT 597
AAAT71630
ID      AAAT71630 standard; DNA; 19 BP.
XX      AC
XX      AAAT71630;
XX      DT
XX      14-DEC-2000 (first entry)
XX      DE
XX      Phosphorothioate 20-mer primer DNA #1.
XX      KM
XX      Phosphorothioate; primer; oligomer synthesis; antisense therapy; ss.
XX      OS
XX      Synthetic.
XX      FH
XX      Key Location/Qualifiers
XX      FT modified_base 1..20
XX      FT /tag= a
XX      FT /mod_base= OTHER
XX      FT /note= "phosphorothioate linkage"
XX      PN
XX      EP1028124-A2.
XX      PD
XX      16-AUG-2000.
XX      PF
XX      06-SEP-1999; 99EP-00307066.
XX      PR
XX      04-FEB-1999; 99US-0118564P.

```

PT bacterial infections, bind to single stranded RNA or DNA.
XX
PS Example 54; Page 69; 132pp; English.
XX
CC Oligonucleotide ISIS 22113 contains a phosphorothioate backbone and has
CC 2'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine
CC the effects of snake venom phosphodiesterase and liver homogenate on the
CC stability of oligonucleotides. Novel oligonucleotides of the invention
CC have both A- and B-form conformational geometry. The A-form geometry
CC modulates the binding affinity and nuclease resistance of the
CC oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC as substrate for RNase-H when bound to a target nucleic acid strand. The
CC oligonucleotides can be used to treat psoriasis and other inflammatory
CC skin conditions, skin cancers and viral, bacterial and fungal infections,
CC and in various diagnostic applications
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482
DB 1 TTTT TTTT TTTT TTTT TTTT 19
RESULT 594
AAA88951 ID AAA88951 standard; DNA; 19 BP.
XX
AC AAA88951;
XX
DT 05-MAR-2001 (first entry)
XX
DE Oligonucleotide ISIS 22114.
XX
KM Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KM dermatological; cytosstatic; virucide; antibacterial; fungicide; therapy;
KM diagnosis; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..15
FT /*tag= e
FT /note= "phosphorothioate linkage"
FT modified_base 16
FT /*tag= a
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl) thymidine"
FT modified_base 17
FT /*tag= b
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl) thymidine"
FT modified_base 18
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl) thymidine"
FT modified_base 19
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl) thymidine"
XX
PN WO200066609-A1.
XX
PD 09-NOV-2000.
XX
PF 03-MAY-2000; 2000WO-US011913.
XX
PR 03-MAY-1999; 99US-00303586.
XX
PA (ISIS-) ISIS PHARM INC.

XX
PI Manoharan M, Mohan V;
XX
DR WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used to
PT treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT bacterial infections, bind to single stranded RNA or DNA.
XX
PS Example 54; Page 69; 132pp; English.
XX
CC Oligonucleotide ISIS 22114 contains a mixed phosphodiester and
CC phosphorothioate backbone and has 3'-O-(2-methoxyethyl) chemistry. It was
CC used in experiments to determine the effects of snake venom
CC phosphodiesterase and liver homogenate on the stability of
CC oligonucleotides. Novel oligonucleotides of the invention have both A-
CC and B-form conformational geometry. The A-form geometry modulates the
CC binding affinity and nuclease resistance of the oligonucleotide. The B-
CC form geometry allows the oligonucleotide to serve as substrate for RNase-
CC H when bound to a target nucleic acid strand. The oligonucleotides can be
CC used to treat psoriasis and other inflammatory skin conditions, skin
CC cancers and viral, bacterial and fungal infections, and in various
CC diagnostic applications
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482
DB 1 TTTT TTTT TTTT TTTT TTTT 19
RESULT 595
AAA88947 ID AAA88947 standard; DNA; 19 BP.
XX
AC AAA88947;
XX
DT 05-MAR-2001 (first entry)
XX
DE Oligonucleotide ISIS 22110.
XX
KM Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KM dermatological; cytosstatic; virucide; antibacterial; fungicide; therapy;
KM diagnosis; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 16
FT /*tag= a
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl) thymidine"
FT modified_base 17
FT /*tag= b
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl) thymidine"
FT modified_base 18
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl) thymidine"
FT modified_base 19
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl) thymidine"
XX
PN WO200066609-A1.
XX
PD 09-NOV-2000.
XX
XX

Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4482
|||||
1 TTTT TTTT TTTT TTTT TTTT 19

Db

RESULT 592
AAA88949
ID AAA88949 standard; DNA; 19 BP.
AC AAA88949;
XX
XX
DT 05-MAR-2001 (first entry)
XX
DE Oligonucleotide ISIS 22112.
XX
XX Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW diagnosis; ss.
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..19
FT /*tag= e
FT /note= "phosphorothioate linkage"
FT modified_base 16
FT /*tag= a
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT modified_base 17
FT /*tag= b
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT modified_base 18
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT modified_base 19
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
XX
PN WO200066609-A1.
XX
PD 09-NOV-2000.
XX
PF 03-MAY-2000; 2000WO-US011913.
XX
PR 03-MAY-1999; 99US-00303586.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Mohan V;
XX
XX Manoharan M, Mohan V;
XX
XX WPI; 2000-672833/65.
XX
DR
XX
PT New oligonucleotides containing sequences with A and B geometry, used to
PT treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT bacterial infections, bind to single stranded RNA or DNA.
XX
XX
XX Example 54; Page 69; 132pp; English.
XX
CC Oligonucleotide ISIS 22112 contains a phosphorothioate backbone and has
CC 3'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine
CC the effects of snake venom phosphodiesterase and liver homogenate on the
CC stability of oligonucleotides. Novel oligonucleotides of the invention
CC have both A- and B-form conformational geometry. The A-form geometry
CC modulates the binding affinity and nuclease resistance of the

CC oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC as substrate for RNase-H when bound to a target nucleic acid strand. The
CC oligonucleotides can be used to treat psoriasis and other inflammatory
CC skin conditions, skin cancers and viral, bacterial and fungal infections,
CC and in various diagnostic applications

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4482
|||||
1 TTTT TTTT TTTT TTTT TTTT 19

Db

RESULT 593
AAA88950
ID AAA88950 standard; DNA; 19 BP.
AC AAA88950;
XX
XX
DT 05-MAR-2001 (first entry)
XX
DE Oligonucleotide ISIS 22113.
XX
XX Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW diagnosis; DNA-RNA hybrid; ss.
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..19
FT /*tag= f
FT /note= "phosphorothioate linkage"
FT modified_base 16
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)thymidine"
FT modified_base 17
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)thymidine"
FT modified_base 18
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)thymidine"
FT misc_RNA 19
FT /*tag= e
FT /label= RNA
FT modified_base 19
FT /*tag= d
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)uridine"
XX
PN WO200066609-A1.
XX
PD 09-NOV-2000.
XX
PF 03-MAY-2000; 2000WO-US011913.
XX
PR 03-MAY-1999; 99US-00303586.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Mohan V;
XX
XX Manoharan M, Mohan V;
XX
XX WPI; 2000-672833/65.
XX
DR
XX
PT New oligonucleotides containing sequences with A and B geometry, used to
PT treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and

DE	Oligonucleotide ISIS 22115.
XX	
KW	Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KM	dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
XV	diagnosis; DNA-RNA hybrid; ss.
XX	
OS	Synthetic.
FX	
FT	Key Location/Qualifiers
PH	modified_base 1..15
FT	/tag= f
FT	/note= "phosphorothioate linkage"
FT	16
FT	modified_base
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "2'-O-(2-methoxyethyl) thymidine"
FT	17
FT	modified_base
FT	/tag= b
FT	/mod_base= OTHER
FT	/note= "2'-O-(2-methoxyethyl) thymidine"
FT	18
FT	/tag= c
FT	/mod_base= OTHER
FT	/note= "2'-O-(2-methoxyethyl) thymidine"
FT	19
FT	misc_RNA
FT	/tag= e
FT	/label= RNA
FT	19
FT	/tag= d
FT	/mod_base= OTHER
FT	/note= "2'-O-(2-methoxyethyl) uridine"
XX	
NN	WO20066609-A1.
PN	
PD	09-NOV--2000.
XX	
PP	03-MAY--2000; 2000WO-US011913.
PR	
PR	03-MAY-1999; 99US-00303586.
PA	(ISIS-) ISIS PHARM INC.
XX	
PX	Manoharan M, Mohan V;
PI	
DR	WPI; 2000-672833/65.
XX	
XX	New oligonucleotides containing sequences with A and B geometry, used to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and bacterial infections, bind to single stranded RNA or DNA.
PS	Example 54; Page 69; 132pp; English.
XX	
CC	Oligonucleotide ISIS 22115 contains a mixed phosphodiester and phosphorothioate backbone and has 2'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine the effects of snake venom
CC	phosphodiesterase and liver homogenate on the stability of
CC	oligonucleotides. Novel oligonucleotides of the invention have both A-
CC	and B-form conformational geometry. The A-form geometry modulates the
CC	binding affinity and nuclease resistance of the oligonucleotide. The B-
CC	form geometry allows the oligonucleotide to serve as substrate for RNase-
CC	H when bound to a target nucleic acid strand. The oligonucleotides can be
CC	used to treat psoriasis and other inflammatory skin conditions, skin
CC	cancers and viral, bacterial and fungal infections, and in various
CC	diagnostic applications
XX	
SQ	Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
	Query Match 0.3%; Score 19; DB 1; Length 19;
	Best Local Similarity 100.0%; Pred.No. 3.8e+02;
	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	4464 TTTT TTTTTTTTTTTTTTTT 4482

DB	1	TTTTTTTTTTTTTTTTTT	19
RESULT 591			
AAA88965			
ID	AAA88965	standard; DNA; 19 BP.	
XX	AAA88965;		
XX			
XX	05-MAR-2001	(first entry)	
DE	2'-Modified chimeric oligonucleotide.		
XX			
KW	Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic; dermatological; cytostatic; virucide; antibacterial; fungicide; therapy; diagnosis; ss.		
XX			
OS	Synthetic.		
XX			
EH	Key	Location/Qualifiers	
FT	modified_base	16	
FT		/*tag= a	
FT		/mod_base= OTHER	
FT		/note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-	
FT		(F), 2'-ara-(OH), -2'-ara-(OMe) "	
FT	modified_base	17	
FT		/*tag= b	
FT		/mod_base= OTHER	
FT		/note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-	
FT		(F), 2'-ara-(OH), -2'-ara-(OMe) "	
FT	modified_base	18	
FT		/*tag= c	
FT		/mod_base= OTHER	
FT		/note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-	
FT		(F), 2'-ara-(OH), -2'-ara-(OMe) "	
FT	modified_base	19	
FT		/*tag= d	
FT		/mod_base= OTHER	
FT		/note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-	
FT		(F), 2'-ara-(OH), -2'-ara-(OMe) "	
XX			
XX	WO200066609-A1.		
PN			
PD	09-NOV-2000.		
XX			
XX	03-MAY-2000; 2000WO-US011913.		
PF			
XX	03-MAY-1999; 99US-00303586.		
PR			
XX			
PA	(ISIS-) ISIS PHARM INC.		
XX			
PI	Manoharan M, Mohan V;		
XX			
DR	WPI; 2000-672833/65.		
XX			
XX			
PT	New oligonucleotides containing sequences with A and B geometry, used to		
PT	treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and		
PT	bacterial infections, bind to single stranded RNA or DNA.		
XX			
PS	Example 86; Page 102; 132pp; English.		
XX			
XX	This sequence represents 2'-modified chimeric oligonucleotides containing		
CC	2'-modified T. The nucleotides were used to examine the effects of the		
CC	modifications on nuclease resistance. Novel oligonucleotides of the		
CC	invention have both A- and B-form conformational geometry. The A-form		
CC	geometry modulates the binding affinity and nuclease resistance of the		
CC	oligonucleotide. The B-form geometry allows the oligonucleotide to serve		
CC	as substrate for RNase-H when bound to a target nucleic acid strand. The		
CC	oligonucleotides can be used to treat psoriasis and other inflammatory		
CC	skin conditions, skin cancers and viral, bacterial and fungal infections,		
CC	and in various diagnostic applications		
XX			
XX	Sequence 19 BP; 0 A; 0 G; 19 T; 0 U; 0 Other;		

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RESULT 588
AA295240
ID AA295240 standard; DNA; 19 BP.
XX
XX AA295240;
AC
XX
XX 05-JUN-2000 (first entry)
DT
XX
XX Modified oligonucleotide #3 ISIS # 22110.
DE
XX
XX Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 22110;
KW research reagent; therapeutic; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH 1.15
FT misc_feature /tag= a
FT /note= "Phosphorothioate internucleotide linkage"
FT misc_feature 15.19
FT /tag= d
FT /note= "Optionally all phosphorothioate internucleotide
FT linkages"
FT 16.19
FT /tag= c
FT /mod_base= OTHER
FT /note= "Optionally all 3'-O-(2-methoxyhexyl) or all 2'-O-
FT (2-methoxyethyl)"
FT
XX
XX WO200004189-A1.
XX
XX 27-JAN-2000.
XX
XX 13-JUL-1999; 99WO-US015886.
XX
XX 14-JUL-1998; 98US-00115043.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD;
XX
XX MPI; 2000-182445/16.
XX
XX Novel modified oligonucleotides, useful in antisense methodologies,
XX diagnostics, therapeutics and as research reagents.
XX
XX Example 54; Page 59; 75pp; English.
XX
XX This sequence represents a modified oligonucleotide used in the course of
XX the invention. The invention relates to oligonucleotides comprising
XX nucleotides covalently linked together by internucleotide linkages where
XX at least 1 nucleotide is linked to adjacent nucleotide by a 2',5'-
XX internucleotide linkage and bears a 3'-substituent. The oligonucleotides
XX can be used in gene therapy and are also useful in antisense
XX methodologies, diagnostics, therapeutics and as research reagents
XX
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

```

```

DT 19-JUN-2000 (first entry)
XX
XX Modified T-containing oligonucleotide, SEQ ID NO:14.
DE
XX
XX Modified nucleoside; aminoxy group;
KW 2'-deoxy-erythro-pentofuranosyl sugar moiety; nuclease resistant;
XX hybridisation; binding affinity; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH 16.19
FT modified_base /tag= a
FT /note= "These nucleotides are substituted with 2'-O-(2-
FT (N-(2-amino)ethyl-N-(methyl))aminoxyethyl) group"
FT
XX
XX WO200008042-A1.
XX
XX 17-FEB-2000.
XX
XX 09-AUG-1999; 99WO-US017988.
XX
XX 07-AUG-1998; 98US-00130973.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD, Prakash TP, Kawasaki AM;
XX
XX MPI; 2000-224020/19.
XX
XX Aminoxy-modified nucleosides and oligonucleotides useful in diagnostic,
XX therapeutic and research reagents and for modulating the expression of
XX protein in organisms.
XX
XX Example 99; Page 120; 195pp; English.
XX
XX The invention relates to aminoxy-modified nucleosides and
XX oligonucleotides and to oligonucleotides that elicit RNase H for cleavage
XX in a complementary nucleic acid strand. It also relates to
XX oligonucleotides wherein at least some of the nucleotides are
XX functionalised to be nuclease resistant, at least some of the
XX include a substituent that potentiates hybridisation of the
XX oligonucleotide to a complementary strand, and at least some of the
XX nucleotides include a 2'-deoxy-erythro-pentofuranosyl sugar moiety. The
XX inclusion of one or more aminoxy moieties in such oligonucleotides
XX provides for improved binding of such oligonucleotides to a complementary
XX strand. The oligonucleotides of the invention are used as diagnostic,
XX therapeutic or research reagents, and can be used to modulate gene
XX expression in organisms. The oligonucleotides containing the modified
XX nucleosides have increased nuclease resistance and increased binding
XX affinity to a complementary strand. The present sequence represents an
XX oligonucleotide containing nucleotides substituted with a 2'-O-(2-
XX (N-(2-amino)ethyl-N-(methyl))aminoxyethyl) group
XX
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

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```

RESULT 589
AA06839
ID AA06839 standard; DNA; 19 BP.
XX
XX
XX AAA06839;
AC
XX
XX

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```

RESULT 590
AA08952
ID AA08952 standard; DNA; 19 BP.
XX
XX
XX AAA08952;
AC
XX
XX
XX 05-MAR-2001 (first entry)
DT
XX

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```

PT used in diagnostic, therapeutic and research reagents.
XX
XX Disclosure; Page 51; 60pp; English.
XX
XX The present sequence represents an oligomeric compound containing 2'-O-
CC modified ribosyl nucleosides. The oligomeric compound contains
CC phosphodiester linkages. The 2'-O-modified nucleosides include ring
CC structures that position the sugar moiety of the nucleosides
CC preferentially in 3' endo geometries. The modified oligomeric compounds
CC have increased binding affinity and increased nuclease resistance. The
CC oligomeric compounds can be used in diagnostic, therapeutic and research
CC reagents
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4482
1 TTTT TTTT TTTT TTTT TTTT 19

```

```

RESULT 586
AAC62422
ID AAC62422 standard; DNA; 19 BP.
XX
XX AAC62422;
XX
XX 07-FEB-2001 (first entry)
XX
XX T19 diester for use in nuclease stability assay.
DE
XX T19 diester; nuclease stability assay; polymerase chain reaction; PCR;
KW molecular cloning; disease diagnosis; disease treatment; ss.
XX
XX Synthetic.
OS
XX US6127124-A.
PN
XX 03-OCT-2000.
PD
XX 20-JAN-1999; 99US-00234237.
PF
XX 20-JAN-1999; 99US-00234237.
PR
XX 20-JAN-1999; 99US-00234237.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Leeds JM, Cummins LL;
PI
XX WPI; 2000-637737/61.
DR
XX
XX Determining the nuclease stability and relative binding affinity of an
PT oligomeric compound comprises capillary gel electrophoresis using laser-
PT induced fluorescence.
XX
XX Example 3; Col 19-20; 14pp; English.
PS
XX The present invention is concerned with methods of determining the
CC nuclease stability of oligomeric compounds using capillary-gel
CC electrophoresis and laser-induced fluorescence. The methods are useful in
CC the polymerase chain reaction (PCR), molecular cloning and disease
CC diagnosis and treatment. The present sequence was used in a demonstration
CC of the methods of the invention
CC
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4482

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Db 1 TTTT TTTT TTTT TTTT TTTT 19

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RESULT 587
AAZ95241
ID AAZ95241 standard; DNA; 19 BP.
XX
XX AAZ95241;
XX
XX 05-JUN-2000 (first entry)
XX
XX Modified oligonucleotide #3 ISIS # 22111.
DE
XX Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 22111;
KW research reagent; therapeutic; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH 1..15
FT misc_feature /*tag= a
FT /*note= "Phosphorothioate internucleotide linkage"
FT 15..19
FT misc_feature /*tag= d
FT /*note= "Optionally all phosphorothioate internucleotide
FT linkages"
FT 16..19
FT modified_base /*tag= c
FT /*mod_base= OTHER
FT /*note= "Optionally all 3'-O-(2-methoxyhexyl) or all 2'-O-
FT (2-methoxyethyl)"
FT 19
FT misc_RNA /*tag= d
FT
XX WO200004189-A1.
XX
XX 27-JAN-2000.
PD
XX
XX 13-JUL-1999; 99WO-US015886.
PF
XX 14-JUL-1998; 98US-00115043.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Manoharan M, Cook PD;
PI
XX WPI; 2000-182445/16.
DR
XX
XX Novel modified oligonucleotides, useful in antisense methodologies,
PT diagnostics, therapeutics and as research reagents.
PT
XX
XX Example 54; Page 59; 75pp; English.
PS
XX
XX This sequence represents a modified oligonucleotide used in the course of
CC the invention. The invention relates to oligonucleotides comprising
CC nucleotides covalently linked together by internucleotide linkages where
CC at least 1 nucleotide is linked to adjacent nucleotide by a 2',5'-
CC internucleotide linkage and bears a 3'-substituent. The oligonucleotides
CC can be used in gene therapy and are also useful in antisense
CC methodologies, diagnostics, therapeutics and as research reagents
CC
XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;
SQ
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.8e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4482
1 TTTT TTTT TTTT TTTT TTTT 19

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```
PR 09-SEP-1998; 98US-0099658P.
XX
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I, Bougueteleret L;
XX
XX WPI; 1999-405178/34.
XX
XX Use of a prostate cancer associated gene and biallelic markers derived
XX from it.
XX
XX Claim 4; Page 374; 385pp; English.
XX
XX The invention relates to a mammalian Pgl gene and protein, and a set of
XX Pgl biallelic markers. The Pgl polynucleotide and biallelic markers are
XX used in a hybridization assay, a sequencing assay, or in an allele-
XX specific amplification assay for determining the identity of a nucleotide
XX at a Pgl-related biallelic marker. The methods can be used to detect and
XX to assess the risk of developing cancer or prostate cancer. Early-stage
XX diagnosis of prostate cancer relies on prostate specific antigen (PSA)
XX dosage. However, the effectiveness of this is limited due to its
XX inability to discriminate between malignant and non-malignant affections
XX of the organ. A need exists for both a reliable diagnostic procedure
XX which would enable early-stage diagnosis, and for preventative and
XX curative treatments of the disease. The Pgl gene can be used for
XX detection of prostate cancer, and the risk of developing it in the
XX future, and can also be used to determine therapies for the disease
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No.3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4482
Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 584
AAZ61390
ID AAZ61390 standard; DNA; 19 BP.
XX
XX AAZ61390;
AC
XX
XX 19-JUN-2000 (first entry)
DT
XX
XX Uniform phosphodiester oligonucleotide.
DE
XX
XX Oligomeric compound; 2'-O-modified ribosyl nucleoside; 3' endo geometry;
KW nuclease resistance; phosphodiester; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 16 /tag= a
FT /note= "2'-modified T"
FT modified_base 17 /tag= b
FT /note= "2'-modified T"
FT modified_base 18 /tag= c
FT /note= "2'-modified T"
FT modified_base 19 /tag= d
FT /note= "2'-modified T"
XX
XX WO200008044-A1.
XX
XX 17-FEB-2000.
PD
XX
XX 06-AUG-1999; 99WO-US017895.
PF
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XX
XX 07-AUG-1998; 98US-00130566.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD;
XX
XX WPI; 2000-205668/18.
XX
XX Novel 2'-O-aminoethyloxyethyl modified nucleosides and oligonucleotides
XX used in diagnostic, therapeutic and research reagents.
XX
XX Disclosure; Page 44; 60pp; English.
XX
XX The present sequence represents an uniform phosphodiester
XX oligonucleotide. The specification describes oligomeric compounds
XX containing 2'-O-modified ribosyl nucleosides. The 2'-O-modified
XX nucleosides include ring structures that position the sugar moiety of the
XX nucleosides preferentially in 3' endo geometries. The modified oligomeric
XX compounds have increased binding affinity and increased nuclease
XX resistance. The oligomeric compounds can be used in diagnostic,
XX therapeutic and research reagents
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No.3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4482
Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 585
AAZ61404
ID AAZ61404 standard; DNA; 19 BP.
XX
XX AAZ61404;
AC
XX
XX 19-JUN-2000 (first entry)
DT
XX
XX 2'-O-modified ribosyl oligonucleotide with phosphodiester linkages.
DE
XX
XX Oligomeric compound; 2'-O-modified ribosyl nucleoside; 3' endo geometry;
KW nuclease resistance; phosphorothioate; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_feature 1..19 /tag= a
FT /note= "nucleosides linked by phosphodiester linkages"
FT modified_base 16..19 /tag= b
FT /note= "2'-O-[2-N,N-dimethylaminoethyl]oxyethyl-5- methyl
FT uridine"
XX
XX WO200008044-A1.
XX
XX 17-FEB-2000.
PD
XX
XX 06-AUG-1999; 99WO-US017895.
PF
XX
XX 07-AUG-1998; 98US-00130566.
PR
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD;
XX
XX WPI; 2000-205668/18.
XX
XX Novel 2'-O-aminoethyloxyethyl modified nucleosides and oligonucleotides
XX
```

```

XX Sosnowski RG, Butler WF, Tu E, Nerenberg MI, Heller MJ, Edman CF,
PI WPI; 1999-385567/32.
XX
XX
XX New microelectronic device designed to carry out and control multi-step
PT and multiplex molecular biological reactions in microscopic format.
XX
XX Example 1; Page 90; 179pp; English.
XX
CC The specification describes a self-addressable, self-assembling
CC microelectronic device which is designed to actively carry out and
CC control multi-step and multiplex molecular biological reactions in
CC microscopic formats. A key aspect of this invention is played by the ion
CC -permeable permeation layer which overlies the electrode. This permeation
CC layer allows attachment of nucleic acids to permit immobilization but
CC also separates the attached oligonucleotides and hybridized target DNA
CC sequences from the highly reactive electrochemical environment generated
CC immediately at the electrode surface. The microelectronic device is
CC designed and fabricated to actively carry out and control reactions such
CC as nucleic acid hybridizations, antibody/antigen reactions, sample
CC preparation, diagnostics and biopolymer synthesis. The device can
CC electronically control the transport and attachment of specific binding
CC entities, such as nucleic acids and polypeptides, to specific micro-
CC locations. The device can subsequently control the transport and reaction
CC of analytes or reactants at the addressed specific micro-locations. The
CC device is able to concentrate analytes and reactants, remove non-
CC specifically bound molecules, provide stringency control for DNA
CC hybridization reactions and improve the detection of analytes. The
CC present sequence represents a probe used to exemplify the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
QY
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 TTTT TTTT TTTT TTTT TTTT 4482
1 TTTT TTTT TTTT TTTT TTTT 19
RESULT 582
AAZ81927
ID AAZ81927 standard; DNA; 19 BP.
XX
AC AAZ81927;
XX
XX 07-SEP-1999 (first entry)
XX
XX Polynucleotide strand with amino groups.
XX
XX Enzyme-specific cleavable polynucleotide substrate;
XX quenched fluorescent moiety; biological assay; detection; identification;
XX microorganism; sterilization assurance; nuclease; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 7
FT /*tag= a
FT /note= "amine-modified C6 derivative of deoxythymidine
FT (dt) "
FT modified_base 9
FT /*tag= b
FT /note= "amine-modified C6 derivative of deoxythymidine
FT (dt) "
FT modified_base 11
FT /*tag= c
FT /note= "amine-modified C6 derivative of deoxythymidine
FT (dt) "
FT modified_base 13
FT /*tag= d

```

```

FT /note= "amine-modified C6 derivative of deoxythymidine
FT (dt) "
XX
XX WO9935288-A1.
XX
XX 15-JUL-1999.
XX
XX 20-AUG-1998; 98WO-US017311.
XX
XX 13-JAN-1998; 98US-00005260.
XX
XX (MINN ) MINNESOTA MINING & MFG CO.
XX
XX Wei A, Mach PA;
XX
XX WPI; 1999-419356/35.
XX
XX An enzyme-specific cleavable polynucleotide substrate bearing quenched
PT fluorescent moieties.
XX
XX Example 2; Page 20; 34pp; English.
XX
CC The specification describes an enzyme-specific cleavable polynucleotide
CC substrate bearing quenched fluorescent moieties. The enzyme-specific
CC cleavable polynucleotide substrate is useful in biological assays for
CC detection and identification of microorganisms, sterilization assurance,
CC pharmaceutical discovery, enzyme assays, immunoassays and other
CC biological assays. The method provides a rapid and convenient approach
CC for detection and identification of microorganisms. It can be adapted to
CC sequence-dependent or sequence-independent tests. The invention provides
CC improved accuracy, faster detection, and overall lower cost in detection
CC and identification of microorganisms. The presence of nuclease is
CC measured more accurately and sensitively by red-shifting the emission
CC wavelength from far UV region (350-400 nm) to the 500-600 nm region of
CC the electromagnetic spectrum and reducing the effect of background signal
CC levels of intact reagents. The present sequence is used in the course of
CC the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
QY
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 TTTT TTTT TTTT TTTT TTTT 4482
1 TTTT TTTT TTTT TTTT TTTT 19
RESULT 583
AAZ01358
ID AAZ01358 standard; DNA; 19 BP.
XX
AC AAZ01358;
XX
XX 27-SEP-1999 (first entry)
XX
XX PCR primer for PGI biallelic marker 4-4-187.
XX
XX PGI gene; biallelic marker; PCR primer; PGI-related biallelic marker;
XX cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
XX PSA; human; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX WO9932644-A2.
XX
XX 01-JUL-1999.
XX
XX 22-DEC-1998; 98WO-IB002133.
XX
XX 22-DEC-1997; 97US-00996306.
XX

```


KW		phosphorothioate; ras gene; malignant cell growth; aminoxy-modified;
XV		nuclease resistance; reporter group; ss.
XX		Synthetic.
OS		
FH	Key	Location/Qualifiers
FT	modified_base	15..18
FT	/tag=	a
FT	/note=	"5-methyl, 2'-aminoxyethoxy-thymidine"
XX		
PN	WO9835978-A1.	
PD	20-Aug-1998.	
XX		
FP	13-FEB-1998;	98WO-US002405.
XX		
PR	14-FEB-1997;	97US-0037143P.
XX	30-JAN-1998;	98US-00016520.
PA	(ISIS-) ISIS PHARM INC.	
XX		
P1	Cook PD, Manoharan M, Kawasaki AM;	
XX		
DR	WPI; 1998-568232/48.	
XX		
PT	New aminoxy-modified oligonucleotides - which can show improved binding	
FT	to complementary strands and improved resistance to nuclease.	
XX		
PS	Disclosure; Page 84; 131pp; English.	
XX		
CC	The invention relates to aminoxy-modified(oligo)nucleotides or	
CC	nucleosides which are useful as therapeutics, diagnostics, and research	
CC	reagents. They may be used, e.g., for modulation of the ras gene and may	
CC	be able to modulate the process of transformation from normal to	
CC	malignant cell growth. They may be prepared using known methods.	
CC	Inclusion of the aminoxy moieties can improve binding of	
CC	oligonucleotides to complementary strands. The moieties can also provide	
CC	conjugation sites useful for conjugation of useful ligands (e.g. reporter	
CC	groups and groups for modifying uptake, distribution or other	
CC	pharmacodynamic properties) to oligonucleotides. The present sequence	
CC	represents an example of an aminoxy-modified oligonucleotide disclosed	
CC	in the specification	
XX		
SQ	Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;	
OY	Query Match	0.3%; Score 19; DB 1; Length 19;
	Best Local Similarity	100.0%; Pred. No. 3.8e+02;
	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	4464 TTTTTTTTTTTTTTTTTT 4482	
DB	1 TTTTTTTTTTTTTTTTTT 19	
RESULT 580		
ID	AAV06820	
XX	AAV06820 standard; DNA; 19 BP.	
AC	AAV06820;	
DT	13-OCT-1998 (first entry)	
XX		
DE	Oligonucleotide containing modified internucleotide linkage.	
XX		
KX	oligonucleotide; ss.	
XX		
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	modified_base	16..18
FT	/tag=	a
FT	/note=	"these T residues are formed as part of a conventional phosphoramidite oligonucleotide synthesis

[illegible]


```

XX (TEXA ) UNIV TEXAS A & M SYSTEM.
PA Carson DD, Hoeoek M, Liu S;
XX WPI; 1998-495388/42.
XX Use of heparin sulphate/heparin interacting protein - for modulating
PT blood coagulation, e.g. for neutralising heparin, treating diseases
XX involving excessive bleeding or administration to wound sites.
XX Example 1; Page 78; 148pp; English.
XX A method has been developed for identifying a heparin (Hp) component that
CC binds to antithrombin-3 (At-3). The method comprises: (a) contacting a Hp
CC sample suspected of containing a Hp component that binds to At-3 with a
CC heparan sulphate (HS)/Hp interacting protein (HHP) to allow binding of
CC the Hp component; and (b) detecting the binding of the Hp component to
CC the HS/HHP. The present sequence represents a primer for reverse
CC transcriptase PCR of heparan sulfate/heparin interacting protein
CC (HS/HHP). Products from the present invention can be used for modulating
CC blood coagulation. They can be used for neutralising heparin, treating
CC diseases characterised by excessive bleeding or administration to wound
CC sites. The HS/HHPs can also be used for the production of antibodies and
CC in diagnostic applications
XX
SQ Sequence 28 BP; 0 A; 6 C; 4 G; 18 T; 0 U; 0 Other;
Query Match 0.3%; Score 19.2; DB 1; Length 28;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4460 GGAAGCTTTTCTTTTCTTTTCTTTT 4483
DB 5 GCGCCGCTTTTCTTTTCTTTTCTTTT 28

```

RESULT 575
AAZ61254 standard; DNA; 28 BP.

AAZ61254;
30-MAY-2000 (first entry)

Oligo dT primer for honey bee venom PX3.101 cDNA.

Protein PX3.101; honey bee; venom; interleukin-8; IL-8; receptor; CXCR1,
CXCR2; cyclooxygenase; lipoxigenase; phospholipase; protease;
inflammatory disease; gene therapy; cancer; autoimmune disease; pain;
chemokine imbalance; rheumatoid arthritis; multiple sclerosis; psoriasis;
systemic lupus erythematosus; Crohn's disease; vasculitis; scleroderma;
metastatic cancer; Alzheimer's disease; wound healing; aging process;
antigen; primer; ss.

Apis mellifera.
GB2341389-A.
15-MAR-2000.
13-SEP-1999; 99GB-00021605.
14-SEP-1998; 98US-0100172P.
(PAMP-) PAN PACIFIC PHARM INC.
Chi X, Lu Y;
WPI; 2000-185368/17.
Isolated nucleic acids encoding the bee venom protein PX3.101 useful for
treating autoimmune and inflammatory disorders such as rheumatoid

```

PT arthritis.
XX Example 3; Page 43; 83pp; English.
XX The present primer was used for cDNA encoding the protein PX3.101, which
CC is a honey bee venom isolated Apis mellifera. PX3.101 inhibits the
CC binding of interleukin-8 (IL-8) to its receptor (e.g. CXCR1 and CXCR2)
CC and inhibits a variety of enzymes (e.g. cyclooxygenases, lipoxigenases,
CC phospholipases and proteases) associated with inflammatory diseases. The
CC nucleic acids may be used for the recombinant production of PX3.101
CC proteins either in vivo (as part of a gene therapy protocol) or in vitro
CC (as a fermentation culture). The nucleic acids may also be used as probes
CC to identify similar sequences in samples. The PX3.101 protein may be used
CC for the treatment of inflammatory diseases, cancers, autoimmune diseases,
CC pain and/or diseases associated with chemokine (especially IL-8)
CC imbalances such as rheumatoid arthritis, multiple sclerosis, psoriasis,
CC systemic lupus erythematosus (SLE), Crohn's disease, vasculitis,
CC scleroderma, metastatic cancer and Alzheimer's disease in humans. It is
CC also disclosed that the proteins may be used to accelerate wound healing,
CC reduce several aging processes and protect against ultraviolet light. The
CC proteins may also be used as antigens in the production of antibodies to
CC specific for PX3.101. The antibodies may be used as diagnostic agents to
CC detect PX3.101 protein in samples and to down regulate PX3.101 activity
XX
SQ Sequence 28 BP; 0 A; 4 C; 4 G; 20 T; 0 U; 0 Other;
Query Match 0.3%; Score 19.2; DB 1; Length 28;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4460 GGAAGCTTTTCTTTTCTTTTCTTTT 4483
DB 5 GCGCCGCTTTTCTTTTCTTTTCTTTT 28

```

RESULT 576
AAQ43973/C
AAQ43973 standard; DNA; 32 BP.

AAQ43973;
25-MAR-2003 (revised)
28-OCT-1993 (first entry)

Triple helix forming oligonucleotide I.

Purine; pyrimidine; tracts; intramolecular triplex; therapeutic;
diagnostic; control; gene expression; mRNA synthesis suppression; ss.

Synthetic.
WO9312230-A1.
24-JUN-1993.
11-DEC-1992; 92MO-US010792.
13-DEC-1991; 91US-00808452.
21-JAN-1992; 92US-00826934.
(STRI) SRI INT.
Jayasena SD, Johnston BH;
WPI; 1993-214172/26.
New oligo:nucleotide(s) forming triple helix with target nucleic acid -
contain purine and pyrimidine tracts in specific orientations, useful
therapeutically or diagnostically e.g. for inactivating HIV RNA, etc.
Disclosure; Page 47; 101pp; English.
The sequence is that of an oligonucleotide, I, which is able to form a

QY 4470 TTTTGTCTTGAGAC 4493
 |||
 DB 2 TTTTGTCTTGAGAC 25

RESULT 572

ID ADB04574 standard; DNA; 25 BP.

AC ADB04574;

DT 20-NOV-2003 (first entry)

XX Human MD27 scanning oligonucleotide SEQ ID 5560.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;

KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;

XX developmental disorder; ss.

OS Homo sapiens.

XX EPI281758-A2.

XX 05-FEB-2003.

PF 30-JUL-2002; 2002EP-00016874.

PR 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

DR WPI; 2003-423107/40.

PT New zinc finger-containing proteins and nucleic acids, useful in

PT manufacturing a medicament for treating or preventing a disorder

PT associated with decreased or increased expression or activity of MD23,

PT MD24, MD27 or MD212, e.g. cancer.

XX Example 8; SEQ ID NO 5560; 103pp; English.

XX The present invention relates to novel human zinc finger-containing

CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is

CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,

CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome

CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

CC or in manufacturing a medicament for treating or preventing a disorder

CC associated with decreased or increased expression or activity of MD23,

CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic

CC acids and proteins are also useful for diagnosing or monitoring a disease

CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic

CC acids can also be used as probes to detect and characterize gross

CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are

CC useful in constructing microarrays for measuring gene expression. The

CC proteins are useful as therapeutic agents for gene therapy or as

CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 25 BP; 3 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

QY Query Match 0.3%; Score 19.2; DB 1; Length 25;

Best Local Similarity 87.5%; Pred. No. 5.2e+02;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4471 TTTTGTCTTGAGACA 4494

DB 1 TTTTGTCTTGAGACA 24

RESULT 573

AAK15434

ID AAK15434 standard; DNA; 27 BP.

XX AAK15434;
 AC |||
 XX 07-MAY-1999 (first entry)

DT PCR primer used to amplify DNA encoding trehalose phosphorylase.

XX Trehalose phosphorylase; trehalose; D-glucose;

KM alpha-D-glucose-1-phosphate; PCR primer; ss.

XX Synthetic.

OS Grifolia frondosa.

XX WO9844116-A1.

XX 08-OCT-1998.

PF 30-MAR-1998; 98WO-UP001423.

PR 31-MAR-1997; 97JP-00098173.

XX (KURE) KUREHA CHEM IND CO LTD.

XX Horinouchi S, Saitoh K, Takahashi E;

DR WPI; 1998-557113/47.

PT Trehalose phosphorylase from Grifolia frondosa and gene encoding it - for

PT producing enzyme for industrial scale production of trehalose.

XX Example 5; Page 25; 52pp; Japanese.

XX The present PCR primer was used to amplify DNA encoding a trehalose

CC phosphorylase enzyme, and is derived from Grifolia frondosa. Vectors and

CC cells containing the nucleic acid sequence can be used in the large scale

CC production of trehalose phosphorylase for industrial-scale manufacture of

CC trehalose from D-glucose and alpha-D-glucose-1-phosphate. Trehalose is

XX used in the foodstuff and drug industries

XX Sequence 27 BP; 1 A; 3 C; 4 G; 19 T; 0 U; 0 Other;

QY Query Match 0.3%; Score 19.2; DB 1; Length 27;

Best Local Similarity 87.5%; Pred. No. 5.8e+02;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4460 GGAATTTTGTCTTGAGTTT 4483

DB 4 GGAATTTTGTCTTGAGTTT 27

RESULT 574

AAV61015

ID AAV61015 standard; DNA; 28 BP.

AC AAV61015;

XX 03-DEC-1998 (first entry)

DT HS/HIP reverse transcriptase PCR primer #4.

XX Human; heparan sulfate/heparin interacting protein; HIP; diagnosis;

XX blood coagulation; antithrombin-3; bleeding; wound; PCR primer; ss.

XX Synthetic.

XX Homo sapiens.

XX WO9838214-A1.

XX 03-SEP-1998.

XX 27-FEB-1998; 98WO-US003788.

XX 28-FEB-1997; 97US-00810609.

RESULT 570
ABN13917
ID ABN13917 standard; DNA; 25 BP.
XX
XX
AC ABN13917;
XX
DT 29-MAY-2002 (first entry)
XX
XX Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13909.
DE
XX
XX Human: genome-derived myosin-like protein 1; hGDMLP-1; heart;
KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KM skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
OS
XX
XX MO200192524-A2.
PN
XX
PD 06-DEC-2001.
XX
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PR 30-JAN-2001; 2001WO-US000661.
XX
PR 30-JAN-2001; 2001WO-US000662.
XX
PR 30-JAN-2001; 2001WO-US000663.
XX
PR 30-JAN-2001; 2001WO-US000664.
XX
PR 30-JAN-2001; 2001WO-US000665.
XX
PR 30-JAN-2001; 2001WO-US000666.
XX
PR 30-JAN-2001; 2001WO-US000667.
XX
PR 30-JAN-2001; 2001WO-US000668.
XX
PR 30-JAN-2001; 2001WO-US000669.
XX
PR 30-JAN-2001; 2001WO-US000670.
XX
PR 05-FEB-2001; 2001US-0266860P.
XX
XX (ABOM-) AEOMICA INC.
XX
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PI
XX
XX WPI; 2002-179446/23.
XX
XX
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX
XX disclosure; SEQ ID NO 13909; 214pp; English.
XX
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMLP-1
XX nucleic acids can be used as probes to detect, characterize and quantify
XX hGDMLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognize hGDMLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption/ionization, as
XX therapeutic supplement in patients having specific deficiency in hGDMLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMLP-1, in particular heart
XX and skeletal muscle disorders. hGDMLP-1 is localized to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 25 BP; 6 A; 3 C; 12 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.3%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 5542 GGTGTCATGCAGTCGAGAAGT 5565
DB 1 GGCGGTGCATGCAGTCGAGAAGT 24
RESULT 571
ADB04572
ID ADB04572 standard; DNA; 25 BP.
XX
XX
AC ADB04572;
XX
XX
DT 20-NOV-2003 (first entry)
XX
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5558.
XX
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX
XX EP1281758-A2.
PN
XX
PD 05-FEB-2003.
XX
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
XX
PR 02-AUG-2001; 2001US-00922181.
XX
XX
XX (ABOM-) AEOMICA INC.
XX
XX
XX Shannon M, Gu Y, Nguyen C;
PI
XX
XX WPI; 2003-423107/40.
XX
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX
XX Example 8; SEQ ID NO 5558; 103pp; English.
XX
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic loci. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
SQ
Sequence 25 BP; 3 A; 2 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 0.3%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CC diseases and various inflammations. The present sequence is a PCR primer,
CC which was used in an example from the invention
XX
SQ Sequence 24 BP; 1 A; 2 C; 1 G; 20 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 4.9e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4457 CATGACTTTTCTTTT 4480
Db 1 CATGCTTTTCTTTT 24

RESULT 568
AAL51806
ID AAL51806 standard; DNA; 24 BP.

XX AAL51806;

XX 24-APR-2003 (first entry)

XX Short chain dehydrogenase 9-35 PCR primer #2.

XX PCR; primer; ss; short chain dehydrogenase; 9.35; cancer; HIV.

XX Unidentified.

XX CNI363664-A.

XX 14-AUG-2002.

XX 05-JAN-2001; 2001CN-00105049.

XX 05-JAN-2001; 2001CN-00105049.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-751778/82.

XX Polypeptide-short-chain dehydrogenase 9.35 and polynucleotide for coding
PT it.

XX Example 2; Page 17 (Disclosure); 32pp; Chinese.

XX The invention comprises the amino acid and coding sequence of a short
CC chain dehydrogenase 9.35. The DNA and protein sequences of the invention
CC are useful for treating cancer and HIV infection. The present DNA
CC sequence represents a PCR primer for the short chain dehydrogenase 9.35
CC gene

SQ Sequence 24 BP; 2 A; 3 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 4.9e+02;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4470 TTTTCTTTTCTTTGCTGAGAC 4493
Db 1 TTTTCTTTTCTTTGCTGAGAC 24

RESULT 569

ABN13916
ID ABN13916 standard; DNA; 25 BP.

XX ABN13916;

XX 29-MAY-2002 (first entry)

XX Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13908.

XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.

XX Homo sapiens.

XX WO200192524-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US016981.

XX 25-MAY-2000; 2000US-0207456P.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX 30-JAN-2001; 2001WO-US000661.

XX 30-JAN-2001; 2001WO-US000662.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 05-FEB-2001; 2001US-0266860P.

XX (AEOM-) AEOMICA INC.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX WPI; 2002-179446/23.

XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.

XX Disclosure; SEQ ID NO 13908; 214pp; English.

XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognize hGDMLP-
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionization, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localized to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence for the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence

SQ Sequence 25 BP; 5 A; 4 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5542 GGTGTGTCATGCAGATGAGAAAGT 5565

Db 2 GGCGGTGTCATGCAGCTGAGAAAGT 25

CC than conventional libraries. This sequence represents an PCR primer
CC involved in the generation of the gene library described in the method of
CC the invention

SO Sequence 28 BP; 3 A; 1 C; 5 G; 19 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.4; DB 1; Length 28;
Best Local Similarity 95.2%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4459 TGGACTTTTCTTTTCTTTT 4479
DB 8 TGGAGTTTCTTTTCTTTT 28

RESULT 564
ABV76937
ID ABV76937 standard; DNA; 28 BP.

AC ABV76937;

DT 03-MAR-2003 (first entry)

DE Nucleotide sequence of PCR primer SAPCR-2.

XX Nucleic acid synthesis; blocking agent; polymerase; DNA library; PCR;
KM primer; ss.

XX Synthetic.

PN EPI253205-A1.

XX 30-OCT-2002.

PD 24-APR-2001; 2001EP-00109971.

PF 24-APR-2001; 2001EP-00109971.

PR 24-APR-2001; 2001EP-00109971.

XX (LION-) LION BIOSCIENCE AG.

PI Hoefer M, Kranz H, Klink M;

XX WPI; 2003-077619/08.

PT Preferential nucleic acid synthesis reaction of selected regions of
PT target nucleic acids, by using a blocking agent which preferentially
PT binds templates which are not desirable when amplifying the nucleic
PT acids.

XX Example 2; Page 6; 20pp; English.

CC The specification describes a nucleic acid synthesis reaction of selected
CC regions of target nucleic acids from a group of two different target
CC nucleic acids. The method comprises combining in a reaction mixture, two
CC different target nucleic acids, polymerase, additionally combining a
CC blocking agent capable of binding a nucleic acid template molecule so
CC that the polymerase is not able to utilize bound target nucleic acids as
CC a template, and exposing the reaction mixture to a temperature at which
CC nucleic acids are synthesized by the polymerase. The method is useful for
CC nucleic acid synthesis reactions, and is especially useful for creating
CC DNA libraries. The present PCR primer was used in the course of the
CC invention

SO Sequence 28 BP; 3 A; 1 C; 5 G; 19 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.4; DB 1; Length 28;
Best Local Similarity 95.2%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4459 TGGACTTTTCTTTTCTTTT 4479
DB 8 TGGAGTTTCTTTTCTTTT 28

RESULT 565
ACC48482
ID ACC48482 standard; DNA; 21 BP.

AC ACC48482;

DT 11-AUG-2003 (first entry)

DE Locked nucleic acid anchored oligo(I) primer ON12.

XX Locked nucleic acid; LNA; gene therapy; primer; ss.

XX Synthetic.

OS Key

FT modified_base

FT modified_base

FT modified_base

FT modified_base

FT modified_base

FT modified_base

FT modified_base

FT modified_base

FT modified_base

FT modified_base

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FT modified_base

FT modified_base

WO2003020739-A2.

13-MAR-2003.

04-SEP-2002; 2002WO-IB003911.

04-SEP-2001; 2001US-0317034P.

22-SEP-2001; 2001US-0323967P.


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XX WO2003037931-A2.
XX
XX 08-MAY-2003.
XX
XX 01-NOV-2002; 2002WO-US035129.
XX
XX 01-NOV-2001; 2001US-0334773P.
XX
XX (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
XX Shannon M, Phan T;
XX
XX WPI; 2003-430501/40.
XX
XX
XX New isolated nucleic acid molecule encoding a human angiomotin-like
XX protein, useful for treating or preventing a disorder associated with
XX decreased or increased expression or activity of AMLP1.
XX
XX Example 2; SEQ ID NO 537; 172pp; English.
XX
XX The present invention describes the human angiomotin-like protein 1
XX (AMLPI). human AMLPI has cytostatic activity, and can be used in gene
XX therapy. The AMLPI protein, nucleic acid molecules, antibodies, and
XX compositions of the present invention can be used for treating or
XX preventing a disorder associated with decreased or increased expression
XX or activity of AMLPI. The present sequence represents a scanning
XX oligonucleotide for human AMLPI, which is used in an example from the
XX present invention.
XX
XX Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.3%; Score 19.4; DB 1; Length 25;
XX Best Local Similarity 95.2%; Pred. No. 4.8e+02;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 7415 GCAGCAGCAGCAGCAGCAGCA 7435
XX |||||||||||||||||||
XX 2 GCAGCAGCAGCAGCAGCAGCA 22
XX
XX
XX RESULT 562
XX ADC38185
XX ID ADC38185 standard; DNA; 25 BP.
XX
XX ADC38185;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human AMLPIa scanning 25-mer oligonucleotide SEQ ID NO:534.
XX
XX human; angiomotin-like protein 1; AMLPI; cytostatic; gene therapy;
XX AMLPIa; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO2003037931-A2.
XX
XX 08-MAY-2003.
XX
XX 01-NOV-2002; 2002WO-US035129.
XX
XX 01-NOV-2001; 2001US-0334773P.
XX
XX (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
XX Shannon M, Phan T;
XX
XX WPI; 2003-430501/40.
XX
XX New isolated nucleic acid molecule encoding a human angiomotin-like
XX protein, useful for treating or preventing a disorder associated with

```

```

PT decreased or increased expression or activity of AMLPI.
XX
XX Example 2; SEQ ID NO 534; 172pp; English.
XX
XX The present invention describes the human angiomotin-like protein 1
XX (AMLPI). human AMLPI has cytostatic activity, and can be used in gene
XX therapy. The AMLPI protein, nucleic acid molecules, antibodies, and
XX compositions of the present invention can be used for treating or
XX preventing a disorder associated with decreased or increased expression
XX or activity of AMLPI. The present sequence represents a scanning
XX oligonucleotide for human AMLPI, which is used in an example from the
XX present invention.
XX
XX Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.3%; Score 19.4; DB 1; Length 25;
XX Best Local Similarity 95.2%; Pred. No. 4.8e+02;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 7415 GCAGCAGCAGCAGCAGCAGCA 7435
XX |||||||||||||||||||
XX 5 GCAGCAGCAGCAGCAGCAGCA 25
XX
XX
XX RESULT 563
XX AAH48768
XX ID AAH48768 standard; DNA; 28 BP.
XX
XX AAH48768;
XX
XX 16-NOV-2001 (first entry)
XX
XX Murine liver cDNA library PCR primer #2.
XX
XX Murine; liver; gene library; amino acid synthesis; binding protein;
XX cell metabolism; energy metabolism; fatty acid metabolism; synthesis;
XX phospholipid metabolism; purine; pyrimidine; nucleoside; nucleotide;
XX replication; transcription; translation; transport protein; PCR primer;
XX ss.
XX
XX Mus musculus.
XX
XX
XX Key Location/Qualifiers
XX modified_base 1
XX /tag= a
XX /mod_base= OTHER
XX /note= "5'-biotinylated"
XX
XX DE20103510-U1.
XX
XX 07-JUN-2001.
XX
XX 28-FEB-2001; 2001DE-02003510.
XX
XX 28-FEB-2001; 2001DE-02003510.
XX
XX (LION-) LION BIOSCIENCE AG.
XX
XX WPI; 2001-368570/39.
XX
XX Gene library containing sequences with specific 3'-ends and no polyA
XX tail, encoding proteins involved in a wide range of cellular processes.
XX
XX Example; Page 7; 251pp; German.
XX
XX This invention describes a novel gene library (A) comprises a gene
XX sequence (or its part) encoding a protein involved in amino acid
XX synthesis, cellular/energy metabolism, metabolism of fatty
XX acids/phospholipids, synthesis or breakdown of
XX purines/pyrimidines/nucleosides/nucleotides, DNA
XX replication/transcription/translation, or is a transport/binding protein.
XX (A) are produced that correspond to the 3'-end of mRNA but without the
XX polyA tail. They can be prepared more efficiently and with less effort

```

CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX
SQ Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
Query Match 0.3%; Score 19.4; DB 1; Length 25;
Best Local Similarity 95.2%; Pred. No. 4.8e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7415 GCAGCAGCAGCAGCAGCAGCA 7435
Db 3 GCAGCAGCAGCAGCAGCAGCA 23
RESULT 559
ID ADC38189 standard; DNA; 25 BP.
XX
AC ADC38189;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:538.
XX
KW human; angiotensin-like protein 1; AMLP1; cytostatic; gene therapy;
KM AMLP1a; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003037931-A2.
XX
PD 08-MAY-2003.
XX
PF 01-NOV-2002; 2002WO-US035129.
XX
PR 01-NOV-2001; 2001US-0334773P.
XX
PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX
PI Shannon M, Phan T;
XX
DR WPI; 2003-430501/40.
XX
PT New isolated nucleic acid molecule encoding a human angiotensin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX
PS Example 2; SEQ ID NO 538; 172bp; English.
XX
CC The present invention describes the human angiotensin-like protein 1
CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX
SQ Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
Query Match 0.3%; Score 19.4; DB 1; Length 25;
Best Local Similarity 95.2%; Pred. No. 4.8e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7415 GCAGCAGCAGCAGCAGCAGCA 7435
Db 1 GCAGCAGCAGCAGCAGCAGCA 21

RESULT 560
ID ADC38186 standard; DNA; 25 BP.
XX
AC ADC38186;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:535.
XX
KW human; angiotensin-like protein 1; AMLP1; cytostatic; gene therapy;
KM AMLP1a; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003037931-A2.
XX
PD 08-MAY-2003.
XX
PF 01-NOV-2002; 2002WO-US035129.
XX
PR 01-NOV-2001; 2001US-0334773P.
XX
PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX
PI Shannon M, Phan T;
XX
DR WPI; 2003-430501/40.
XX
PT New isolated nucleic acid molecule encoding a human angiotensin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX
PS Example 2; SEQ ID NO 535; 172bp; English.
XX
CC The present invention describes the human angiotensin-like protein 1
CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX
SQ Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
Query Match 0.3%; Score 19.4; DB 1; Length 25;
Best Local Similarity 95.2%; Pred. No. 4.8e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7415 GCAGCAGCAGCAGCAGCAGCA 7435
Db 4 GCAGCAGCAGCAGCAGCAGCA 24
RESULT 561
ID ADC38188 standard; DNA; 25 BP.
XX
AC ADC38188;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:537.
XX
KW human; angiotensin-like protein 1; AMLP1; cytostatic; gene therapy;
KM AMLP1a; ss.
XX
OS Synthetic.
OS Homo sapiens.

```

XX 20-FEB-1998 (first entry)
XX
XX DNA probe used in fingerprinting technique.
XX
XX probe; screening; fingerprinting; assay; 3' termini; hybridisation; ss.
XX
XX Synthetic.
XX
XX EP778351-A2.
XX
XX 11-JUN-1997.
XX
XX 26-NOV-1996; 96EP-00118921.
XX
XX 30-NOV-1995; 95JP-00311949.
XX
XX (HITA ) HITACHI LTD.
XX
XX Kambara H, Okano K, Uematsu C;
XX
XX WPI, 1997-300347/28.
XX
XX Nucleic acid assay methods - based on restriction fragment length
XX determination.
XX
XX Example 1; Page 7; 21pp; English.
XX
XX The present sequence is a DNA probe used in a novel method of analysis or
XX assay for nucleotides, which comprises: (i) digesting DNA with a
XX restriction enzyme; (ii) discriminating a difference in sequences of the
XX DNA fragments obtained around the 3' termin with a DNA probe and
XX extending the DNA probe by a complementary strand synthesis to
XX fractionate the DNA fragments into groups; and (iii) measuring lengths of
XX the DNA fragments which belong to the groups, or length of the extended
XX DNA probe, and using the lengths obtained for the fragments around the 3'
XX termin as fingerprints. Where polyA is present, the presence of
XX recognition sequence GCG is critical for clarifying the terminal site,
XX this is because the length of polyA cannot be controlled. The method is
XX useful for assaying a large number of cDNA molecules or DNA fragments and
XX for assaying long DNA sequences
XX
XX Sequence 24 BP; 0 A; 2 C; 1 G; 19 T; 0 U; 2 Other;
XX
XX Query Match 0.3%; Score 19.4; DB 1; Length 24;
XX Best Local Similarity 95.2%; Pred. No. 4.5e+02;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT G 4464
XX ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT CG 21
XX
XX RESULT 557
XX ID ADC38190 standard; DNA; 25 BP.
XX
XX AC ADC38190;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:539.
XX
XX human; angiotensin-like protein 1; AMLP1; cytosstatic; gene therapy;
XX AMLP1a; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX WO2003037931-A2.
XX
XX 08-MAY-2003.
XX

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PF      01-NOV-2002; 2002WO-US035129.
XX
XX      01-NOV-2001; 2001US-0334773P.
XX
XX      (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
XX      Shannon M, Phan T;
XX
XX      WPI; 2003-430501/40.
XX
XX      New isolated nucleic acid molecule encoding a human angiomotin-like
XX      PT protein, useful for treating or preventing a disorder associated with
XX      PT decreased or increased expression or activity of AMLP1.
XX
XX      Example 2; SEQ ID NO 539; 172bp; English.
XX
XX      The present invention describes the human angiomotin-like protein 1
XX      CC (AMLPI). human AMLPI has cytostatic activity, and can be used in gene
XX      CC therapy. The AMLPI protein, nucleic acid molecules, antibodies, and
XX      CC compositions of the present invention can be used for treating or
XX      CC preventing a disorder associated with decreased or increased expression
XX      CC or activity of AMLPI. The present sequence represents a scanning
XX      CC oligonucleotide for human AMLPIa, which is used in an example from the
XX      CC present invention.
XX
XX      Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
XX
SQ      Query Match      0.3%; Score 19.4; DB 1; Length 25;
XX      Beet local Similarity 95.2%; Pred. No. 4.8e+02;
XX      Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY      7413 CAGCAGCAGCAGCAGCAGCAG 7433
XX      1 CAGCAGCAGCAACAGCAGCAG 21
XX
DB
XX
RESULT 558
ADCC3187
XX      ID      ADC3187 standard; DNA; 25 BP.
XX
XX      AC      ADC3187;
XX
XX      DT      18-DEC-2003 (first entry)
XX
XX      DE      Human AMLPIa scanning 25-mer oligonucleotide SEQ ID NO:536.
XX
XX      KW      human; angiomotin-like protein 1; AMLPI, cytostatic; gene therapy;
XX      KW      AMLPIa; ss.
XX
XX      OS      Synthetic.
XX      OS      Homo sapiens.
XX
XX      PN      WO2003037931-A2.
XX
XX      PD      08-MAY-2003.
XX
XX      PF      01-NOV-2002; 2002WO-US035129.
XX
XX      PR      01-NOV-2001; 2001US-0334773P.
XX
XX      PA      (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
XX      PI      Shannon M, Phan T;
XX
XX      WPI; 2003-430501/40.
XX
XX      New isolated nucleic acid molecule encoding a human angiomotin-like
XX      PT protein, useful for treating or preventing a disorder associated with
XX      PT decreased or increased expression or activity of AMLPI.
XX
XX      Example 2; SEQ ID NO 536; 172bp; English.
XX
XX      The present invention describes the human angiomotin-like protein 1

```

Oy	4464	TTTTTTTTTTTTTTTTTTTG 4464
Db	1	TTTTTTTTTTTTTTTTTTG 21
RESULT	554	
ID	ABK99283/C	
XX	ABK99283 standard; RNA; 21 BP.	
AC	ABK99283;	
XX		
DT	21-OCT-2002 (first entry)	
XX		
DE	Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #13.	
KM		
XX	Hepatitis C virus; HCV, NS5B replicase; ss, RNA polymerase.	
OS	Synthetic.	
XX		
PN	US2002064771-A1.	
XX		
PD	30-MAY-2002.	
XX		
PF	06-APR-2001; 2001US-00828034.	
XX		
PR	07-APR-2000; 2000US-0195852P.	
XX		
PA	(ZHON/) ZHONG W.	
PA	(HONG/) HONG Z.	
XX	(FERR/) FERRARI E.	
XX		
PI	Zhong W, Hong Z, Ferrari E;	
XX		
DR	WPI; 2002-582330/62.	
XX		
PT	Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3	
PT	nucleotide-long template to which a 2 nucleotide-long primer is annealed,	
PT	and template and primer which do not form a stable duplex in the absence	
XX	of HCV NS5B.	
XX		
XX	Example; Page 6; 17pp; English.	
XX		
XX	The invention relates to a replicase complex comprising a hepatitis C	
CC	virus (HCV) NS5B replicase protein, a linear nucleic acid template and a	
CC	complementary nucleic acid primer which is annealed to the 3' terminus of	
CC	the template, where the template is at least three nucleotides and the	
CC	primer is two or three nucleotides, and the template and primer do not	
CC	form a stable duplex in solution in the absence of the HCV NS5B protein.	
CC	The complex is useful for determining HCV replicase activity and permits	
CC	establishment of sensitive RNA-dependent RNA polymerase assays to screen	
CC	and evaluate antiviral inhibitors and to improve the specificity and	
CC	efficacy of the inhibitors. The complex is also useful in the development	
CC	of a reliable system for determining kinetic and thermodynamic constants	
CC	of HCV NS5B-catalysed nucleotide incorporation and investigation of	
CC	mechanistic inhibitors for mis-incorporation or chain termination.	
CC	Specifically, the short RNA template and primer pairs are useful in	
CC	screening assays which are used for determining kinetic, thermodynamic	
CC	and mechanistic properties of NS5B replication and ultimately in the	
CC	development of inhibitors of NS5B. Newly identified inhibitors of	
CC	replicase activity may be used for developing anti-HCV pharmaceuticals.	
CC	Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis	
CC	templates	
XX		
XX		
SQ	Sequence 21 BP; 16 A; 3 C; 1 G; 0 T; 1 U; 0 Other;	
XX		
Qy	Query Match	0.3%; Score 19.4; DB 1; Length 21;
XX	Best Local Similarity	95.2%; Pred. No. 3.7e+02;
Db	Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
XX		
XX	4460 GGACTTTTTTTTTTTTTTTT 4460	
XX		
XX	21 GGACTGTTTTTTTTTTTTTTT 1	
XX		

RESULT	555
ID	ABZ81769 standard; DNA; 21 BP.
XX	
AC	ABZ81769;
XX	
DT	11-JUN-2003 (first entry)
XX	
DE	Huntington's disease gene mutated exon 1 region.
XX	
KW	Huntington's disease; neurotropic; anticonvulsant; huntingtin; human;
XX	
RW	gene therapy; mutant; ds.
XX	
OS	Homo sapiens.
OS	Synthetic.
FH	
FT	Key Location/Qualifiers
FT	mutation replace(10,C)
FT	/tag= a
PX	
PN	MO2003013437-A2.
XX	
PD	20-FEB-2003.
XX	
PF	07-AUG-2002; 2002WO-US025352.
XX	
PR	07-AUG-2001; 2001US-0310757P.
PR	08-AUG-2001; 2001US-0310770P.
PR	08-AUG-2001; 2001US-0310889P.
PR	04-DEC-2001; 2001US-0337219P.
XX	
PA	(UYDE) UNIV DELAWARE.
PI	
PI	Kmiec EB, Parekh-Olimedo H;
DR	WPI; 2003-256476/25.
XX	
PT	New single stranded oligonucleotides comprising a DNA domain having at
PT	least one mismatch with respect to the genetic sequence of the
PT	Huntington's disease gene to be altered, useful for treating or
PT	preventing Huntington's disease.
XX	
PS	Example 1, Fig 6b; 133pp; English.
CC	The present sequence is that of a portion of a mutated glutamine (CAG)
CC	triplet repeat region of exon 1 of the human Huntington's disease (HD)
CC	gene (see also ABZ81769). The triplet repeat region (see ABZ81767) is
CC	mutated following treatment with an RNA/DNA chimeric oligonucleotide (see
CC	ABZ81768) that causes a CAG (Gln) to TAG (stop) gene alteration in the HD
CC	exon 1 repeats due to sliding of the repeat region, a phenomenon that can
CC	occur with the methods of this invention. The RNA/DNA chimeric
CC	oligonucleotide is an example of oligonucleotides of the invention for
CC	targased alteration of the HD gene. Such oligonucleotides can be used for
CC	the treatment or prevention of HD
XX	
SQ	Sequence 21 BP; 7 A; 6 C; 7 G; 1 T; 0 U; 0 Other;
QY	
Query Match	0.3%; Score 19.4; DB 1; Length 21;
Best Local Similarity	95.2%; Pred. No. 3.7e+02;
Matches 20; Conservative % 0; Mismatches 1; Indels 0; Gaps 0;	
DB	
7413 CAGCAGCAGCAGCAGCAG 7433	
1 CAGCAGCAGTAGCAGCAGCAG 21	
RESULT 556	
AAT68615	
ID	AAT68615 standard; DNA; 24 BP.
XX	
AC	AAT68615;


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XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX
XX Disclosure; Page 6; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTTGTGCT 4487
Db 1 TTTTGTGCT 21

RESULT 549
AAQ75685
ID AAQ75685 standard; DNA; 21 BP.
XX
XX AAQ75685;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX 16-APR-1993; 93JP-00112515.
PA
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX
XX Disclosure; Page 7; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTTGTGCT 4487
Db 1 TTTTGTGCT 21

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CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTTGTGCT 4487
Db 1 TTTTGTGCT 21

RESULT 550
AAQ75645
ID AAQ75645 standard; DNA; 21 BP.
XX
XX AAQ75645;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX 16-APR-1993; 93JP-00112515.
PA
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX
XX Disclosure; Page 6; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTTGTGCT 4487
Db 1 TTTTGTGCT 21

RESULT 551
AAQ75673
ID AAQ75673 standard; DNA; 21 BP.
XX

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XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c) the
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 3.7e+02;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 4464 TTTTGTGCTC 4484
DB 1 TTTTGTGCTC 21
XX
XX RESULT 546
XX ID .AAQ75621 standard; DNA; 21 BP.
XX AC AAQ75621;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX PT Analysis; gene expression; reverse transcription; primer; cDNA;
XX KM aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 3.7e+02;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Query Match 0.3%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 3.7e+02;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 4467 TTTTGTGCTC 4487
DB 1 TTTTGTGCTC 21
XX
XX RESULT 547
XX ID AAQ75746 standard; DNA; 21 BP.
XX AC AAQ75746;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX PT Analysis; gene expression; reverse transcription; primer; cDNA;
XX KM aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 3.7e+02;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 4466 TTTTGTGCTC 4486
DB 1 TTTTGTGCTC 21
XX
XX RESULT 548
XX ID AAQ75637 standard; DNA; 21 BP.
XX AC AAQ75637;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX PT Analysis; gene expression; reverse transcription; primer; cDNA;
XX KM aggregate; restriction enzyme; ss.
XX OS Synthetic.

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```

CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;
Query Match 0.3%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4465 TTTTCTTTTCTTTTCTG 4485
DB 1 TTTTCTTTTCTTTTCTG 21

RESULT 543
AAQ75649
ID AAQ75649 standard; DNA; 21 BP.
XX
AC AAQ75649;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
DR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
Query Match 0.3%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4467 TTTTCTTTTCTTTTCTG 4487
DB 1 TTTTCTTTTCTTTTCTG 21

RESULT 544
AAQ75714
ID AAQ75714 standard; DNA; 21 BP.

```

```

XX
XX AAQ75714;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 0.3%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4466 TTTTCTTTTCTTTTCTG 4486
DB 1 TTTTCTTTTCTTTTCTG 21

RESULT 545
AAQ75775
ID AAQ75775 standard; DNA; 21 BP.
XX
XX
XX AAQ75775;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 0.3%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4466 TTTTCTTTTCTTTTCTG 4486
DB 1 TTTTCTTTTCTTTTCTG 21

```


OS		Streptococcus dysgalactiae.
XX		
XX	MO200196380-A2.	
PN		
PD	20-DEC-2001.	
XX		
PF	11-JUN-2001; 2001WO-CA000837.	
FR	12-JUN-2000; 2000US-0211016P.	
XX		
PA	(UYSA-) UNIV SASRATCHEMAN.	
PI	Potter AA, Bolton AJ, Song XM;	
XX		
DR	WPI; 2002-106467/14.	
XX		
PT	Novel vaccine composition comprising Mlg protein (Fc receptor) of	
PT	Streptococcus dysgalactiae useful for treating or preventing	
PT	streptococcal infection such as mastitis in vertebrates.	
XX		
PS	Example 1; Page 33; 60pp; English.	
XX		
CC	The invention relates to a vaccine composition comprising a vehicle and	
CC	an Fc receptor protein. Streptococcus dysgalactiae Mlg protein. The	
CC	sequence and composition are useful for treating or preventing a	
CC	bacterial infection e.g. a streptococcal infection which causes mastitis	
CC	in a vertebrate subject. The vaccine compositions can also be used to	
CC	treat other streptococcal infections caused by S. agalactiae, such as	
CC	septicemia, meningitis, bacteraemia, impetigo, arthritis, urinary tract	
CC	infections, abscesses and spontaneous abortion. This sequence represents	
CC	a sequencing primer used to determine the DNA sequence encoding the S.	
CC	dysgalactiae Mlg protein of the invention	
SO		
	Sequence 30 BP; 14 A; 5 C; 8 G; 3 T; 0 U; 0 Other;	
	Query Match	0.3%; Score 19.6; DB 1; Length 30;
	Best Local Similarity 84.6%; Pred.No. 5.7e+02;	
	Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
OY	7203 GGTTTCACTTAGTTCTTAACATT 7228	
DB	30 GTTTTCGCTTAGTTCTAGACTCT 5	
	RESULT 538	
	AAQ75669	
ID	AAQ75669 standard; DNA; 21 BP.	
AC		
XX	AAQ75669;	
XX		
DT	04-AUG-1995 (first entry)	
XX		
DE	Reverse transcription primer used in cDNA analysis technique.	
KM	Analysis; gene expression; reverse transcription; primer; cDNA;	
KX	aggregate; restriction enzyme; ss.	
XX		
OS	Synthetic.	
XX		
FN	JF06303997-A.	
XX		
PD	01-NOV-1994.	
XX		
PF	16-APR-1993; 93JP-00112515.	
XX		
RR	16-APR-1993; 93JP-00112515.	
XX		

```

PA      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR      WPI; 1995-018287/03.
XX
PT      Analysis of cDNA and gene expression - by amplification of mRNA followed
PT      by digestion with restriction enzymes.
XX
PS      Disclosure; Page 7; 11pp; Japanese.
XX
CC      A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC      labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC      and using the aggregate of mRNAs as the template for each reverse
CC      transcription primer; (b) digesting each of the prepared aggregates of
CC      the double-stranded cDNAs with restriction enzyme and; (c)
CC      electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC      method can be used to analyse gene expression rapidly and easily
XX
SQ      Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
SO
Query Match          0.3%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.7e+02;
Matches    20; Conservative   0; Mismatches    1; Indels     0; Gaps    0;

Cy      4467 TTTTGTGCTC 4487
           |||||
Db       1 TTTTTTTTTTGCTT 21

RESULT 539
AAQ75618
ID      AAQ75618 standard; DNA; 21 BP.
XX
AC      AAQ75618;
XX
DT      04-AUG-1995 (first entry)
XX
DE      Reverse transcription primer used in cDNA analysis technique.
XX
KW      Analysis; gene expression; reverse transcription; primer; cDNA;
KW      aggregate; restriction enzyme; ss.
XX
OS      Synthetic.
XX
PN      JP06303997-A.
PD
PP      01-NOV-1994.
PX
PF      16-APR-1993; 93JP-00112515.
PR
PR      16-APR-1993; 93JP-00112515.
XX
PA      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
WPI; 1995-018287/03.
XX
PT      Analysis of cDNA and gene expression - by amplification of mRNA followed
PT      by digestion with restriction enzymes.
XX
PS      Disclosure; Page 6; 11pp; Japanese.
XX
CC      A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC      labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC      and using the aggregate of mRNAs as the template for each reverse
CC      transcription primer; (b) digesting each of the prepared aggregates of
CC      the double-stranded cDNAs with restriction enzyme and; (c)
CC      electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC      method can be used to analyse gene expression rapidly and easily
XX
SQ      Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
SO
Query Match          0.3%; Score 19.4; DB 1; Length 21;

```

```
DE Primer for PR-Q gene.
XX
XX Chemically regulatable DNA promoter; expression control; pesticide;
XX herbicide tolerance; pathogenesis-related gene; PR gene; primer; ss.
OS Synthetic.
OS Nicotiana acuminata.
XX
XX US5851766-A.
XX
XX
XX 22-DEC-1998.
PD
PF 31-MAY-1995; 95US-00456262.
XX
PR 31-MAY-1995; 95US-00456262.
PA (NOVS ) NOVARTIS FINANCE CORP.
XX
XX Harms C, Ryals JA;
PI WPI; 1999-080396/07.
XX
DR Isolating chemically regulatable DNA sequences in plants - useful for
PT chemically controlling expression in transformed plants.
XX
PS Example 72; Col 96; 175pp; English.
XX
XX This sequence represents a primer used to isolate the tobacco
CC pathogenesis-related (PR) gene. The PR gene can be isolated using the
CC method of the invention. The method is for isolating a chemically
CC regulatable DNA promoter fragment from the 5' flanking region of a
CC chemically regulatable gene in a plant tissue. The method allows
CC isolation of sequences which will be useful for the controlled expression
CC of genes, under the control of a non-coding regulatable sequence. This is
CC useful in plants with a herbicide or pesticide detoxification mechanism
CC under the control of a chemical regulator, the regulator being applied
CC before or with the herbicide or pesticide to give optimal tolerance. The
CC promoter fragment is useful for controlling sequences which encode traits
CC such as height, shape, development, male or female sterility, and the
CC ability of the plant to withstand cold, heat, salt and drought. The
CC chemical induction of the promoter allows the regulation of production of
CC compounds, e.g. flavours, fragrances, pigments, natural sweeteners,
CC industrial feedstocks, antimicrobials and pharmaceuticals, by
CC biosynthesis or metabolic conversion, whose biosynthesis is controlled
CC by endogenous or foreign genes. The method allows control over the time
CC and rate of gene expression either throughout the whole plant, or in
CC localised tissues, to achieve e.g. fungal or insect resistance by for
CC instance dusting the leaves with the chemical regulator. Controlling the
CC developmental processes by the application of a regulating chemical in
CC e.g. the commercial production of cultivated crops allows processes such
CC as germination, flower formation and fruit ripening to be synchronised at
CC a given time
XX
XX
SQ Sequence 30 BP; 20 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
OY
Query Match 0.3%; Score 19.6; DB 1; Length 30;
Best Local Similarity 84.6%; Pred.No.5.7e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0
4463 CTTTTTTTCTTTTTCGCTT 4488
DB 30 CTTATGTTTTTTTTTTTGATT 5
RESULT 536
AAV81666/C
ID AAV81666 standard; DNA; 30 BP.
XX
XX AAV81666;
AC
XX 25-FEB-1999 (first entry)
DT
XX Oligonucleotide SEQ ID NO:85 used in Example 72.
DE
```

```

XX      Regulation; transcription; plant tissue; chimeric construction; PR;
KM      pathogenesis-related protein; anti-pathogenic; transgenic plant;
KW      beta-1,3-glucanase activity; pest resistance; primer; ss.
XX
XX      Synthetic.
OS
XX      US5847258-A.
PN
XX      08-DEC-1998.
PD
XX
XX      31-MAY-1995;      95US-00457364.
PF
XX
XX      08-MAR-1988;      88US-00165667.
PR      06-FEB-1989;      89US-00305566.
PR      24-MAR-1989;      89US-00329018.
PR      20-JUN-1989;      89US-00368672.
PR      20-OCT-1989;      89US-00425504.
PR      07-SEP-1990;      90US-00580431.
PR      21-DEC-1990;      90US-00632441.
PR      01-APR-1991;      91US-00678378.
PR      27-SEP-1991;      91US-00768122.
PR      06-MAR-1992;      92US-00848506.
PR      06-NOV-1992;      92US-00973197.
PR      06-APR-1993;      93US-00042847.
PR      12-APR-1993;      93US-00045957.
PR      16-JUL-1993;      93US-00093301.
PR      13-JAN-1994;      94US-00181271.
PR      31-MAY-1995;      95US-00457364.
XX
XX      (NOVS ) NOVARTIS FINANCE CORP.
PA
XX
XX      Payne GB, Ward ER, Moyer MB, Ryals JA;
PI
XX      WPI; 1999-059180/05.
XX
XX      DNA encoding pathogenesis-related glucanase proteins - useful for
PT      producing transgenic plants with enhanced disease or pest resistance.
XX
XX      Example 72; Col 93; 169pp; English.
XX
XX      The present invention describes a DNA molecule encoding a pathogenesis-
CC      related (PR) protein having beta-1,3-glucanase activity selected from PR-
CC      2, PR-2', PR-2'', PR-N, PR-O and PR-O'. Also described are: (i) a
CC      chimeric gene comprising the above DNA molecule linked to a heterologous
CC      promoter; (ii) a vector containing the chimeric gene; (iii) a host cell
CC      containing the chimeric gene; (iv) a transgenic plant containing the
CC      chimeric gene; and (v) a seed from the transgenic plant. The DNA molecule
CC      is used to produce transgenic plants with enhanced disease or pest
CC      resistance. The present sequence represents an oligonucleotide from the
CC      present invention
XX
XX      SQ      Sequence 30 BP; 20 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX      Query Match      0.3%; Score 19.6; DB 1; Length 30;
XX      Best Local Similarity 84.6%; Pred. No. 5.7e+02;
XX      Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX      QY      4463 CTTTCTTTTCTTTTCTTTTCTT 4488
XX      ||| ||| ||| ||| ||| ||| ||| |||
XX      DB      30 CTTATGTTTTTTTTTTTTTTGGAATT 5
XX
XX      RESULT 537
XX      AAS1818/c
XX      ID      AAS18118 standard; DNA; 30 BP.
XX
XX      AC      AAS18118;
XX
XX      DT      26-MAR-2002 (first entry)
XX
XX      Streptococcus dysgalactiae Mig DNA sequencing primer mig-7.
XX

```


KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
 XX antiinflammatory; inflammatory disease; autoimmune disease; ds.
 OS Homo sapiens.
 XX WO200119844-A1.
 XX PD 22-MAR-2001.
 XX PF 13-SEP-2000; 2000WO-US024966.
 XX PR 13-SEP-1999; 99US-0153625P.
 XX PA (NYRB-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
 XX PI Crow MK, Li Y;
 XX WI; 2001-244776/25.
 XX DR WPI; 2001-244776/25.
 XX PT New altered CD40L promoter for use in the study, diagnosis and treatment
 PT of a variety of inflammatory disorders and autoimmune diseases, such as
 PT rheumatoid arthritis.
 XX PS Example 1; Fig 3; 90pp; English.
 XX CC The present invention describes an isolated, purified nucleic acid, which
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
 CC residues 331-455 of the sequence comprising 455 nucleotides given in
 CC AAF74905 where A in the wild type sequence at position 331 (corresponding
 CC to position -125) is replaced with C. (I) has antiarthritic,
 CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
 CC be used in gene therapy. (I) is useful in the study, diagnosis and
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in
 CC which elevated expression of CD40L is a factor, e.g., rheumatoid
 CC arthritis. The present sequence represents a CD40L poly-A tract sequence
 CC which is used in an example from the present invention
 SQ Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
 QY Query Match 0.3%; Score 19.6; DB 1; Length 28;
 Best Local Similarity 84.6%; Pred. No. 5.2e+02;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 DB 4458 ATGACTTTTGTGTTTTTTTTTTT 4483
 27 AAGGTTTGTGTTTTTTTTTTT 2
 RESULT 531
 AAF74916/C
 ID AAF74916 standard; DNA; 28 BP.
 XX AAF74916;
 XX AC 23-MAY-2001 (first entry)
 XX DT 23-MAY-2001 (first entry)
 XX DE CD40L poly-A tract sequence SEQ ID NO:13.
 XX KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
 KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
 KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
 XX OS Homo sapiens.
 XX PN WO200119844-A1.
 XX PD 22-MAR-2001.
 XX PF 13-SEP-2000; 2000WO-US024966.
 XX PR 13-SEP-1999; 99US-0153625P.
 XX PA (NYRB-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

XX Crow MK, Li Y;
 XX WI; 2001-244776/25.
 XX DR WPI; 2001-244776/25.
 XX PT New altered CD40L promoter for use in the study, diagnosis and treatment
 PT of a variety of inflammatory disorders and autoimmune diseases, such as
 PT rheumatoid arthritis.
 XX PS Example 1; Fig 3; 90pp; English.
 XX CC The present invention describes an isolated, purified nucleic acid, which
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
 CC residues 331-455 of the sequence comprising 455 nucleotides given in
 CC AAF74905 where A in the wild type sequence at position 331 (corresponding
 CC to position -125) is replaced with C. (I) has antiarthritic,
 CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
 CC be used in gene therapy. (I) is useful in the study, diagnosis and
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in
 CC which elevated expression of CD40L is a factor, e.g., rheumatoid
 CC arthritis. The present sequence represents a CD40L poly-A tract sequence
 CC which is used in an example from the present invention
 SQ Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
 QY Query Match 0.3%; Score 19.6; DB 1; Length 28;
 Best Local Similarity 84.6%; Pred. No. 5.2e+02;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 DB 4458 ATGACTTTTGTGTTTTTTTTTTT 4483
 27 AAGGTTTGTGTTTTTTTTTTT 2
 RESULT 532
 AAF74927/C
 ID AAF74927 standard; DNA; 28 BP.
 XX AAF74927;
 XX AC 23-MAY-2001 (first entry)
 XX DT 23-MAY-2001 (first entry)
 XX DE CD40L poly-A tract sequence SEQ ID NO:24.
 XX KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
 KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
 KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
 XX OS Homo sapiens.
 XX PN WO200119844-A1.
 XX PD 22-MAR-2001.
 XX PF 13-SEP-2000; 2000WO-US024966.
 XX PR 13-SEP-1999; 99US-0153625P.
 XX PA (NYRB-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
 XX PI Crow MK, Li Y;
 XX WI; 2001-244776/25.
 XX DR WPI; 2001-244776/25.
 XX PT New altered CD40L promoter for use in the study, diagnosis and treatment
 PT of a variety of inflammatory disorders and autoimmune diseases, such as
 PT rheumatoid arthritis.
 XX PS Example 1; Fig 3; 90pp; English.
 XX CC The present invention describes an isolated, purified nucleic acid, which
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
 CC residues 331-455 of the sequence comprising 455 nucleotides given in

CC be used in gene therapy. (I) is useful in the study, diagnosis and
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in
 CC which elevated expression of CD40L is a factor, e.g., rheumatoid
 CC arthritis. The present sequence represents a CD40L poly-A tract sequence
 CC which is used in an example from the present invention
 XX
 SQ Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.6; DB 1; Length 27;
 Best Local Similarity 84.6%; Pred. No. 4.9e+02;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4458 ATGACTTTTGTGTTTTTTTTTTTTTTT 4483
 DB 26 AAGCTTTTGTGTTTTTTTTTTTTTTT 1

RESULT 528
 AAF74934/c
 ID AAF74934 standard; DNA; 27 BP.

XX AAF74934;

DT 23-MAY-2001 (first entry)

XX CD40L poly-A tract sequence SEQ ID NO:31.

XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
 KM diagnosis; antiarthritic; antirheumatic; immunosuppressive;
 KM antiinflammatory; inflammatory disease; autoimmune disease; ds.

XX Homo sapiens.

XX WO200119844-A1.

XX 22-MAR-2001.

XX 13-SEP-2000; 2000WO-US024966.

XX 13-SEP-1999; 99US-0153625P.

XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

XX Crow MK, L1 Y;

XX WPI; 2001-244776/25.

XX New altered CD40L promoter for use in the study, diagnosis and treatment
 PT of a variety of inflammatory disorders and autoimmune diseases, such as
 PT rheumatoid arthritis.

XX Example 1; Fig 3; 90pp; English.

XX The present invention describes an isolated, purified nucleic acid, which
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
 CC residues 331-455 of the sequence comprising 455 nucleotides given in
 CC AAF74905 where A in the wild type sequence at position 331 (corresponding
 CC to position -125) is replaced with C. (I) has antiarthritic,
 CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
 CC be used in gene therapy. (I) is useful in the study, diagnosis and
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in
 CC which elevated expression of CD40L is a factor, e.g., rheumatoid
 CC arthritis. The present sequence represents a CD40L poly-A tract sequence
 CC which is used in an example from the present invention

XX Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.6; DB 1; Length 27;
 Best Local Similarity 84.6%; Pred. No. 4.9e+02;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4458 ATGACTTTTGTGTTTTTTTTTTTTTTT 4483
 DB 26 AAGCTTTTGTGTTTTTTTTTTTTTTT 1

DB 26 AAGCTTTTGTGTTTTTTTTTTTTTTT 1

RESULT 529
 AAF74920/c
 ID AAF74920 standard; DNA; 28 BP.

XX AAF74920;

DT 23-MAY-2001 (first entry)

XX CD40L poly-A tract sequence SEQ ID NO:17.

XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
 KM diagnosis; antiarthritic; antirheumatic; immunosuppressive;
 KM antiinflammatory; inflammatory disease; autoimmune disease; ds.

XX Homo sapiens.

XX WO200119844-A1.

XX 22-MAR-2001.

XX 13-SEP-2000; 2000WO-US024966.

XX 13-SEP-1999; 99US-0153625P.

XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

XX Crow MK, L1 Y;

XX WPI; 2001-244776/25.

XX New altered CD40L promoter for use in the study, diagnosis and treatment
 PT of a variety of inflammatory disorders and autoimmune diseases, such as
 PT rheumatoid arthritis.

XX Example 1; Fig 3; 90pp; English.

XX The present invention describes an isolated, purified nucleic acid, which
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
 CC residues 331-455 of the sequence comprising 455 nucleotides given in
 CC AAF74905 where A in the wild type sequence at position 331 (corresponding
 CC to position -125) is replaced with C. (I) has antiarthritic,
 CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
 CC be used in gene therapy. (I) is useful in the study, diagnosis and
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in
 CC which elevated expression of CD40L is a factor, e.g., rheumatoid
 CC arthritis. The present sequence represents a CD40L poly-A tract sequence
 CC which is used in an example from the present invention

XX Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.6; DB 1; Length 28;
 Best Local Similarity 84.6%; Pred. No. 5.2e+02;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4458 ATGACTTTTGTGTTTTTTTTTTTTTTT 4483
 DB 27 AAGCTTTTGTGTTTTTTTTTTTTTTT 2

RESULT 530
 AAF74906/c
 ID AAF74906 standard; DNA; 28 BP.

XX AAF74906;

DT 23-MAY-2001 (first entry)

XX CD40L poly-A tract sequence SEQ ID NO:3.

XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;

```

OS Homo sapiens.
XX
XX WO200119844-A1.
XX
XX 22-MAR-2001.
XX
XX 13-SEP-2000; 2000WO-US024966.
XX
XX 13-SEP-1999; 99US-0153625P.
XX
XX (NTRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
XX PA
XX
XX PI Crow MK, Li Y;
XX
XX DR WPI, 2001-244776/25.
XX
XX PT New altered CD40L promoter for use in the study, diagnosis and treatment
XX of a variety of inflammatory disorders and autoimmune diseases, such as
XX rheumatoid arthritis.
XX
XX PS Example 1; Fig 3; 90pp; English.
XX
XX CC The present invention describes an isolated, purified nucleic acid, which
XX is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
XX residues 331-455 of the sequence comprising 455 nucleotides given in
XX AAF74905 where A in the wild type sequence at position 331 (corresponding
XX to position -125) is replaced with C. (II) has antiarthritic,
XX antiinflammatory, immunosuppressive and antiinflammatory activities, and can
XX be used in gene therapy. (I) is useful in the study, diagnosis and
XX treatment of inflammatory and autoimmune diseases, as well as diseases in
XX which elevated expression of CD40L is a factor, e.g., Rheumatoid
XX arthritis. The present sequence represents a CD40L poly-A tract sequence
XX which is used in an example from the present invention
XX
XX SQ Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 19.6; DB 1; Length 27;
XX Best Local Similarity 84.6%; Pred. No. 4.9e+02;
XX Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0
XX
XX Oy 4458 ATGACATTTTTTTTTTTTTTTTTTTT 4483
XX |||||
XX 26 AAGCTTTTTCGTTTTTTTTTTTTTTTTTT 1
XX
XX DB
XX
XX RESULT 526
XX AAF74932/C
XX ID AAF74932 standard; DNA; 27 BP.
XX
XX AC AAF74932;
XX
XX DT 23-MAY-2001 (first entry)
XX
XX DE CD40L poly-A tract sequence SEQ ID NO:29.
XX
XX KM Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
XX diagnosis; antiarthritic; antirheumatic; immunosuppressive; ds.
XX antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200119844-A1.
XX
XX PD 22-MAR-2001.
XX
XX PF 13-SEP-2000; 2000WO-US024966.
XX
XX PR 13-SEP-1999; 99US-0153625P.
XX
XX PA (NTRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
XX PI Crow MK, Li Y;
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XX FT
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[illegible]

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XX

CC distinguishing morphology. The present sequence represents a rice sd-1
CC DNA fragment, which is given in the exemplification of the present
CC invention. Rice sd-1 is located on chromosome 1.
XX
SQ Sequence 30 BP; 0 A; 3 C; 0 G; 27 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.8; DB 1; Length 30;
Best Local Similarity 91.3%; Pred. No. 5.3e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4463 CTTTCTTTCTTTCTTTCTTTCTT 4485
DB 8 CTTTCTTTCTTTCTTTCTTTCTT 30

RESULT 519
AAQ47176
ID AAQ47176 standard; DNA; 26 BP.
XX
XX AAQ47176;

AC 25-MAR-2003 (revised)
DT 25-JAN-1994 (first entry)
XX
XX

DE MHC DR A intron binding oligomer DRA.

XX MHC; major histocompatibility complex; class II; control oligomers; DR A;
KM transplacation; antigen; autoimmune disease; ss.
XX

OS Synthetic.

PN WO9314769-A1.

XX 05-AUG-1993.

XX 29-JAN-1993; 93WO-US000797.

XX 31-JAN-1992; 92US-00830427.

PR 14-SEP-1992; 92US-00944868.

XX (REGC) UNIV CALIFORNIA.

XX Weiss TL, Garovoy MR, Hunt A, Huey B, Tam S;

PI WPI; 1993-258367/32.

DR Depletion of transplacation antigens in donor cells - using anti-sense
PT or triplex-forming oligonucleotide(s), used for treating auto-immune
PT disease and in transplants.

XX Example; Page 22; 71pp; English.

XX The sequences given in AAQ47176-77 represent triplex forming oligo-
CC nucleotides which bind to the mRNA sequence of the MHC class II locus DR
CC A structural gene at positions 851-876. The sequences given in AAQ47178-
CC 80 represent control oligomers which contain base compositions similar to
CC that around this DR A region but not containing the correct sequences. DR
CC A is a transplacation antigen. Binding of this sequence to the DR A gene
CC inhibits antigen production. This method may be used for treating
CC individuals with autoimmune disease, characterised by dysfunctional
CC expression of a transplacation antigen. It may also be used to produce
CC cells which are more easily transplanted into a recipient. (Updated on 25
CC -MAR-2003 to correct PN field.)
XX
SQ Sequence 26 BP; 1 A; 0 C; 22 G; 3 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 4.7e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3615 GGGGATGGGGTGGGGTGGGAGAGG 3640
DB 1 GGGGGTGGGGTGGGGTGGGGAGG 26

RESULT 520
AAS01617/C
ID AAS01617 standard; DNA; 26 BP.
XX
XX AAS01617;

AC 18-JUL-2001 (first entry)
DT
XX
XX

DE Human MINT31/CACNA1G region 6 bisulfite Gm6 reverse PCR primer.

XX Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;
KM cellular proliferative disorder; colorectal cancer; age related disease;
KM apolipoprotein B; APOB; caudal type homeobox transcription factor 2;

XX CDX2; epidermal growth factor receptor; EGFR; fibroblastin-1; FBN1;

XX G protein-coupled receptor 37; GPR37; heat shock 70KD protein 6; HSP70B';

XX HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;

XX PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;

XX patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;

XX chromosome 17; PCR primer; ss.

XX Homo sapiens.

XX WO200119845-A1.

XX 22-MAR-2001.

XX 14-SEP-2000; 2000WO-US025479.

XX 15-SEP-1999; 99US-00398522.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Issa J;

XX WPI; 2001-244777/25.

XX Claim 21; Page 35; 125pp; English.

XX The present sequence for bisulfite Gm6 reverse PCR primer is used to

CC study the methylation state of region 6 in human MINT31/T-type calcium

CC channel CACNA1G which map to chromosome 17. The methylation state of

CC specific regions within CpG islands associated with the CACNA1G gene

CC correlate with several cancerous phenotypes involving various tissue and

CC cell types. Since aberrant methylation of normally unmethylated CpG

CC islands is often observed in immortalised and transformed cells, CACNA1G

CC is implicated in cellular proliferative disorders e.g. leukaemia,

CC colorectal, lung, breast and other cancers. The nucleic acid coding for

CC CACNA1G is useful as a marker for screening cancer and age related

CC diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for

CC amplification of a CpG-containing nucleic acid, where the primer

CC hybridises with a target polynucleotide sequence (AAS01627-AAS01676), can

CC be used for detecting aberrant methylation. The CpG island sequences

CC (AAS01677-AAS01692) are selected from genes encoding CACNA1G,
CC apolipoprotein B (APOB), caudal type homeobox transcription factor 2
CC (CDX2), epidermal growth factor receptor (EGFR), fibroblastin-1 (FBN1), G
CC protein-coupled receptor 37 (GPR37), heat shock 70KD protein 6 (HSP70B';
CC HSPA6), RasGAP-related protein (IQGAP2), klotho (KL), proteinase-
CC activated receptor 2 (PAR2), paired-like homeodomain transcription factor
CC 2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1;
CC SDC4) or a MINT31 sequence
XX
SQ Sequence 26 BP; 18 A; 3 C; 0 G; 4 T; 0 U; 1 Other;

Query Match 0.3%; Score 19.6; DB 1; Length 26;
Best Local Similarity 95.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

PF 10-SEP-2001; 2001BP-00307665.
XX
PR 11-SEP-2000; 2000US-0065173.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Mobler PK, Delenstarr GC;
XX
DR WPI; 2002-282886/33.
XX
PT Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target
PT molecules, and molecular arrays incorporating sets of calibration probes.
XX
XX Disclosure; Page 14; 32pp; English.
XX
XX The invention relates to a method for calibrating data scanned from a
CC molecular array. The method involves employing calibration probes that
CC generate signals proportional to the total concentrations of labelled
CC target molecules to which the molecular array probes are directed over an
CC entire range of sample solutions and molecular arrays incorporating sets
CC of calibration probes. Method is useful for calibrating different types
CC of signals scanned from a molecular array, or calibrating signals scanned
CC from different molecular arrays. The present sequence is poly (A)
CC normalisation probe used in calibration of molecular array data
XX
SQ Sequence 29 BP; 23 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 19.8; DB 1; Length 29;
Best Local Similarity 91.3%; Pred. No. 5.1e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4460 GGACTTTT TTTT TTTT TTTT TTTT 4482
DB 23 GGAGATTT TTTT TTTT TTTT TTTT 1
RESULT 517
AAD33517/C
ID AAD33517 standard; DNA; 30 BP.
XX
XX AAD33517;
AC
XX
DT 01-JUL-2002 (first entry)
XX
XX T7T18Apad_PSS-30-0001 probe for calibration of molecular array data.
DE
XX
XX Molecular array; probe; ss.
KM
XX
XX Unidentified.
OS
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XX EP1186673-A2.
PN
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XX 13-MAR-2002.
PD
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XX 10-SEP-2001; 2001BP-00307665.
PF
XX
XX 11-SEP-2000; 2000US-0065173.
PR
XX
XX (AGIL-) AGILENT TECHNOLOGIES INC.
PA
XX
XX Mobler PK, Delenstarr GC;
PI
XX
XX WPI; 2002-282886/33.
DR
XX
XX Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target
PT molecules, and molecular arrays incorporating sets of calibration probes.
XX
XX Disclosure; Page 14; 32pp; English.
XX
XX The invention relates to a method for calibrating data scanned from a
CC molecular array. The method involves employing calibration probes that

CC generate signals proportional to the total concentrations of labelled
CC target molecules to which the molecular array probes are directed over an
CC entire range of sample solutions and molecular arrays incorporating sets
CC of calibration probes. Method is useful for calibrating different types
CC of signals scanned from a molecular array, or calibrating signals scanned
CC from different molecular arrays. The present sequence is poly (A)
CC normalisation probe used in calibration of molecular array data
XX
SQ Sequence 30 BP; 24 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 19.8; DB 1; Length 30;
Best Local Similarity 91.3%; Pred. No. 5.3e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4460 GGACTTTT TTTT TTTT TTTT TTTT 4482
DB 23 GGAGATTT TTTT TTTT TTTT TTTT 1
RESULT 518
ADA26181
ID ADA26181 standard; DNA; 30 BP.
XX
XX ADA26181;
AC
XX
DT 20-NOV-2003 (first entry)
XX
XX Rice semi-dwarf (sd-1) DNA fragment SEQ ID NO:26.
DE
XX
XX genotype; plant; rice; semi-dwarf; sd-1; polymorphism; detection;
KW characteristic; single nucleotide polymorphism; SNP; genotyping;
KM chromosome 1; gene; ds.
XX
XX Synthetic.
OS
XX
XX Oryza sativa.
OS
XX
XX WO2003070934-A1.
PN
XX
XX 28-AUG-2003.
PD
XX
XX 07-FEB-2003; 2003WO-JP001317.
PF
XX
XX 25-FEB-2002; 2002JP-00048115.
PR
XX
XX (PLAN-) PLANT GENOME CENT CO LTD.
PA
XX
XX Minobe Y, Moma L, Kitazawa N, Yoshino R, Suzuki J;
PI
XX
XX WPI; 2003-697617/66.
DR
XX
XX Judging the genotype of a region around a plant sd-1 gene with
PT polymorphism-obtained markers isolated by positional cloning, useful in
PT genotyping for examination of semi-dwarf character of rice.
XX
XX Disclosure; Page 15; 104pp; Japanese.
XX
XX The present invention describes a method for judging the genotype of a
CC region around a plant semi-dwarf (sd-1) gene in which polymorphisms are
CC present, by detecting the polymorphisms. Also described: (1) examining
CC semi-dwarf characteristics of a plant using the judgment method with
CC detection of polymorphisms; (2) oligonucleotides for amplifying sd-1 DNA
CC regions, which are primers for judging the genotype of a region around a
CC plant sd-1 gene; (3) reagents for judging the genotype of a region around
CC a plant sd-1 gene containing these oligonucleotides; and (4) reagents for
CC examining the semi-dwarf character of a plant containing the
CC oligonucleotides. The method is for judging the genotype of a region
CC around a plant sd-1 gene, which is applicable in genotyping by (d) CAPS
CC (derived) cleaved amplified polymorphic sequence) for examination of the
CC semi-dwarf character of rice to identify desirable strains e.g. with high
CC crop yield, pest resistance and resistance to flooded water. The method
CC is easy and quick, in which a seedling is required for studying single
CC nucleotide polymorphisms (SNPs) for genotyping, without needing
CC cultivation of seedling to fully-grown plant for judging heterozygote and

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XX 18-NOV-1999.
PD 12-MAY-1999; 99WO-US010361.
PP 12-MAY-1998; 98US-00076404.
PR 12-MAY-1998; 98US-0085092P.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
XX WPI, 2000-086439/07.
DR
XX Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
XX Example 8; Fig 134; 405pp; English.
XX
XX This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming a first side of a second
CC region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUUACACUAUAUUCUAGUACAGAAAUUC (11). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
XX
XX Sequence 29 BP; 21 A; 2 C; 1 G; 3 T; 0 U; 2 Other;
SQ
XX
XX Query Match 0.3%; Score 19.8; DB 1; Length 29;
XX Best Local Similarity 91.3%; Pred. No. 5, 1e-02;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0.
XX
OY 4465 TTTTTTTTTTTTTTTGGTCT 4487
XX |||||||||||||||||
XX 27 TTTTTTTTTTTTTTTAGTCT 5
XX
XX RESULT 515
XX ID AAA71193/C AAA71193 standard; RNA; 29 BP.
XX
XX AAA71193;
XX
XX 27-APR-2001 (first entry)
XX
XX Molecular interaction site RNA #210.
XX
XX Modulator; identification; molecular interaction; virtual library; ss.
XX
XX Canis familiaris.
XX
XX WO9958947-A2.
XX
XX 18-NOV-1999.
XX

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XX	PS	12-MAY-1999;	99MO-US010361.
XX	PR	12-MAY-1998;	98US-00076404.
XX	PR	12-MAY-1998;	98US-0085092P.
XX	PA	(ISIS-) ISIS PHARM INC.	
XX	F1	Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V,	
XX	F1	Hofstadler S, Mcneil J;	
DR	XX	WPI; 2000-086439/07.	
XX	PT	Identifying compounds which modulate activity of target biomolecules,	
PT	PT	used to provide compounds which can be used as pharmacological,	
PT	XX	agricultural and industrial compounds.	
PS	XX	Example 8; Fig 135; 405pp; English.	
CC	CC	This invention describes a novel method for identifying compounds which	
CC	CC	modulate the activity of a target biomolecule. The method uses 3-	
CC	CC	dimensional representations of the biomolecule and a library of compounds	
CC	CC	and comprises (a) identifying at least one molecular interaction site of	
CC	CC	the target RNA; (b) generating in silico a virtual library of compounds	
CC	CC	predicted or calculated to interact with the molecular interaction site;	
CC	CC	and (c) comparing 3-dimensional (3-D) representations of the target RNA	
CC	CC	with members of the virtual library of compounds to generate a hierarchy	
CC	CC	of the compounds ranked in accordance with their respective ability to	
CC	CC	form physical interactions with the molecular interaction site. The	
CC	CC	method also describes (1) RNA comprising a joined sequence of at least 24	
CC	CC	nucleotides but not more than 70 nucleotides and having secondary	
CC	CC	structure defined by: (a) 3 nucleotides forming a first side of a first	
CC	CC	double stranded (ds) region; (b) 2 nucleotides forming a first side of an	
CC	CC	internal loop region; (c) 4 nucleotides forming a first side of a second	
CC	CC	ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4	
CC	CC	nucleotides forming a second side of the second ds region; (f) 4	
CC	CC	nucleotides forming a second side of the internal loop region; and (g) 3	
CC	CC	nucleotides forming a second side of the first ds region; (2) a purified	
CC	CC	and isolated RNA fragment comprising the human sequence	
CC	CC	UUUACAGCAUAUCUGAUCUUCAGAAAUAUC (II). The methods and products can be	
CC	CC	used for identifying agents which modulate the activity of biomolecules,	
CC	CC	particularly RNA. Such agents can be used as pharmaceutical, agricultural	
CC	CC	or industrial compounds	
XX	SQ	Sequence 29 BP; 21 A; 2 C; 1 G; 0 T; 3 U; 2 Other;	
		Query Match 0.3%; Score 19.8; DB 1; Length 29;	
		Best Local Similarity 91.3%; Pred No.5.1e+02;	
		Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0	
QY		4465 TTTT TTTTTTTTTTTTTTTTGCT 4487	
DB		27 TTTT TTTTTTTTTTTTTTAGGCT 5	
RESULT 516		AAD33515/c	
ID		AAD33515 standard; DNA; 29 BP.	
XX		AAD33515;	
XX		01-JUL-2002 (first entry)	
XX		TTT18pad_P86-29-0001 probe for calibration of molecular array data.	
XX		Molecular array; probe; ss.	
XX		Unidentified.	
XX		OS	
XX		EP186673-A2.	
XX		FN	
XX		13-MAR-2002.	
XX		DD	
XX		XX	

XX	08-SEP-2003	(first entry)
DT	Oligo dT primer.	
DE		
XX		
KM	Rat: Czf-1; chondrocyte; zinc finger; osteopathic; antiarthritic;	
KW	antirheumatic; PCR; primer; ss.	
XX		
XX	Synthetic.	
OS		
XX		
PN	MO2003044159-A2.	
XX		
PD	30-MAY-2003.	
XX		
PF	20-NOV-2002; 2002WO-IL000925.	
XX		
PR	20-NOV-2001; 2001US-0331626P.	
XX		
PA	(PROC-) PROCHON BIOTECH LTD.	
XX		
PI	Yayon A, Blumenstein S, Harari D,	
XX		
DR	WPI. 2003-457599/43.	
XX		
PT	New chondrocyte-derived zinc finger polypeptides and encoding	
PT	polynucleotides, useful for detecting, diagnosing and treating	
PT	protein-related diseases, such as osteoarthritis and rheumatoid	
PT	arthritis.	
XX		
PS	Example 1, Page 27; 64pp; English.	
XX		
CC	The present sequence is that of an oligo-dT primer, which was used in the	
CC	PCR amplification of cDNA (see ACC83474) encoding a novel rat zinc finger	
CC	protein, designated Czf-1 (see ABR42912). Czf-1 is expressed in	
CC	osteoblasts and chondrocytes, and serves as a marker for osteoarthritis.	
CC	Czf-1 polynucleotides, polypeptides and antibodies can be used in the	
CC	characterisation, diagnosis and treatment of fibroblast growth factor	
CC	receptor-related and skeletal diseases and disorders, such as	
CC	osteoarthritis, rheumatoid arthritis, and cartilage-related diseases	
XX		
SQ	Sequence 28 BP; 2 A; 3 C; 3 G; 20 T; 0 U; 0 Other;	
XX		
Query Match	0.3%;	Score 19.8; DB 1; Length 28;
Beat Local Similarity	91.3%;	Pred. No. 4.8e+02;
Matches 21; Conservative	0;	Mismatches 2; Indels 0; Gaps 0;
QY	4459 TCGACTTTT TTTT TTTT TTTT 4481	
DB	6 TCGAGTTT TTTT TTTT TTTT 28	
XX		
RESULT 513		
AAQ72764		
ID	AAQ72764 standard; DNA; 29 BP.	
XX		
AC	AAQ72764;	
XX		
DT	25-MAR-2003 (revised)	
DT	08-JUN-1995 (first entry)	
DE	Solid phase restriction enzymatic amplification primer #7.	
XX		
KM	Primer; solid phase; restriction enzyme; amplification; cleavage site;	
KM	recognition sequence; complementary region; hybridise; target; detection;	
KM	single strand; hybridisation; probe; enzyme; horseradish peroxidase;	
KW	alkaline phosphatase; quantification; pathogenic; organism; allelic;	
KW	variant; genomic; defect; diagnosis; genetic disease; ss.	
XX		
OS	Synthetic.	
XX		
PN	FR2697851-A1.	
XX		
PD	13-MAY-1994.	

XX	10-NOV-1992;	92FR-00013562.	
XX	10-NOV-1992;	92FR-00013562.	
XX	(INMR) BIO MERIEUX.		
XX	Gruters R, Cleuziat P, Bonnici F, Mallet F,		
XX	WPI; 1994-318696/40.		
XX	Detecting target nucleic acid by restriction enzyme amplification - using		
XX	two immobilised, partially double stranded probes, one complementary to		
XX	target and the other to the first probe cleavage product.		
XX	Example 3; Page 15; 24pp; French.		
XX	A series of primers (AAQ272756-64) used in the novel process solid phase		
XX	restriction enzymatic amplification (SPREA). The method is based on the		
XX	type II restriction enzymes (RE), especially those that cleave outside		
XX	their recognition sequence e.g. BsaI. The process involves binding a		
XX	primer containing one strand of the RE cleavage site, and extending no		
XX	further than the RE cleavage site, to a solid support e.g. the walls of a		
XX	microtiter plate well. A second primer with a region complementary to the		
XX	first primer hybridises to the first primer and extends as a single		
XX	strand from the cleavage site to the RE recognition site. The extension		
XX	region of the second primer, in one case, includes a region complementary		
XX	to the target and, for the other primer, a single strand region which		
XX	will bind the sequence complementary to the target sequence. One of the		
XX	single-stranded regions has a 5' end, the other a 3' end. DNA from the		
XX	sample to be detected e.g. whole cell extract DNA, is added to the well		
XX	such that the target DNA and the first primer hybridise and regenerate		
XX	the RE cleavage site. The RE cleaves the site and releases the target		
XX	sequence and its complement which can then hybridise to the second probe.		
XX	The second round of cleavage results in both strands, equivalent to the		
XX	target sequence, being amplified. Detection of the product is performed		
XX	by hybridisation of probes (e.g. AAQ27261-2) linked to an enzyme e.g.		
XX	horseradish peroxidase or alkaline phosphatase. The method provides a		
XX	rapid and sensitive detection of target sequences without the use of		
XX	radioisotopes. The target sequence to be detected can be determined by		
XX	the sequence of the bound primers and the type II RE involved. This		
XX	system allows the detection and/or quantification of pathogenic		
XX	organisms, allelic variants, genomic defects, specific mRNAs etc., e.g.		
XX	for diagnosis of genetic diseases. (Updated on 25-MAR-2003 to correct PN		
XX	field.)		
XX	Sequence 29 BP; 11 A; 8 C; 9 G; 1 T; 0 U; 0 Other;		
XX	Query Match 0.3%; Score 19.8; DB 1; Length 29;		
XX	Best Local Similarity 91.3%; Pred. No. 5.1e+02;		
XX	Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
XX	7409 ACATCAGCAGCAGCAGCAGCAGC 7431		
XX	7 AGACCAGCAGCAGCAGCAGCAGC 29		
XX	RESULT 514		
XX	AAA71176/C		
XX	ID AAA71176 standard; DNA; 29 BP.		
XX	AAA71176;		
XX	27-APR-2001 (first entry)		
XX	Molecular interaction site DNA #157.		
XX	Modulator; identification; molecular interaction; virtual library; ss.		
XX	Canis familiaris.		
XX	W09958947-A2.		

CC second primer, polyGH (H = A, C or T) locks onto the polyC tail added by
 CC terminal deoxynucleotidyl transferase (Tdt). In the final step, AAT70112-
 CC 17 (polyAB and polyCD primers; B = G, T or C; D = G, A or T) are used to
 CC amplify the first strand and produce a cDNA library with anchored ends.
 CC cDNA libraries produced may be used to identify new (unique) nucleotide
 CC sequences from PCSUB (PCR-based cDNA subtractive) libraries. The new
 CC method produces discrete sized PCR products which would not necessarily
 CC require further subcloning/screening. The method also produces full-
 CC length cDNA's obtainable from the libraries as opposed to specific cDNA
 CC clones, as produced by previously known methods. Other methods such as
 CC PCR and RACE require a knowledge of the target sequence to be amplified,
 CC by using the PCSUB method no previous knowledge is necessary
 XX

SQ Sequence 28 BP; 18 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Qy 4467 TTTTGTCTGCTG 4489
 |||||
 27 TTTTGTCTGCTG 5

Db

Query Match 0.3%; Score 19.8; DB 1; Length 28;
 Best Local Similarity 91.3%; Pred. No. 4.8e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 510
 AAT70113/c
 ID AAT70113 standard; DNA; 28 BP.
 XX
 AC AAT70113;
 XX
 DT 24-SEP-1997 (first entry)
 XX
 DE PolyAB primer 2.
 XX
 KM primer; polymerase chain reaction; cDNA library; anchored end; PCSUB;
 KM lock-docking; screening; PCR-based cDNA subtractive cloning; ss.
 XX
 OS Synthetic.
 XX
 PN MO9640998-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 05-JUN-1996; 96MO-US008582.
 XX
 PR 07-JUN-1995; 95US-00481687.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Wang X, Duvick JP, Briggs SP;
 XX
 DR WPI; 1997-087067/08.
 XX
 PT Method for prodn. of cDNA libraries with anchored ends - useful for
 PT subtractive cloning of sequences of interest.
 XX
 PS Claim 1; Page 28; 56pp; English.
 XX

CC The invention provides a PCR-based method for generating a full-length
 CC cDNA library with anchored ends. The method uses lock-docking primers
 CC (AAT70106-11), where one primer, poly TV (V = G, C or A) locks over the
 CC polyA tail of eukaryotic mRNA producing first strand synthesis and a
 CC second primer, polyGH (H = A, C or T) locks onto the polyC tail added by
 CC terminal deoxynucleotidyl transferase (Tdt). In the final step, AAT70112-
 CC 17 (polyAB and polyCD primers; B = G, T or C; D = G, A or T) are used to
 CC amplify the first strand and produce a cDNA library with anchored ends.
 CC cDNA libraries produced may be used to identify new (unique) nucleotide
 CC sequences from PCSUB (PCR-based cDNA subtractive) libraries. The new
 CC method produces discrete sized PCR products which would not necessarily
 CC require further subcloning/screening. The method also produces full-
 CC length cDNA's obtainable from the libraries as opposed to specific cDNA
 CC clones, as produced by previously known methods. Other methods such as
 CC PCR and RACE require a knowledge of the target sequence to be amplified,

CC by using the PCSUB method no previous knowledge is necessary
 XX

SQ Sequence 28 BP; 18 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

Qy 4467 TTTTGTCTGCTG 4489
 |||||
 27 TTTTGTCTGCTG 5

Db

Query Match 0.3%; Score 19.8; DB 1; Length 28;
 Best Local Similarity 91.3%; Pred. No. 4.8e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 511
 AAD33512/c
 ID AAD33512 standard; DNA; 28 BP.
 XX
 AC AAD33512;
 XX
 DT 01-JUL-2002 (first entry)
 XX
 DE TTT16apad_PS8-28-0001 probe for calibration of molecular array data.
 XX
 KM Molecular array; probe; ss.
 XX
 OS Unidentified.
 XX
 PN EP1166673-A2.
 XX
 PD 13-MAR-2002.
 XX
 PF 10-SEP-2001; 2001EP-00307665.
 XX
 PR 11-SEP-2000; 2000US-00659173.
 XX
 PA (AGIL-) AGILENT TECHNOLOGIES INC.
 XX
 PI Wobler PK, Delenstarr GC;
 XX
 DR WPI; 2002-282886/33.
 XX
 PT Calibration of molecular array data by employing calibration probes that
 PT generate signals proportional to total concentrations of labeled target
 PT molecules, and molecular arrays incorporating sets of calibration probes.
 XX
 PS Disclosure; Page 14; 32pp; English.
 XX

CC The invention relates to a method for calibrating data scanned from a
 CC molecular array. The method involves employing calibration probes that
 CC generate signals proportional to the total concentrations of labeled
 CC target molecules to which the molecular array probes are directed over an
 CC entire range of sample solutions and molecular arrays incorporating sets
 CC of calibration probes. Method is useful for calibrating different types
 CC of signals scanned from a molecular array, or calibrating signals scanned
 CC from different molecular arrays. The present sequence is poly (A)
 CC normalisation probe used in calibration of molecular array data
 XX

SQ Sequence 28 BP; 22 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Qy 4460 GGAAGTTTGTCTGCTG 4482
 |||||
 23 GGAAGTTTGTCTGCTG 1

Db

Query Match 0.3%; Score 19.8; DB 1; Length 28;
 Best Local Similarity 91.3%; Pred. No. 4.8e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 512
 ACC83476
 ID ACC83476 standard; DNA; 28 BP.
 XX
 AC ACC83476;

[illegible]

```

DR      WPI; 1997-087067/08.
XX      Method for prodn. of cDNA libraries with anchored ends - useful for
PT      subtractive cloning of sequences of interest.
XX
XX
PS      Claim 1; Page 29; 56pp; English.
XX
CC      The invention provides a PCR-based method for generating a full-length
CC      cDNA library with anchored ends. The method uses lock-docking primers
CC      (AAAT70106-11), where one primer, poly TV (V = G,C or A) locks over the
CC      polyA tail of eukaryotic mRNA producing first strand synthesis and a
CC      second primer, polyG/H (H = A, C or T) locks onto the polyC tail added by
CC      terminal deoxynucleotidyl transferase (Tdt). In the final step, AAAT70112-
CC      17 (polyAB and polycD primers; B = G, T or C; D = G, A or T) are used to
CC      amplify the first strand and produce a cDNA library with anchored ends.
CC      cDNA libraries produced may be used to identify new (unique) nucleotide
CC      sequences from PCSUB (PCR-based cDNA subtractive) libraries. The new
CC      method produces discrete sized PCR products which would not necessarily
CC      require further subcloning/screening. The method also produces full-
CC      length cDNA's obtainable from the libraries as opposed to specific cDNA
CC      clones, as produced by previously known methods. Other methods such as
CC      PCR and RACE require a knowledge of the target sequence to be amplified,
CC      by using the PCSUB method no previous knowledge is necessary
SQ
SQ      Sequence 28 BP; 18 A; 5 C; 4 G; 1 T; 0 U; 0 Other;
Query Match          0.3%; Score 19.8; DB 1; Length 28;
      Best Local Similarity    91.3%; Pred. No. 4.8e+02;
Matches   21; Conservative    0; Mismatches    2; Indels    0; Gaps    0;
Oy      4467 TTTTTCCTGTCTGTAAG 4489
           |||||
Db       : 27 TTTTTCCTGTCTGTAAG 5
RESULT 509
AAAT70112/C
ID      AAAT70112 standard; DNA; 28 BP.
AC      AAAT70112;
XX      24-SEP-1997 (first entry)
XX
XX      PolyAB primer 1.
DE
XX      primer; polymerase chain reaction; cDNA library; anchored end; PCSUB;
KW      lock-docking; screening; PCR-based cDNA subtractive cloning; ss.
XX
XX      Synthetic.
OS
XX      WO9640998-A1.
PN
XX      19-DEC-1996.
PD
XX      05-JUN-1996; 96WO-US008582.
PF
XX      07-JUN-1995; 95US-00481687.
PR
XX      (PION-) PIONEER HI-BRED INT INC.
PA
XX      Wang X, Duwick JP, Briggs SF;
PI
XX      WPI; 1997-087067/08.
DR
XX      Method for prodn. of cDNA libraries with anchored ends - useful for
PT      subtractive cloning of sequences of interest.
XX
XX      Claim 1; Page 28; 56pp; English.
XX
XX      The invention provides a PCR-based method for generating a full-length
CC      cDNA library with anchored ends. The method uses lock-docking primers
CC      (AAAT70106-11), where one primer, poly TV (V = G,C or A) locks over the
CC      polyA tail of eukaryotic mRNA producing first strand synthesis and a

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AAH43080/C
ID AAH43080 standard; DNA; 27 BP.
XX
XX
AC AAH43080;
XX
XX
DT 15-OCT-2001 (first entry)
XX
XX
DE Nucleotide sequence of a synthetic oligonucleotide.
XX
XX
KW Nucleic acid immobilisation; ss.
XX
XX
OS Synthetic.
XX
XX
PN WO200155365-A1.
XX
XX
PD 02-AUG-2001.
XX
XX
PF 24-JAN-2001; 2001WO-JP000443.
XX
XX
PR 27-JAN-2000; 2000JP-00019301.
XX
XX
PA (TOYO ) TOYO KOHAN CO LTD.
XX
XX
PI Tanga M, Okamura H, Takagi K, Takahashi K;
XX
XX
DR WPI; 2001-488794/53.
XX
XX
PT Support for immobilizing nucleotides.
XX
XX
PS Example 1; Page 8; 18pp; Japanese.
XX
XX
CC The specification describes a support for immobilizing nucleotides which
CC contributes to the efficient clarification of DNA without damaging the
CC terminal parts of the DNA. The support is a chemically treated modified
CC substrate on which oligonucleotides with restriction enzyme cleavage
CC sites are immobilised. The support is useful for immobilizing nucleic
CC acids such as DNA. The present sequence represents a synthetic
CC oligonucleotide used in the course of the invention
XX
XX
SQ Sequence 27 BP; 20 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX
Query Match 0.3%; Score 19.8; DB 1; Length 27;
Best Local Similarity 91.3%; Pred. No. 4.6e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4466 TTTTGTGTGTGTGTGTGTGTGT 4488
DB 23 TTTTGTGTGTGTGTGTGTGTGT 1

```

```

PA (TOYO ) TOYO KOHAN CO LTD.
PA (TAKA/) TAKAHASHI K.
XX
XX
DR WPI; 2002-630904/68.
XX
XX
PT Carrying out a thermal cycle of polymerase chain reaction (PCR) by using
PT a substrate on which a DNA is immobilized used in medical, biochemical,
PT molecular biological and gene engineering fields.
XX
XX
PS Example; Page 10; 13pp; Japanese.
XX
XX
CC The invention relates to performing a thermal cycle of PCR by using a
CC substrate on which a deoxyribonucleic acid (DNA) is immobilized. The
CC method is useful in the medical, biochemical, molecular biological and
CC genetic engineering fields. Sequences ABQ79671-881 represent PCR primers
CC used in the method of the invention
XX
XX
SQ Sequence 27 BP; 20 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX
Query Match 0.3%; Score 19.8; DB 1; Length 27;
Best Local Similarity 91.3%; Pred. No. 4.6e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4466 TTTTGTGTGTGTGTGTGTGTGT 4488
DB 23 TTTTGTGTGTGTGTGTGTGTGT 1

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RESULT 504
ABL41793
ID ABL41793 standard; DNA; 27 BP.
XX
XX
AC ABL41793;
XX
XX
DT 29-MAY-2002 (first entry)
XX
XX
DE Primer for human endometrial specific steroid-binding factor I cDNA.
XX
XX
KW Human; endometrial specific steroid-binding factor; ESF;
KW prostatic steroid-binding protein; hsf I; hsf II; hsf III; asthma;
KW PCR primer; ss.
XX
XX
OS Homo sapiens.
XX
XX
OS Synthetic.
XX
XX
PN US6338948-B1.
XX
XX
PD 15-JAN-2002.
XX
XX
PF 30-MAY-2000; 2000US-00583169.
XX
XX
PR 21-MAR-1996; 96US-0014724P.
XX
XX
PR 21-MAR-1997; 97US-00821451.
XX
XX
PR 08-MAR-1999; 99US-00263810.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Ni J, Yu G, Gentz R;
XX
XX
DR WPI; 2002-215019/27.
XX
XX
PT New antibody specific for human endometrial specific steroid-binding
PT factor (hsf) III; useful for detecting hsf III protein in biological
PT sample and to isolate or identify clones expressing the protein.
XX
XX
PS Example 2; Col 33; 36pp; English.
XX
XX
CC PCR primers ABL41790 and ABL41793 were used to amplify cDNA encoding
CC human endometrial specific steroid-binding factor (hsf) I. The primers
CC were used to introduce restriction sites for cloning. The full length
CC hsf I protein has a molecular weight of 9.8 kDa. The protein has
CC homology to rat prostatic steroid-binding protein. Antibodies which bind
CC hsf proteins, such as hsf I, hsf II, and hsf III are useful for

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XX Homo sapiens.
XX WO200071164-A1.
XX 30-NOV-2000.
XX 24-MAY-2000; 2000WO-AU000498.
XX 24-MAY-1999; 99AU-00000510.
XX (TACH/) TACHAS G.
XX Tachas G;
XX WPI; 2001-025093/03.
XX Treating gastric acid disturbance by administering an oligonucleotide
XX which modulates the activity of a polypeptide involved in gastric acid
XX production or secretion.
XX Example 3; Page 150; 164pp; English.
XX The present invention provides oligonucleotides, and methods for their
XX use, which are useful in modulating the action of proteins involved in
XX gastric acid production. The target protein is preferably the histamine
XX H2 receptor or one of the proteins which form part of the gastric proton
XX pump. The sequences and methods of the invention are useful in the
XX treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
XX duodenal ulcers and other gastric acid disturbances, most of which are
XX caused by Helicobacter pylori
XX
XX Sequence 26 BP; 23 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
XX
Qy 4463 CTTTTTTTTTTTTTTTTTTGT 4485
   ||||| ||||| ||||| |||||
Db 24 CTTTTTTTTTTCTTTTTTTTTT 2
   ||||| ||||| ||||| |||||

RESULT 498
AAD33509/C
ID AAD33509 standard; DNA; 26 BP.
XX AAD33509;
XX
AC 01-JUN-2002 (first entry)
XX
DT T7718Apad_P510-26-0001 probe for calibration of molecular array data.
XX
DE Molecular array; probe; ss.
XX
KM Unidentified.
XX
OS Unidentified.
XX
PN EP1186673-A2.
XX
PD 13-MAR-2002.
XX
PF 10-SEP-2001; 2001EP-00307665.
XX
PR 11-SEP-2000; 2000US-00659173.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Wobler PK, Delenstarr GC;
XX
DR WPI; 2002-282886/33.
XX
PT Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target

```

The invention relates to a method for calibrating data scanned from a molecular array. The method involves employing calibration probes that generate signals proportional to the total concentrations of labelled target molecules to which the molecular array probes are directed over an entire range of sample solutions and molecular arrays incorporating sets of calibration probes. Method is useful for calibrating different types of signals scanned from a molecular array, or calibrating signals scanned from different molecular arrays. The present sequence is poly (A) normalisation probe used in calibration of molecular array data

Sequence 26 BP; 20 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.8; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 4.3e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0

Oy 4460 GGACTTTTTTTTTTTTTTTT 4482
 ||| ||||| ||||| |||||
Db 23 GGAGATTTTTTTTTTTTTTT 1

RESULT 499
AAIT94842
ID AAIT94842 standard; DNA; 27 BP.

AC AAT94842;
DT 27-MAR-1998 (first entry)
DE Human ESF I 3' PCR primer.
XX
XX
KW Endometrial specific steroid-binding factor I; ESF I; human;
KM inflammation; asthma; rhinitis; cystic fibrosis; airway disease;
XX neoplasia; atopy; therapy; diagnosis; primer; PCR; ss.
XX
OS Synthetic.
OS Homo sapiens.
PN WO9734997-A1.
PD 25-SEP-1997.
PP 21-MAR-1996; 96WO-US003857.
PR 21-MAR-1996; 96WO-US003857.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Ni J, Yu G, Gentz RL;
PT WPI, 1997-480206/44.
PT Human endometrial specific steroid-binding factor I, II and III - used to treat inflammation, asthma, rhinitis, cystic fibrosis, airway disease, neoplasia, atopy etc.
PS Example 2; Page 52-53; 92pp; English.
SQ This oligonucleotide contains an Asp718 site followed by 18 nucleotides complementary to a polyA tail. It was used with a 5' primer (see AAT94839), containing a BamHI site and 20 bases of the human endometrial specific steroid binding factor I (ESF I) coding sequence (see AAT94830), to amplify ESF I cDNA deposited as ATCC 97401. The PCR product was incorporated into baculovirus vector pCIG and recombinant ESF I was expressed in Spodoptera frugiperda Sf9 cells. Human ESF I (see AAW35802) can be used to treat inflammation, asthma, rhinitis, cystic fibrosis, airway disease, neoplasia, atopy etc

Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;

CC beer, wine and sake and production of bread. The gene is responsive to
 CC the stresses such as oxidative stress, osmotic pressure stress and
 CC glucose starvation stress. The present sequence represents a PCR primer
 CC for the yeast DOG2 stress responsive gene, which is used in an example
 CC from the present invention

XX
 SQ Sequence 26 BP; 3 A; 2 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.8; DB 1; Length 26;

Best Local Similarity 91.3%; Pred. No. 4.3e+02; Mismatches 2; Indels 0; Gaps 0;

XX
 QY 4464 TTTTGTGTC 4486
 DB 3 TTTTGTGTC 25

RESULT 495

AAA88688 standard; DNA; 26 BP.

XX
 AC AAA88688;

XX
 DT 05-FEB-2001 (first entry)

XX
 DE Oligo-dT-XhoI primer.

XX
 KM Sweetgum; angiosperm; cytochrome P450-1; confert; loblolly pine;

XX
 KM transgenic plant; lignin; paper; pulping; PCR primer; ss.

XX
 OS Synthetic.

XX
 PN WO200058489-A2.

XX
 PD 05-OCT-2000.

XX
 PF 24-MAR-2000; 2000MO-US008083.

XX
 PR 26-MAR-1999; 99US-00277248.

XX
 PA (INTO) INT PAPER CO.

XX
 PI Chiang VL, Carraway DT;

XX
 DR WPI; 2000-647240/62.

XX
 PT Use of angiosperm confertyl aldehyde 5-hydroxylase which catalyzes 5-
 PT hydroxylation of confertyl aldehyde, for modifying lignin biosynthesis in
 PT gymnosperms, involves expressing the enzyme in a gymnosperm plant.

XX
 PS Example 3; Page 23; 123pp; English.

XX
 CC The present sequence is that of an oligo-dT primer including a 5' XhoI
 CC site. The primer was used with a gene-specific primer to amplify sweetgum
 CC cytochrome P450-1 cDNA (see AAA88688). An aim of the invention is to
 CC identify, sequence and clone specific genes such as P450-1 from an
 CC angiosperm that are involved in production of syringyl lignin, and to
 CC then introduce such genes into the genome of a gymnosperm, such as
 CC loblolly pine, to induce production of syringyl lignin and thereby
 CC provide enhanced pulpability to the wood structure

XX
 SQ Sequence 26 BP; 2 A; 1 C; 3 G; 20 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.8; DB 1; Length 26;

Best Local Similarity 91.3%; Pred. No. 4.3e+02; Mismatches 2; Indels 0; Gaps 0;

QY 4459 TGGACTTTT 4481
 DB 4 TGGACTTTT 26

RESULT 496

AAD12516
 ID AAD12516 standard; DNA; 26 BP.

XX
 AC AAD12516;

XX
 DT 25-SEP-2001 (first entry)

XX
 DE Thuja sp. pinoresinol/lariciresinol reductase cDNA cloning linker primer.

XX
 KM Diguent protein; pinoresinol/lariciresinol reductase; stereospecificity;

XX
 KM lignin biosynthetic pathway; secoisolariciresinol; western red cedar;

XX
 KM PCR primer; ss.

XX
 OS Thuja plicata.

XX
 PN WO200149833-A2.

XX
 PD 12-JUL-2001.

XX
 PF 22-DEC-2000; 2000MO-US035265.

XX
 PR 30-DEC-1999; 99US-00475316.

XX
 PA (UNIW) UNIV WASHINGTON STATE RES FOUND.

XX
 PI Lewis NG, Davin LB, Dinkova-Kostova AT, Fujita M, Gang DR;

XX
 DR Ford JD, Sarkanen S;

XX
 DR WPI; 2001-465260/50.

XX
 PT Diguent and/or pinoresinol/lariciresinol reductase proteins useful for

XX
 PT producing optically-pure lignans.

XX
 PS Example 14; Page 56; 183pp; English.

XX
 CC The present invention relates to an isolated diguent and/or pinoresinol
 CC /lariciresinol reductase protein from a lignan biosynthetic pathway.
 CC Diguent and/or pinoresinol/lariciresinol reductase protein and the
 CC nucleic acids that encode it may be expressed either in vivo or in vitro
 CC to produce enzymes involved in the biosynthesis of lignans. The 78-kD
 CC dirigent protein confers stereospecificity in 8,8'-linked lignan
 CC formation and binds to and orients confertyl alcohol-derived free
 CC radicals, which then undergo stereospecific coupling to form (+)-
 CC pinoresinol. Pinoresinol/lariciresinol reductase catalyzes the conversion
 CC of pinoresinol to lariciresinol and then to secoisolariciresinol. The
 CC present sequence is 3' linker PCR primer, XhoI-poly(dT) used in the
 CC cloning of Thuja plicata pinoresinol/ lariciresinol reductase cDNA

XX
 SQ Sequence 26 BP; 1 A; 2 C; 3 G; 20 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.8; DB 1; Length 26;

Best Local Similarity 91.3%; Pred. No. 4.3e+02; Mismatches 2; Indels 0; Gaps 0;

QY 4459 TGGACTTTT 4481
 DB 4 TGGACTTTT 26

RESULT 497

AAF1616/C
 ID AAF1616 standard; DNA; 26 BP.

XX
 AC AAF1616;

XX
 DT 13-MAR-2001 (first entry)

XX
 DE Gastric acid production inhibiting oligonucleotide SEQ ID NO: 103.

XX
 KM Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;

XX
 KM stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;

XX
 KM DNA-RNA hybrid; ss.

```

PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
XX Wobler PK, Delenstarr GC;
XX
XX WPI; 2002-282886/33.
DR
XX Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target
PT molecules, and molecular arrays incorporating sets of calibration probes.
XX
XX Disclosure; Page 14; 32pp; English.
XX
CC The invention relates to a method for calibrating data scanned from a
CC molecular array. The method involves employing calibration probes that
CC generate signals proportional to the total concentrations of labelled
CC target molecules to which the molecular array probes are directed over an
CC entire range of sample solutions and molecular arrays incorporating sets
CC of calibration probes. Method is useful for calibrating different types
CC of signals scanned from a molecular array, or calibrating signals scanned
CC from different molecular arrays. The present sequence is poly (A)
CC normalisation probe used in calibration of molecular array data
CC
SQ Sequence 25 BP; 19 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match          0.3%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 4.1e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4460 GGACTTTTTTTTTTTTTTTTTTTT 4482
DB 23 GGAGATTTTTTTTTTTTTTTTTTT 1

RESULT 493
AB223535/C
ID AB223535 standard; DNA; 25 BP.
XX
AC AB223535;
XX
DT 07-APR-2003 (first entry)
XX
DE fragment of a plasmid used to detect somatic instability.
XX
KM Replication error; drug development; somatic instability; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 4 /tag= a
FT /note= "this base represents an unspecified number of
FT bases"
FT misc_feature 22 /tag= b
FT /note= "this base represents an unspecified number of
FT bases"
XX
XX WO200295071-A2.
XX
XX 28-NOV-2002.
XX
XX 22-MAY-2002; 2002WO-NL000322.
XX
XX 22-MAY-2001; 2001EP-00201936.
XX
PA (NEVA-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.
XX (TJUS/) TIJSTERMAN M.
XX
XX Plaeterk RHA, Tijsterman M;
XX
XX WPI; 2003-129440/12.
XX
XX Determining whether a product of a gene is involved in preventing a
PT

```

```

PT replication error in a cell comprises providing a specific inhibitor for
PT the product and determining the level of expression of a marker gene.
XX
XX Example 1; Fig 3; 47pp; English.
XX
PS The specification describes a method for determining whether a product of
CC a gene is involved in preventing a replication error in a cell. The
CC method comprises providing the cell with a specific inhibitor for the
CC product and determining the level of functional expression of a marker
CC gene in the cell, where the level of expression of the marker gene is
CC dependent on the occurrence of the replication error. The method is used
CC for determining whether a product of a gene is involved in preventing a
CC replication error in a cell. The identified genes are useful for
CC developing diagnostic tools, or as targets for drug development to
CC manipulate cells on the basis of the presence or absence of function of
CC the gene. AB223535-36 represents fragments of plasmids used to detect
XX somatic instability, in the course of the invention
XX
SQ Sequence 25 BP; 21 A; 0 C; 1 G; 1 T; 0 U; 2 Other;

Query Match          0.3%; Score 19.8; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 4.1e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4464 TTTTTTTTTTTTTTTTGCCT 4488
DB 25 TTTNTTTTTTTTTTTTTTTTCAT 1

RESULT 494
AAA13806
ID AAA13806 standard; DNA; 26 BP.
XX
AC AAA13806;
XX
DT 27-JUL-2000 (first entry)
XX
DE Yeast DOG2 stress responsive gene PCR primer SEQ ID NO:5.
XX
KM Yeast; stress responsive gene; promoter; brewing; beer; wine; sake;
XX bread; oxidative stress; osmotic pressure; stress; glucose starvation;
XX PCR primer; ss.
XX
OS Saccharomyces cerevisiae.
XX
XX JP2000078977-A.
XX
XX 21-MAR-2000.
XX
XX 04-SEP-1998; 98JP-00251390.
XX
XX 04-SEP-1998; 98JP-00251390.
XX
PA (TAIF ) MARUHA CORP.
XX
XX WPI; 2000-285929/25.
XX
XX A stress-responsive gene promoter.
XX
XX Example 3; Page 10; 12pp; Japanese.
XX
XX The present invention describes a stress responsive gene promoter
CC isolated from Saccharomyces cerevisiae (yeast). Also described in the
CC present invention are: (1) a promoter containing a DNA hybridising with
CC the above DNA under a stringent condition and having stress-responsive
CC promoter activity; (2) a gene expression cassette containing the above
CC promoter; (3) an expression vector containing the above gene expression
CC cassette; (4) a recombinant vector in which a gene encoding an optional
CC polypeptide is recombined to the above expression vector; (5) a
CC transformant containing the above recombinant vector; and (6) a method
CC for the preparation of the above polypeptide in which the above
CC transformant is cultured and the polypeptide is collected from the
CC resultant culture. Saccharomyces cerevisiae is used for the brewing of
CC

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XX  WO2003057236-A1.
PN
XX
XX  17-JUL-2003.
PD
XX
XX  27-DEC-2002; 2002WO-JP013781.
PF
XX  28-DEC-2001; 2001JP-00403260.
PR
XX  28-MAR-2002; 2002JP-00093096.
XX
XX  (TAKE ) TAKEDA CHEM IND LTD.
PA
XX  Matsumoto H, Noguchi J, Harada M, Mori M;
PI
XX  WPI; 2003-569538/53.
DR
XX
XX  Composition comprising peptide of brain origin binding to orphan G-
PT protein coupled receptor GPR8 for treatment and prevention of obesity and
XX  hyperphagia.
XX
XX  Example 30; SEQ ID NO 46; 277bp; Japanese.
PS
XX
XX  The present invention relates to novel compositions for inhibiting body
CC weight gain, for lowering body weight, for inhibiting fat weight gain,
CC and for suppressing appetite, which contain as active component a peptide
CC ligand (GPR8, ADC51805) of brain origin. The compositions can be used
CC for treatment and prevention of hyperphagia and obesity (including
CC malignant mastocytosis, exogenous obesity, hyperinsulinemic obesity,
CC hyperplasmic obesity, hypophyseal obesity, hypoplastic obesity, infant
CC hypothyroid obesity, hypochalamic obesity, symptomatic obesity, infant
CC obesity, upper body obesity, alimentary obesity, hypogonadal obesity,
CC systemic mastocytosis, simple obesity and central obesity). The present
XX sequence was used to illustrate the invention.
XX
XX  Sequence 24 BP; 8 A; 7 C; 8 G; 1 T; 0 U; 0 Other;
SQ
XX
XX  Query Match 0.3%; Score 19.8; DB 1; Length 24;
XX Best Local Similarity 91.3%; Pred. No. 3.9e+02;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7413 CAGCAGCAGCAGCAGCAGCAGCA 7435
DB 1 CAGCGGCGACGACGACGAGTA 23
XX
XX  RESULT 491
XX AAQ72756/C
XX ID AAQ72756 standard; DNA; 25 BP.
XX
XX  AAQ72756;
AC
XX
XX  25-MAR-2003 (revised)
DT
XX  08-JUN-1995 (first entry)
DT
XX
XX  Solid phase restriction enzymatic amplification primer #1.
DE
XX
XX  Primer; solid phase; restriction enzyme; amplification; cleavage site;
XX recognition sequence; complementary region; hybridise; target; detection;
XX single strand; hybridisation; probe; enzyme; horseradish peroxidase;
XX alkaline phosphatase; quantification; pathogenic; organism; allelic;
XX variant; genomic; defect; diagnosis; genetic disease; ss.
XX
XX  Synthetic.
OS
XX
XX  FR2697851-A1.
PN
XX
XX  13-MAY-1994.
PD
XX
XX  10-NOV-1992; 92FR-00013562.
PF
XX  10-NOV-1992; 92FR-00013562.
PR
XX
XX  (INMR ) BIO MERIEUX.
PA

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```

XX  Gruters R, Cleuziat P, Bonnici F, Mallet F;
XX
XX  WPI; 1994-318696/40.
DR
XX
XX  Detecting target nucleic acid by restriction enzyme amplification - using
PT two immobilised, partially double stranded probes, one complementary to
PT target and the other to the first probe cleavage product.
XX
XX  Example 1; Page 10; 24pp; French.
PS
XX
XX  A series of primers (AAQ72756-64) used in the novel process solid phase
CC restriction enzymatic amplification (SPREA). The method is based on the
CC type II restriction enzymes (RE), especially those that cleave outside
CC their recognition sequence e.g. BsaI. The process involves binding a
CC primer containing one strand of the RE cleavage site, and extending no
CC further than the RE cleavage site, to a solid support e.g. the walls of a
CC microtiter plate well. A second primer with a region complementary to the
CC first primer hybridises to the first primer and extends as a single
CC strand from the cleavage site to the RE recognition site. The extension
CC region of the second primer, in one case, includes a region complementary
CC to the target and, for the other primer, a single strand region which
CC will bind the sequence complementary to the target sequence. One of the
CC single-stranded regions has a 5' end, the other a 3' end. DNA from the
CC sample to be detected e.g. whole cell extract DNA, is added to the well
CC such that the target DNA and the first primer hybridise and regenerate
CC the RE cleavage site. The RE cleaves the site and releases the target
CC sequence and its complement which can then hybridise to the second probe.
CC The second round of cleavage results in both strands, equivalent to the
CC target sequence, being amplified. Detection of the product is performed
CC by hybridisation of probes (e.g. AAQ72761-2) linked to an enzyme e.g
CC horseradish peroxidase or alkaline phosphatase. The method provides a
CC rapid and sensitive detection of target sequences without the use of
CC radioisotopes. The target sequence to be detected can be determined by
CC the sequence of the bound primers and the type II RE involved. This
CC system allows the detection and/or quantification of pathogenic
CC organisms, allelic variants, genomic defects, specific RNAs etc., e.g.
CC for diagnosis of genetic diseases. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX
XX  Sequence 25 BP; 0 A; 9 C; 8 G; 8 T; 0 U; 0 Other;
SQ
XX
XX  Query Match 0.3%; Score 19.8; DB 1; Length 25;
XX Best Local Similarity 91.3%; Pred. No. 4.1e+02;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7409 ACATCGACGACGACGACGACG 7431
DB 23 AGACGACGACGACGACGACGACG 1
XX
XX  RESULT 492
XX AAD33507/C
XX ID AAD33507 standard; DNA; 25 BP.
XX
XX  AAD33507;
AC
XX
XX  01-JUL-2002 (first entry)
DT
XX  TTT18Apad_P811-25-0001 probe for calibration of molecular array data.
DE
XX
XX  Molecular array; probe; ss.
XX
XX  Unidentified.
OS
XX
XX  EP1186673-A2.
PN
XX
XX  13-MAR-2002.
PD
XX
XX  10-SEP-2001; 2001EP-00307665.
PF
XX  11-SEP-2000; 2000US-00659173.
PR
XX
XX

```

CC the compounds or their salts that can alter binding of the G protein-coupled receptors. The proteins and encoded DNAs are useful in diagnosis of and developing drugs for prevention or treatment of obesity and eating disorders. This sequence represents a PCR primer used in production of CC DNA encoding a G protein-coupled receptor protein

XX Sequence 24 BP; 8 A; 7 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.8; DB 1; Length 24;

Best Local Similarity 91.3%; Pred. No. 3.9e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

7413 CAGCAGCAGCAGCAGCAGCA 7435

1 CAGCGCAGCAGCAGCAGCA 23

RESULT 488

AAD33505/c

ID AAD33505 standard; DNA; 24 BP.

XX AAD33505;

DT 01-JUL-2002 (first entry)

DE T7T18Apad_PS12-24-0001 probe for calibration of molecular array data.

KW Molecular array; probe; ss.

OS Unidentified.

PN EP186673-A2.

PD 13-MAR-2002.

PF 10-SEP-2001; 2001EP-00307655.

PR 11-SEP-2000; 2000US-00659173.

PA (AGIL-) AGILENT TECHNOLOGIES INC.

PI Wobler PK, Delenstarr GC;

DR WPI; 2002-282886/33.

PT Calibration of molecular array data by employing calibration probes that generate signals proportional to total concentrations of labeled target molecules, and molecular arrays incorporating sets of calibration probes.

PS Disclosure; Page 14; 32pp; English.

XX The invention relates to a method for calibrating data scanned from a molecular array. The method involves employing calibration probes that generate signals proportional to the total concentrations of labelled target molecules to which the molecular array probes are directed over an entire range of sample solutions and molecular arrays incorporating sets of calibration probes. Method is useful for calibrating different types of signals scanned from a molecular array, or calibrating signals scanned from different molecular arrays. The present sequence is poly (A) normalisation probe used in calibration of molecular array data

XX Sequence 24 BP; 18 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.8; DB 1; Length 24;

Best Local Similarity 91.3%; Pred. No. 3.9e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

4460 GGACTTTTCTTTTCTTTTCTTTT 4482

23 GGAGATTTTCTTTTCTTTTCTTTT 1

RESULT 489

ABX2931
ID ABX2931 standard; DNA; 24 BP.

XX ABX2931;

DT 14-MAY-2003 (first entry)

DE Screening method related primer #13.

XX G protein-coupled receptor; GPR7; primer; ss; anorectic; cibophobia;
KW anorexia; appetite loss; excessive appetite; obesity-related disorder;
KW adipocyte malignancy; obesity; excessive insulin; blood volume change;
KW thyroid disorder; paediatric obesity; upper body obesity;
KW dietary obesity; cardiac obesity; whole body adipocyte disorder.

OS Synthetic.

PN WO200293161-A1.

PD 21-NOV-2002.

PF 14-MAY-2002; 2002WO-JP004635.

PR 15-MAY-2001; 2001JP-00145411.

PA (TAKE) TAKEDA CHEM IND LTD.

PI Mori M, Shimomura Y, Goto M;

DR WPI; 2003-129320/12.

PT Screening compounds that modify the binding of G-protein coupled receptor GPR7 to its ligands for treatment of obesity and cibophobia.

PS Disclosure; Page 176; 222pp; Japanese.

XX The invention relates to a method for screening compounds for their ability to modify the binding of G protein-coupled receptor protein GPR7 to its polypeptide, ligands and their amides, esters and salts, by measuring the binding in the presence and absence of the test compound. The method is used for prevention and treatment of cibophobia, anorexia, loss of appetite, excessive appetite and a broad range of obesity-related disorders including adipocyte malignancy, obesity due to external factors, excessive insulin, blood volume changes, thyroid disorders, paediatric obesity, upper body obesity, dietary obesity, cardiac obesity, and whole body adipocyte disorder. This sequence represents a primer used in the scope of the invention

XX Sequence 24 BP; 8 A; 7 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 0.3%; Score 19.8; DB 1; Length 24;

Best Local Similarity 91.3%; Pred. No. 3.9e+02; Mismatches 2; Indels 0; Gaps 0;

7413 CAGCAGCAGCAGCAGCAGCA 7435

1 CAGCGCAGCAGCAGCAGCA 23

RESULT 490

ADC51835

ID ADC51835 standard; DNA; 24 BP.

XX ADC51835;

DT 18-DEC-2003 (first entry)

DE GPR8 PCR primer, SEQ ID 46.

KW Body weight; GPR8L; brain; hyperphagia; obesity; anorectic; GPR8; PCR; primer; ss.

OS Unidentified.

DE 5' anchored (ISSR)-PCR primer - SEQ ID 20.
 XX inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;
 KM animal; Basmati rice; ss.
 XX Synthetic.
 XX WO2003085133-A2.
 XX
 PD 16-OCT-2003.
 XX
 PF 09-JAN-2003; 2003WO-IB000041.
 XX
 PR 08-APR-2002; 2002IN-CH000260.
 XX
 PA (DNMF-) CENT DNA FINGERPRINTING & DIAGNOSTICS.
 XX
 PI Nagaraaju JG;
 XX
 DR WPI; 2003-804317/75.
 XX
 PT New set of inter-simple sequence repeats (ISSR)-PCR primers for
 PT genotyping eukaryotes, useful for genotyping diverse genomes of plant and
 PT animal systems.
 XX
 PS Claim 1; SEQ ID NO 20; 60pp; English.
 XX
 CC The invention relates to a novel set of inter-simple sequence repeats
 CC (ISSR)-PCR primers for genotyping eukaryotes. The primers of the
 CC invention may be useful for genotyping diverse genomes of plant and
 CC animal systems, in particular for distinguishing Basmati rice varieties
 CC from non-Basmati rice varieties and traditional Basmati rice varieties
 CC from evolved Basmati rice varieties. The current sequence is that of the
 CC 5' anchored (ISSR)-PCR primer of the invention.
 XX
 SQ Sequence 23 BP; 3 A; 6 C; 7 G; 7 T; 0 U; 0 Other;
 XX
 Query Match 0.3%; Score 19.8; DB 1; Length 23;
 Best Local Similarity 91.3%; Pred. No. 3.6e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 7417 AGCAGCAGCAGCAGCAGCAGCAT 7439
 DB 23 AGCAGCAGCAGCAGCAGCAGCTCTAT 1
 XX
 RESULT 486
 ID ABL61611 standard; DNA; 24 BP.
 XX
 AC ABL61611;
 XX
 DT 13-MAY-2002 (first entry)
 XX
 DE Porcine GPR8-related PCR primer #3.
 XX
 KM Anorectic; GPR8 ligand; central nervous system; obesity; pig;
 KM appetite-stimulating agent; prolactin; porcine; PCR primer; ss.
 XX
 OS Sus scrofa.
 XX
 PN WO200198494-A1.
 XX
 PD 27-DEC-2001.
 XX
 PF 20-JUN-2001; 2001WO-JP005257.
 XX
 PR 21-JUN-2000; 2000JP-00191089.
 PR 06-SEP-2000; 2000JP-00275013.
 PR 13-APR-2001; 2001JP-00116000.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX

PI Mori M, Shimomura Y, Harada M, Kurihara M, Kitada C, Asami T;
 PI Matsumoto Y, Adachi Y, Watanabe T, Sugo T, Abe M;
 XX
 DR WPI; 2002-139790/18.
 XX
 PT Ligand to GPR8 and encoded gene, useful in developing receptor-binding
 PT assay system, diagnosis and screening candidate compounds for central
 PT nervous system function-regulating drugs to treat e.g. obesity.
 XX
 PS Example 30; Page 184; 221pp; Japanese.
 XX
 CC The present invention relates to GPR8 ligands. The ligands as well as
 CC their precursor proteins and DNAs are useful in developing receptor-
 CC binding assay systems, diagnosis and screening candidate compounds for
 CC central nervous system function-regulating drugs as preventives or
 CC remedies for obesity, appetite-stimulating agents and prolactin
 CC production promoters or inhibitors. The present PCR primer was used to
 CC illustrate the invention
 XX
 SQ Sequence 24 BP; 8 A; 7 C; 8 G; 1 T; 0 U; 0 Other;
 XX
 Query Match 0.3%; Score 19.8; DB 1; Length 24;
 Best Local Similarity 91.3%; Pred. No. 3.9e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 7413 CAGCAGCAGCAGCAGCAGCA 7435
 DB 1 CAGCGCAGCAGCAGCAGCAGTA 23
 XX
 RESULT 487
 ID ABR94601 standard; DNA; 24 BP.
 XX
 AC ABR94601;
 XX
 DT 28-AUG-2002 (first entry)
 XX
 DE G-protein-coupled receptor DNA PCR primer #17.
 XX
 KM Human; rat; primer; ss; G protein-coupled receptor; anorectic; anabolic;
 KM obesity; appetite enhancement; prolactin production; eating disorder;
 KM PCR; pig; mouse.
 XX
 OS Sus scrofa.
 XX
 PN WO200244368-A1.
 XX
 PD 06-JUN-2002.
 XX
 PF 29-NOV-2001; 2001WO-JP010418.
 XX
 PR 30-NOV-2000; 2000JP-00364801.
 PR 26-MAR-2001; 2001JP-00087482.
 PR 15-MAY-2001; 2001JP-00145434.
 PR 06-SEP-2001; 2001JP-00270838.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Terao Y, Shintani Y, Harada M, Shimomura Y, Mori M;
 PI WPI; 2002-471832/50.
 XX
 DR New rat and mouse brain-originated G protein-coupled receptor proteins
 PT TGR26, useful in diagnosis and developing drugs for prevention or
 PT treatment of obesity or an eating disorder.
 XX
 PS Example 11; Page 244; 312pp; Japanese.
 XX
 CC The invention relates to G protein-coupled receptor proteins and their
 CC associated nucleic acids. The sequences are used in diagnosis of diseases
 CC relating to function of the protein and can be used for treating obesity,
 CC enhancing appetite or inhibiting prolactin production by administering

PF 27-JUN-2001; 2001WO-IB001147.
 XX
 PR 27-JUN-2000; 2000JP-00193133.
 PR 03-AUG-2000; 2000JP-00236115.
 PR 26-SEP-2000; 2000JP-00292483.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (KANK-) KANKYO ENG CO LTD.
 XX
 PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
 PI Yokomaku T;
 DR WPI; 2002-195876/25.
 XX
 PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
 PT their polymorphism and mutation, particularly useful in science and
 PT medicine for e.g. analytical applications, disease diagnosis and
 PT microbial identification.
 XX
 PS Example 12; Page 60; 152pp; Japanese.
 CC The present invention relates to nucleic acid probes, which are useful
 CC for assaying nucleic acids by hybridizing with a target nucleic acid, in
 CC which a single-stranded oligonucleotide is labelled with a fluorescent
 CC substance and a quencher in a manner that the fluorescence intensity of
 CC the hybridization reaction system is increased after completion of the
 CC hybridization but no stem loop structure is formed. The probes are useful
 CC for assaying nucleic acids and their polymorphism and mutation,
 CC particularly useful for e.g. analytical applications, disease diagnosis
 CC and microbial identification. The present sequence was used to illustrate
 CC the invention
 XX
 SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
 Query Match 0.3%; Score 20; DB 1; Length 30;
 Best Local Similarity 82.1%; Pred. No. 4.9e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 4458 ATGACCTTTTCTTTTCTTTTCTTTTCT 4485
 DB 3 ATATATTTTCTTTTCTTTTCTTTTCTTTT 30
 RESULT 481
 ABL95888
 ID ABL95888 standard; DNA; 30 BP.
 XX
 AC ABL95888;
 XX
 DT 19-JUN-2002 (first entry)
 XX
 DE Probe poly d for assaying nucleic acids.
 XX
 KW Probe; polymorphism detection; mutation detection; disease diagnosis;
 KW microbial identification; ss.
 XX
 OS Unidentified.
 XX
 PN WO200208414-A1.
 XX
 PD 31-JAN-2002.
 XX
 PF 27-JUN-2001; 2001WO-IB001147.
 XX
 PR 27-JUN-2000; 2000JP-00193133.
 PR 03-AUG-2000; 2000JP-00236115.
 PR 26-SEP-2000; 2000JP-00292483.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (KANK-) KANKYO ENG CO LTD.
 XX
 PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
 PI Yokomaku T;

XX
 DR WPI; 2002-195876/25.
 XX
 PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
 PT their polymorphism and mutation, particularly useful in science and
 PT medicine for e.g. analytical applications, disease diagnosis and
 PT microbial identification.
 XX
 PS Example 12; Page 60; 152pp; Japanese.
 CC The present invention relates to nucleic acid probes, which are useful
 CC for assaying nucleic acids by hybridizing with a target nucleic acid, in
 CC which a single-stranded oligonucleotide is labelled with a fluorescent
 CC substance and a quencher in a manner that the fluorescence intensity of
 CC the hybridization reaction system is increased after completion of the
 CC hybridization but no stem loop structure is formed. The probes are useful
 CC for assaying nucleic acids and their polymorphism and mutation,
 CC particularly useful for e.g. analytical applications, disease diagnosis
 CC and microbial identification. The present sequence was used to illustrate
 CC the invention
 XX
 SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;
 Query Match 0.3%; Score 20; DB 1; Length 30;
 Best Local Similarity 82.1%; Pred. No. 4.9e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 4458 ATGACCTTTTCTTTTCTTTTCTTTTCT 4485
 DB 3 ATATATTTTCTTTTCTTTTCTTTTCTTTT 30
 RESULT 482
 ABL95889
 ID ABL95889 standard; DNA; 30 BP.
 XX
 AC ABL95889;
 XX
 DT 19-JUN-2002 (first entry)
 XX
 DE Probe poly e for assaying nucleic acids.
 XX
 KW Probe; polymorphism detection; mutation detection; disease diagnosis;
 KW microbial identification; ss.
 XX
 OS Unidentified.
 XX
 PN WO200208414-A1.
 XX
 PD 31-JAN-2002.
 XX
 PF 27-JUN-2001; 2001WO-IB001147.
 XX
 PR 27-JUN-2000; 2000JP-00193133.
 PR 03-AUG-2000; 2000JP-00236115.
 PR 26-SEP-2000; 2000JP-00292483.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (KANK-) KANKYO ENG CO LTD.
 XX
 PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
 PI Yokomaku T;
 DR WPI; 2002-195876/25.
 XX
 PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
 PT their polymorphism and mutation, particularly useful in science and
 PT medicine for e.g. analytical applications, disease diagnosis and
 PT microbial identification.
 XX
 PS Example 12; Page 60; 152pp; Japanese.
 CC The present invention relates to nucleic acid probes, which are useful

Db 3 AATAATTTTTTTGTTTTTTTTTTT 30

RESULT 478
ID ABL95891
XX ABL95891 standard; DNA; 30 BP.
XX
AC ABL95891;
XX
DT 19-JUN-2002 (first entry)
XX
DE Probe poly g for assaying nucleic acids.
XX
KM Probe: polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX
OS Unidentified.
XX
PN WO200208414-A1.
XX
PD 31-JUN-2002.
XX
PF 27-JUN-2001; 2001WO-IB001147.
XX
PR 27-JUN-2000; 2000JP-00193133.
XX
PR 03-AUG-2000; 2000JP-00236115.
XX
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
DR WPI; 2002-195876/25.
XX
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
PS Example 12; Page 60; 152pp; Japanese.
XX
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 4.9e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4458 ATGACCTTTTTTTTTTTTTTTTGT 4485
DB 3 AATAATTTTTTTCTTTTTTTTTTTT 30

RESULT 479
ID ABL95892
XX ABL95892 standard; DNA; 30 BP.
XX
AC ABL95892;
XX
DT 19-JUN-2002 (first entry)
XX

DE Probe poly h for assaying nucleic acids.
XX
KM Probe: polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX
OS Unidentified.
XX
PN WO200208414-A1.
XX
PD 31-JUN-2002.
XX
PF 27-JUN-2001; 2001WO-IB001147.
XX
PR 27-JUN-2000; 2000JP-00193133.
XX
PR 03-AUG-2000; 2000JP-00236115.
XX
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
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PA (KANK-) KANKYO ENG CO LTD.
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PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
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DR WPI; 2002-195876/25.
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PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
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PS Example 12; Page 60; 152pp; Japanese.
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CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 4.9e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4458 ATGACCTTTTTTTTTTTTTTTTGT 4485
DB 3 AATAATTTTTTTCTTTTTTTTTTTT 30

RESULT 480
ID ABL95894
XX ABL95894 standard; DNA; 30 BP.
XX
AC ABL95894;
XX
DT 19-JUN-2002 (first entry)
XX
DE Probe poly j for assaying nucleic acids.
XX
KM Probe: polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX
OS Unidentified.
XX
PN WO200208414-A1.
XX
PD 31-JUN-2002.
XX

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XX Example 12; Page 60; 152pp; Japanese.
PS
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridizing with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labeled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;
Query Match 0.3%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 4.9e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0
QY 4458 ATGACATTTTGTCTTTTTTTTTTTTTTTGGT 4485
Dd ||| | | | | | | | | | | | | | | | |
3 ATATATTATTTTGTCTTTTTTTTTTTTTTTT 30
RESULT 476
ABLJ95886
ID ABLJ95886 standard; DNA; 30 BP.
XX
XX ABLJ95886;
XX
DT 19-JUN-2002 (first entry)
DE Probe poly b for assaying nucleic acids.
XX
XX Probe; polymorphism detection; mutation detection; disease diagnosis;
XX microbial identification; se.
XX
XX Unidentified.
OS
XX WO200208414-A1.
PN
XX 31-JAN-2002.
PD
XX 27-JUN-2001; 2001WO-IB001147.
XX
XX 27-JUN-2000; 2000JP-00193113. PR
XX 03-AUG-2000; 2000JP-00236115. PR
XX 26-SEP-2000; 2000JP-00292483. PR
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX (KANR-) KANKYO ENG CO LTD.
PA
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K,
PI Yokomaku T;
DR
WI; 2002-195876/25.
XX
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
XX Example 12; Page 60; 152pp; Japanese.
PS
XX The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridizing with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labeled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention

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CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 30 BP, 4 A, 0 C, 1 G, 25 T, 0 U, 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 4.9e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0
OY 4458 ATGACACTTTTTTTTTTTTTTTTTTTGCT 4485
DB 3 ATATATTTTTTTTTTGGTTTTTTTTTTTT 30
RESULT 477
ABL95887
ID ABL95887 standard; DNA; 30 BP.
XX
AC ABL95887;
XX
DT 19-JUN-2002 (first entry)
XX
DE Probe poly c for assaying nucleic acids.
XX
KW Probe: polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX
OS Unidentified.
XX
OS MO200208414-A1.
XX
PN 31-JAN-2002.
XX
PD 27-JUN-2001; 2001WO-IB001147.
XX
PF 27-JUN-2000; 2000JP-00193133.
XX
PR 03-AUG-2000; 2000JP-00236115.
XX
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
PA (KANR-) KANRKO ENG CO LTD.
XX
FI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
XX
FI Yokomaku T;
XX
DR WPI; 2002-195876/25.
XX
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
XX
PS Example 12; Page 60; 152pp; Japanese.
XX
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 4.9e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 4458 ATGACACTTTTTTTTTTTTTTTTTTTGCT 4485

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DT 11-APR-2002 (first entry)
 XX Poly g nucleotide sequence.
 DE ss; fluorochrome; nucleic acid probe; fluorescence.
 XX
 XX
 OS Unidentified.
 XX JP2001286300-A.
 PN 16-OCT-2001.
 PD 20-APR-2000; 2000JP-00120097.
 XX
 PF 20-APR-1999; 99JP-00111601.
 PR 24-AUG-1999; 99JP-00236666.
 PR 30-AUG-1999; 99JP-00242693.
 PR 01-FEB-2000; 2000JP-00028896.
 XX
 PA (BIOT-) BIOINDUSTRY KYOKAI SH.
 PA (KANK-) KANKYO ENG KK.
 PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIUTSU SOGO KEN.
 DR WPI; 2002-134193/18.
 XX
 PT Measurement of nucleic acid, using a nucleic acid probe and analysis of
 PT the obtained data.
 PS Example 5; Page 17; 34pp; Japanese.
 XX
 CC This invention relates to a method for measuring nucleic acids using a
 CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
 CC decreases the fluorescence of the fluorochrome when hybridised with a
 CC target nucleic acid, the decrease in the fluorescence is measured. The
 CC method can be used for measuring a target nucleic acid
 SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
 Query Match 0.3%; Score 20; DB 1; Length 30;
 Best Local Similarity 82.1%; Pred. No. 4.9e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 4458 ATGACCTTTTCTTTTCTTTTCTTTTCTTGT 4485
 DB 3 ATATATTTTCTTTTCTTTTCTTTTCTTTTCTT 30
 RESULT 474
 ABL95890
 ID ABL95890 standard; DNA; 30 BP.
 AC ABL95890;
 XX
 DT 19-JUN-2002 (first entry)
 XX
 DE Probe poly f for assaying nucleic acids.
 XX
 KW Probe; polymorphism detection; mutation detection; disease diagnosis;
 KW microbial identification; ss.
 XX
 OS Unidentified.
 XX WO200208414-A1.
 PN 31-JAN-2002.
 PD 27-JUN-2001; 2001WO-IB001147.
 PF 27-JUN-2000; 2000JP-00193133.
 PR 03-AUG-2000; 2000JP-00236115.
 PR 26-SEP-2000; 2000JP-00292483.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (KANK-) KANKYO ENG CO LTD.
 XX
 XX Kuraie R, Kanagawa T, Kanagata Y, Torimura M, Kurata S, Yamada K;
 PI Yokomaku T;
 XX
 DR WPI; 2002-195876/25.
 XX
 PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
 PT their polymorphism and mutation, particularly useful in science and
 PT medicine for e.g. analytical applications, disease diagnosis and
 PT microbial identification.
 PS Example 12; Page 60; 152pp; Japanese.
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 CC The present invention relates to nucleic acid probes, which are useful
 CC for assaying nucleic acids by hybridising with a target nucleic acid, in
 CC which a single-stranded oligonucleotide is labelled with a fluorescent
 CC substance and a quencher in a manner that the fluorescence intensity of
 CC the hybridisation reaction system is increased after completion of the
 CC hybridisation but no stem loop structure is formed. The probes are useful
 CC for assaying nucleic acids and their polymorphism and mutation,
 CC particularly useful for e.g. analytical applications, disease diagnosis
 CC and microbial identification. The present sequence was used to illustrate
 the invention
 SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
 Query Match 0.3%; Score 20; DB 1; Length 30;
 Best Local Similarity 82.1%; Pred. No. 4.9e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 4458 ATGACCTTTTCTTTTCTTTTCTTTTCTTGT 4485
 DB 3 ATATATTTTCTTTTCTTTTCTTTTCTTTTCTT 30
 RESULT 475
 ABL95885
 ID ABL95885 standard; DNA; 30 BP.
 AC ABL95885;
 XX
 DT 19-JUN-2002 (first entry)
 XX
 DE Probe poly a for assaying nucleic acids.
 XX
 KW Probe; polymorphism detection; mutation detection; disease diagnosis;
 KW microbial identification; ss.
 XX
 OS Unidentified.
 XX WO200208414-A1.
 PN 31-JAN-2002.
 PD 27-JUN-2001; 2001WO-IB001147.
 PF 27-JUN-2000; 2000JP-00193133.
 PR 03-AUG-2000; 2000JP-00236115.
 PR 26-SEP-2000; 2000JP-00292483.
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 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (KANK-) KANKYO ENG CO LTD.
 XX
 PI Kuraie R, Kanagawa T, Kanagata Y, Torimura M, Kurata S, Yamada K;
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 DR WPI; 2002-195876/25.
 XX
 PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
 PT their polymorphism and mutation, particularly useful in science and
 PT medicine for e.g. analytical applications, disease diagnosis and
 PT microbial identification.

```
XX 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 5; Page 17; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 4.9e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4458 ATGACCTTTTCTTTTCTTTTCTTTTCTTGT 4485
Db 3 ATATATTTTCTTTTCTTTTCTTTTCTTTT 30
XX
RESULT 471
ABA97616
ID ABA97616 standard; DNA; 30 BP.
XX
AC ABA97616;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly e nucleotide sequence.
XX
KM ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
XX (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
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PT the obtained data.
XX
PS Example 5; Page 17; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
```

```
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 4.9e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4458 ATGACCTTTTCTTTTCTTTTCTTTTCTTGT 4485
Db 3 ATATATTTTCTTTTCTTTTCTTTTCTTTT 30
XX
RESULT 472
ABA97617
ID ABA97617 standard; DNA; 30 BP.
XX
AC ABA97617;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly f nucleotide sequence.
XX
KM ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
XX (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 5; Page 17; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 4.9e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4458 ATGACCTTTTCTTTTCTTTTCTTTTCTTGT 4485
Db 3 ATATATTTTCTTTTCTTTTCTTTTCTTTT 30
XX
RESULT 473
ABA97618
ID ABA97618 standard; DNA; 30 BP.
XX
AC ABA97618;
XX
```

PT the obtained data.

XX Example 5; Page 17; 34pp; Japanese.

XX This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid

XX Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 30;

Best Local Similarity 82.1%; Pred. No. 4.9e+02; Mismatches 5; Indels 0; Gaps 0;

QY 4458 ATGACCTTTTCTTTTCTTTTCTTTTGT 4485
DB 3 ATATATTTTCTTTTCTTTTCTTTTCTTTT 30

RESULT 468

ABA97614
ID ABA97614 standard; DNA; 30 BP.

AC ABA97614;

DT 11-APR-2002 (first entry)

XX Poly c nucleotide sequence.

XX ss; fluorochrome; nucleic acid probe; fluorescence.

XX Unidentified.

PN JP2001286300-A.

PD 16-OCT-2001.

XX 20-APR-2000; 2000JP-00120097.

XX 20-APR-1999; 99JP-00111601.

PR 24-AUG-1999; 99JP-00236666.

PR 30-AUG-1999; 99JP-00242693.

PR 01-FEB-2000; 2000JP-00028896.

XX (BIOI-) BIOINDUSTRY KYOKAI SH.

PA (KANK-) KANKYO ENG KK.

PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIUTSU SOGO KEN.

DR WPI; 2002-134193/18.

XX Measurement of nucleic acids, using a nucleic acid probe and analysis of

PT the obtained data.

XX Example 5; Page 17; 34pp; Japanese.

XX This invention relates to a method for measuring nucleic acids using a

CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe

CC decreases the fluorescence of the fluorochrome when hybridised with a

CC target nucleic acid, the decrease in the fluorescence is measured. The

CC method can be used for measuring a target nucleic acid

XX Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

QY Query Match 0.3%; Score 20; DB 1; Length 30;

Best Local Similarity 82.1%; Pred. No. 4.9e+02; Mismatches 5; Indels 0; Gaps 0;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4458 ATGACCTTTTCTTTTCTTTTCTTTTGT 4485

DB 3 ATATATTTTCTTTTCTTTTCTTTTCTTTT 30

RESULT 469
ABA97612
ID ABA97612 standard; DNA; 30 BP.

XX ABA97612;

DT 11-APR-2002 (first entry)

XX Poly a nucleotide sequence.

XX ss; fluorochrome; nucleic acid probe; fluorescence.

XX Unidentified.

PN JP2001286300-A.

PD 16-OCT-2001.

XX 20-APR-2000; 2000JP-00120097.

XX 20-APR-1999; 99JP-00111601.

PR 24-AUG-1999; 99JP-00236666.

PR 30-AUG-1999; 99JP-00242693.

PR 01-FEB-2000; 2000JP-00028896.

XX (BIOI-) BIOINDUSTRY KYOKAI SH.

PA (KANK-) KANKYO ENG KK.

PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIUTSU SOGO KEN.

DR WPI; 2002-134193/18.

XX Measurement of nucleic acids, using a nucleic acid probe and analysis of

PT the obtained data.

XX Example 5; Page 17; 34pp; Japanese.

XX This invention relates to a method for measuring nucleic acids using a

CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe

CC decreases the fluorescence of the fluorochrome when hybridised with a

CC target nucleic acid, the decrease in the fluorescence is measured. The

CC method can be used for measuring a target nucleic acid

XX Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

QY Query Match 0.3%; Score 20; DB 1; Length 30;

Best Local Similarity 82.1%; Pred. No. 4.9e+02; Mismatches 5; Indels 0; Gaps 0;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4458 ATGACCTTTTCTTTTCTTTTCTTTTGT 4485

DB 3 ATATATTTTCTTTTCTTTTCTTTTCTTTT 30

RESULT 470
ABA97615
ID ABA97615 standard; DNA; 30 BP.

XX ABA97615;

DT 11-APR-2002 (first entry)

XX Poly d nucleotide sequence.

XX ss; fluorochrome; nucleic acid probe; fluorescence.

XX Unidentified.

PN JP2001286300-A.

PD 16-OCT-2001.

XX 20-APR-2000; 2000JP-00120097.

Best Local Similarity 82.1%; Pred. No. 4.9e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4077 ATTTGGAATCTCCATGCGCATGA 4104
DB 30 ATTTGAAAAATTTCCATGCGCATGA 3

RESULT 465

ABA97613
ID ABA97613 standard; DNA; 30 BP.

AC ABA97613;

DT 11-APR-2002 (first entry)

XX Poly b nucleotide sequence.

XX ss; fluorochrome; nucleic acid probe; fluorescence.

OS Unidentified.

XX JP2001286300-A.

PD 16-OCT-2001.

PF 20-APR-2000; 2000JP-00120097.

PR 20-APR-1999; 99JP-00111601.

PR 24-AUG-1999; 99JP-00236666.

PR 30-AUG-1999; 99JP-00242693.

PR 01-FEB-2000; 2000JP-00028896.

XX (BIOI-) BIOINDUSTRY KYOKAI SH.

PA (KANK-) KANKYO ENG KK.

PA (KEIZ-) KEIZAI SANGYOSHIO SANGYO GIUTSU SOGO KEN.

WPI; 2002-134193/18.

XX Measurement of nucleic acids, using a nucleic acid probe and analysis of

PT the obtained data.

XX Example 5; Page 17; 34pp; Japanese.

XX This invention relates to a method for measuring nucleic acids using a

CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe

CC decreases the fluorescence of the fluorochrome when hybridised with a

CC target nucleic acid, the decrease in the fluorescence is measured. The

CC method can be used for measuring a target nucleic acid

XX

XX Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 30;

Best Local Similarity 82.1%; Pred. No. 4.9e+02;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4458 ATGACCTTTTTTTTTTTTTTTTGT 4485

DB 3 ATATATTTTTTTTTTTGTTTTTTTTTTT 30

RESULT 466

ABA97619
ID ABA97619 standard; DNA; 30 BP.

AC ABA97619;

DT 11-APR-2002 (first entry)

XX Poly h nucleotide sequence.

XX ss; fluorochrome; nucleic acid probe; fluorescence.

OS

XX

XX

OS Unidentified.

XX JP2001286300-A.

PD 16-OCT-2001.

PF 20-APR-2000; 2000JP-00120097.

PR 20-APR-1999; 99JP-00111601.

PR 24-AUG-1999; 99JP-00236666.

PR 30-AUG-1999; 99JP-00242693.

PR 01-FEB-2000; 2000JP-00028896.

XX (BIOI-) BIOINDUSTRY KYOKAI SH.

PA (KANK-) KANKYO ENG KK.

PA (KEIZ-) KEIZAI SANGYOSHIO SANGYO GIUTSU SOGO KEN.

WPI; 2002-134193/18.

XX Measurement of nucleic acids, using a nucleic acid probe and analysis of

PT the obtained data.

XX Example 5; Page 17; 34pp; Japanese.

XX This invention relates to a method for measuring nucleic acids using a

CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe

CC decreases the fluorescence of the fluorochrome when hybridised with a

CC target nucleic acid, the decrease in the fluorescence is measured. The

CC method can be used for measuring a target nucleic acid

XX

XX Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 30;

Best Local Similarity 82.1%; Pred. No. 4.9e+02;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4458 ATGACCTTTTTTTTTTTTTTTTGT 4485

DB 3 ATATATTTTTTTTTTTCTTTTTTTTTTTT 30

RESULT 467

ABA97620
ID ABA97620 standard; DNA; 30 BP.

AC ABA97620;

DT 11-APR-2002 (first entry)

XX Poly l nucleotide sequence.

XX ss; fluorochrome; nucleic acid probe; fluorescence.

OS Unidentified.

XX JP2001286300-A.

PD 16-OCT-2001.

PF 20-APR-2000; 2000JP-00120097.

PR 20-APR-1999; 99JP-00111601.

PR 24-AUG-1999; 99JP-00236666.

PR 30-AUG-1999; 99JP-00242693.

PR 01-FEB-2000; 2000JP-00028896.

XX (BIOI-) BIOINDUSTRY KYOKAI SH.

PA (KANK-) KANKYO ENG KK.

PA (KEIZ-) KEIZAI SANGYOSHIO SANGYO GIUTSU SOGO KEN.

WPI; 2002-134193/18.

XX Measurement of nucleic acids, using a nucleic acid probe and analysis of

CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribonucleotide that was used for investigating the base
CC selectivity of a target nucleic acid
XX

SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 4.9e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4458 ATGCACTTTTCTTTTCTTTTCTTTTGT 4485
Db 3 ATATATTTTCTTTTCTTTTCTTTTCTTTT 30

RESULT 463
ABL56889
ID ABL56889 standard; DNA; 30 BP.
XX
XX ABL56889;
XX
XX 26-JUL-2002 (first entry)
XX
XX Synthetic deoxyribonucleotide poly b.
XX
XX Concentration; quantification; mutation detection; polymorphic;
XX polymerase chain reaction; PCR; ss.
XX
XX Synthetic.
XX
XX EP1046717-A2.
XX
XX 25-OCT-2000.
XX
XX 20-APR-2000; 2000EP-00108643.
XX
XX 20-APR-1999; 99JP-00111601.
XX
XX (NIBI-) JAPAN BIOINDUSTRY ASSOC.
XX (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
XX (KANK-) KANKYO ENG CO LTD.
XX
XX Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
XX Koyama O, Furusho K;
XX
XX WPI; 2000-657765/64.
XX
XX Determining the concentration of a target nucleic acid, useful e.g. for
XX detecting genetic mutations, comprises using a fluorescently labeled
XX probe in which emission is reduced by binding to the target nucleic acid.
XX
XX Example 5; Page 21; 55pp; English.
XX
XX The invention relates to the determination of the concentration of a
XX nucleic acid target, using a fluorescently labeled probe which produces
XX reduced fluorescence emission when hybridised to the target nucleic acid.
XX The method comprises measuring the reduction in emission caused by
XX hybridisation. The new method is particularly used to quantify target
XX nucleic acids by a real-time polymerase chain reaction, e.g. for
XX quantifying microbial cells in co-cultures or symbiotic systems, for
XX detecting gene mutations or polymorphisms, and for analysing melting

CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribonucleotide that was used for investigating the base
CC selectivity of a target nucleic acid
XX

SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 4.9e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4458 ATGCACTTTTCTTTTCTTTTCTTTTGT 4485
Db 3 ATATATTTTCTTTTCTTTTCTTTTCTTTT 30

RESULT 464
ABX68103/G
ID ABX68103 standard; DNA; 30 BP.
XX
XX ABX68103;
XX
XX 07-MAY-2003 (first entry)
XX
XX Novel Helicobacter pylori gene PCR primer #1074.
XX
XX Protein-protein interaction; ulcer; selected interacting domain; SID;
XX PCR; primer; ss.
XX
XX Helicobacter pylori.
XX
XX WO200266501-A2.
XX
XX 29-AUG-2002.
XX
XX 28-DEC-2001; 2001WO-EP015428.
XX
XX 02-JAN-2001; 2001US-0259302P.
XX
XX (HYBR-) HYBRIGENICS.
XX (INSP) INST PASTEUR.
XX
XX Legrain P, Rain J, Colland F, De Reuse H, Labigne A;
XX
XX WPI; 2002-674910/72.
XX
XX New complexes of protein-protein interactions in Helicobacter pylori,
XX useful for identifying modulating compounds for treating or preventing
XX ulcers in mammals.
XX
XX Example 9; Page 521; 642pp; English.
XX
XX The invention describes a complex of protein-protein interactions in
XX Helicobacter pylori selected from 421 complexes given in the
XX specification. The complex of protein-protein interactions are useful for
XX screening for agents which modulate the interaction of proteins.
XX Modulating compounds which binds to a targeted bacterial protein may be
XX used for treating or preventing ulcers in a human or animal. This
XX sequence represents a primer used to isolate polynucleotides encoding
XX Helicobacter pylori proteins for studies on protein-protein interactions
XX
XX Sequence 30 BP; 11 A; 5 C; 4 G; 7 T; 3 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 30;

PS Example 5; Page 21; 55pp; English.

XX The invention relates to the determination of the concentration of a

CC nucleic acid target, using a fluorescently labeled probe which produces

CC reduced fluorescence emission when hybridised to the target nucleic acid.

CC The method comprises measuring the reduction in emission caused by

CC hybridisation. The new method is particularly used to quantify target

CC nucleic acids by a real-time polymerase chain reaction, e.g. for

CC quantifying microbial cells in co-cultures or symbiotic systems, for

CC detecting gene mutations or polymorphisms, and for analysing melting

CC curves of target nucleic acids to determine a Tm value. Methods of the

CC invention allow target nucleic acids to be quantified quickly, easily and

CC accurately. Particularly there is no need to remove unbound probe, and no

CC materials are introduced that inhibit amplification by Taq polymerase (so

CC conventional PCR conditions can be used). The specificity of PCR is kept

CC high (amplification of primer dimers is delayed), and the limit of

CC quantitation is reduced. Complex probes are not needed, and amplification

CC can be monitored in real time. The working graph for data analysis

CC (automatically generated by a computer) has a higher correlation

CC coefficient than conventional graphs so more accurate quantitation is

CC possible. The current sequence represents a synthetic

CC deoxyribonucleotide that was used for investigating the base

CC selectivity of a target nucleic acid

XX

SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 30;

Best Local Similarity 82.1%; Pred. No. 4.9e+02;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4458 ATGAGCTTTTCTTTTCTTTTCTTTTGT 4485

DB 3 ATATATTTTCTTTTCTTTTCTTTTCTTTT 30

RESULT 459

ABLS6893

ID ABL56893 standard; DNA; 30 BP.

XX

AC ABL56893;

XX

DT 26-JUL-2002 (first entry)

XX

DE Synthetic deoxyribonucleotide poly f.

XX

KW Concentration; quantification; mutation detection; polymorphic;

KM polymerase chain reaction; PCR; ss.

XX

OS Synthetic.

XX

PN EP1046717-A2.

XX

PD 25-OCT-2000.

XX

PF 20-APR-2000; 2000EP-00108643.

XX

PR 20-APR-1999; 99JP-00111601.

XX

PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.

PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.

PA (KANR-) KANKYO ENG CO LTD.

XX

PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;

PI Koyama O, Furuho K;

XX

DR WPI; 2000-657765/64.

XX

PT Determining the concentration of a target nucleic acid, useful e.g. for

PT detecting genetic mutations, comprises using a fluorescently labeled

PT probe in which emission is reduced by binding to the target nucleic acid.

XX

PS Example 5; Page 21; 55pp; English.

XX

CC The invention relates to the determination of the concentration of a

CC nucleic acid target, using a fluorescently labeled probe which produces

CC reduced fluorescence emission when hybridised to the target nucleic acid.

CC The method comprises measuring the reduction in emission caused by

CC hybridisation. The new method is particularly used to quantify target

CC nucleic acids by a real-time polymerase chain reaction, e.g. for

CC quantifying microbial cells in co-cultures or symbiotic systems, for

CC detecting gene mutations or polymorphisms, and for analysing melting

CC curves of target nucleic acids to determine a Tm value. Methods of the

CC invention allow target nucleic acids to be quantified quickly, easily and

CC accurately. Particularly there is no need to remove unbound probe, and no

CC materials are introduced that inhibit amplification by Taq polymerase (so

CC conventional PCR conditions can be used). The specificity of PCR is kept

CC high (amplification of primer dimers is delayed), and the limit of

CC quantitation is reduced. Complex probes are not needed, and amplification

CC can be monitored in real time. The working graph for data analysis

CC (automatically generated by a computer) has a higher correlation

CC coefficient than conventional graphs so more accurate quantitation is

CC possible. The current sequence represents a synthetic

CC deoxyribonucleotide that was used for investigating the base

CC selectivity of a target nucleic acid

XX

SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 30;

Best Local Similarity 82.1%; Pred. No. 4.9e+02;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4458 ATGAGCTTTTCTTTTCTTTTCTTTTGT 4485

DB 3 ATATATTTTCTTTTCTTTTCTTTTCTTTT 30

RESULT 460

ABLS6895

ID ABL56895 standard; DNA; 30 BP.

XX

AC ABL56895;

XX

DT 26-JUL-2002 (first entry)

XX

DE Synthetic deoxyribonucleotide poly h.

XX

KW Concentration; quantification; mutation detection; polymorphic;

KM polymerase chain reaction; PCR; ss.

XX

OS Synthetic.

XX

PN EP1046717-A2.

XX

PD 25-OCT-2000.

XX

PF 20-APR-2000; 2000EP-00108643.

XX

PR 20-APR-1999; 99JP-00111601.

XX

PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.

PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.

PA (KANR-) KANKYO ENG CO LTD.

XX

PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;

PI Koyama O, Furuho K;

XX

DR WPI; 2000-657765/64.

XX

PT Determining the concentration of a target nucleic acid, useful e.g. for

PT detecting genetic mutations, comprises using a fluorescently labeled

PT probe in which emission is reduced by binding to the target nucleic acid.

XX

PS Example 5; Page 21; 55pp; English.

XX

CC The invention relates to the determination of the concentration of a

CC nucleic acid target, using a fluorescently labeled probe which produces

PT Determining the concentration of a target nucleic acid, useful e.g. for
 PT detecting genetic mutations, comprises using a fluorescently labeled
 PT probe in which emission is reduced by binding to the target nucleic acid.
 XX
 PS Example 5; Page 21; 55pp; English.
 CC The invention relates to the determination of the concentration of a
 CC nucleic acid target, using a fluorescently labeled probe which produces
 CC reduced fluorescence emission when hybridised to the target nucleic acid.
 CC The method comprises measuring the reduction in emission caused by
 CC hybridisation. The new method is particularly used to quantify target
 CC nucleic acids by a real-time polymerase chain reaction, e.g. for
 CC quantifying microbial cells in co-cultures or symbiotic systems, for
 CC detecting gene mutations or polymorphisms, and for analysing melting
 CC curves of target nucleic acids to determine a Tm value. Methods of the
 CC invention allow target nucleic acids to be quantified quickly, easily and
 CC accurately. Particularly there is no need to remove unbound probe, and no
 CC materials are introduced that inhibit amplification by Taq polymerase (so
 CC conventional PCR conditions can be used). The specificity of PCR is kept
 CC high (amplification of primer dimers is delayed), and the limit of
 CC quantitation is reduced. Complex probes are not needed, and amplification
 CC can be monitored in real time. The working graph for data analysis
 CC (automatically generated by a computer) has a higher correlation
 CC coefficient than conventional graphs so more accurate quantitation is
 CC possible. The current sequence represents a synthetic
 CC deoxyribooligonucleotide that was used for investigating the base
 CC selectivity of a target nucleic acid
 XX
 SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
 Query Match 0.3%; Score 20; DB 1; Length 30;
 Best Local Similarity 82.1%; Pred. No. 4.9e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 4458 ATGACCTTTTCTTTTCTTTTCTTTTCT 4485
 DB 3 ATATATTTTCTTTTCTTTTCTTTTCTTTT 30
 RESULT 457
 ABL56890
 ID ABL56890 standard; DNA; 30 BP.
 XX
 AC ABL56890;
 XX
 DT 26-JUL-2002 (first entry)
 XX
 DE Synthetic deoxyribooligonucleotide poly c.
 XX
 KM Concentration; quantification; mutation detection; polymorphic;
 KM polymerase chain reaction; PCR; ss.
 XX
 OS Synthetic.
 XX
 PN EP1046717-A2.
 XX
 PD 25-OCT-2000.
 XX
 PF 20-APR-2000; 2000EP-00108643.
 XX
 PR 20-APR-1999; 99JP-00111601.
 XX
 PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 PA (KANK-) KANKYO ENG CO LTD.
 XX
 PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
 PI Koyama O, Furusho K;
 XX
 DR WPI; 2000-657765/64.
 XX
 PT Determining the concentration of a target nucleic acid, useful e.g. for
 PT detecting genetic mutations, comprises using a fluorescently labeled
 PT probe in which emission is reduced by binding to the target nucleic acid.

PT probe in which emission is reduced by binding to the target nucleic acid.
 XX
 PS Example 5; Page 21; 55pp; English.
 CC The invention relates to the determination of the concentration of a
 CC nucleic acid target, using a fluorescently labeled probe which produces
 CC reduced fluorescence emission when hybridised to the target nucleic acid.
 CC The method comprises measuring the reduction in emission caused by
 CC hybridisation. The new method is particularly used to quantify target
 CC nucleic acids by a real-time polymerase chain reaction, e.g. for
 CC quantifying microbial cells in co-cultures or symbiotic systems, for
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 CC curves of target nucleic acids to determine a Tm value. Methods of the
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 CC accurately. Particularly there is no need to remove unbound probe, and no
 CC materials are introduced that inhibit amplification by Taq polymerase (so
 CC conventional PCR conditions can be used). The specificity of PCR is kept
 CC high (amplification of primer dimers is delayed), and the limit of
 CC quantitation is reduced. Complex probes are not needed, and amplification
 CC can be monitored in real time. The working graph for data analysis
 CC (automatically generated by a computer) has a higher correlation
 CC coefficient than conventional graphs so more accurate quantitation is
 CC possible. The current sequence represents a synthetic
 CC deoxyribooligonucleotide that was used for investigating the base
 CC selectivity of a target nucleic acid
 XX
 SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;
 Query Match 0.3%; Score 20; DB 1; Length 30;
 Best Local Similarity 82.1%; Pred. No. 4.9e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 4458 ATGACCTTTTCTTTTCTTTTCTTTTCT 4485
 DB 3 ATATATTTTCTTTTCTTTTCTTTTCTTTT 30
 RESULT 458
 ABL56888
 ID ABL56888 standard; DNA; 30 BP.
 XX
 AC ABL56888;
 XX
 DT 26-JUL-2002 (first entry)
 XX
 DE Synthetic deoxyribooligonucleotide poly a.
 XX
 KM Concentration; quantification; mutation detection; polymorphic;
 KM polymerase chain reaction; PCR; ss.
 XX
 OS Synthetic.
 XX
 PN EP1046717-A2.
 XX
 PD 25-OCT-2000.
 XX
 PF 20-APR-2000; 2000EP-00108643.
 XX
 PR 20-APR-1999; 99JP-00111601.
 XX
 PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 PA (KANK-) KANKYO ENG CO LTD.
 XX
 PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
 PI Koyama O, Furusho K;
 XX
 DR WPI; 2000-657765/64.
 XX
 PT Determining the concentration of a target nucleic acid, useful e.g. for
 PT detecting genetic mutations, comprises using a fluorescently labeled
 PT probe in which emission is reduced by binding to the target nucleic acid.

```

F1 Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
XX detecting genetic mutations, comprises using a fluorescently labeled
XX probe in which emission is reduced by binding to the target nucleic acid.
PS Example 5; Page 21; 55pp; English.
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
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CC materials are introduced that inhibit amplification by Taq polymerase (so
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CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribonucleotide that was used for investigating the base
CC selectivity of a target nucleic acid
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match          0.3%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 4.9e+02;
Matches   23; Conservative    0; Mismatches     5; Indels      0; Gaps       0.

OY         4458 ATGCACCTTTTGTGTTTTTGTTGGT 4485
           ||| | | | | | | | | | | | | | | |
DB         3 ATATATTTCCTTTTGTGTTTGTTCCTTTT 30

RESULT 455
ABLS56896
ID ABLS56896 standard; DNA; 30 BP.
AC ABLS56896;
XX
DT 26-JUL-2002 (first entry)
DE Synthetic deoxyribonucleotide poly I.
XX
KM Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; ss.
OS Synthetic.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99UP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
KI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T,
PI Koyama O, Furusho K;
XX
```

```

DR  WPI; 2000-657765/64.
XX
PT  Determining the concentration of a target nucleic acid, useful e.g. for
PT  detecting genetic mutations, comprises using a fluorescently labeled
PT  probe in which emission is reduced by binding to the target nucleic acid.
XX
XX  Example 5; Page 21; 55pp; English.
XX
CC  The invention relates to the determination of the concentration of a
CC  nucleic acid target, using a fluorescently labeled probe which produces
CC  reduced fluorescence emission when hybridised to the target nucleic acid.
CC  The method comprises measuring the reduction in emission caused by
CC  hybridisation. The new method is particularly used to quantify target
CC  nucleic acids by a real-time polymerase chain reaction, e.g. for
CC  quantifying microbial cells in co-cultures or symbiotic systems, for
CC  detecting gene mutations or polymorphisms, and for analysing melting
CC  curves of target nucleic acids to determine a Tm value. Methods of the
CC  invention allow target nucleic acids to be quantified quickly, easily and
CC  accurately. Particularly there is no need to remove unbound probe, and no
CC  materials are introduced that inhibit amplification by Taq polymerase (so
CC  conventional PCR conditions can be used). The specificity of PCR is kept
CC  high (amplification of primer dimers is delayed), and the limit of
CC  quantitation is reduced. Complex probes are not needed, and amplification
CC  can be monitored in real time. The working graph for data analysis
CC  (automatically generated by a computer) has a higher correlation
CC  coefficient than conventional graphs so more accurate quantitation is
CC  possible. The current sequence represents a synthetic
CC  deoxyribooligonucleotide that was used for investigating the base
CC  selectivity of a target nucleic acid
XX
SQ  Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 4.9e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy 4458 ATGACCTTTTTTTTTTTTTTTTTTTTGT 4485
||| ||||| ||||| ||||| |||||
Db 3 ATATATTTTTTTTTTCTTTTTTTTTTTT 30
XX
RESULT 456
ABL56894
ID ABL56894 standard; DNA; 30 BP.
XX
AC ABL56894;
XX
DT 26-JUN-2002 (first entry)
XX
DE Synthetic deoxyribooligonucleotide poly g.
XX
KM Concentration; quantification; mutation detection; polymorphic;
KM polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN EPI046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANR-) KANKYO ENG CO LTD.
XX
PT Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PT Koyama O, Furusho K;
XX
DR WPI, 2000-657765/64.
XX

```

ID	AAAT69677	standard; DNA; 30 BP.
XX		
AC	AAT69677;	
XX		
DT	25-MAR-2003	(revised)
DT	19-FEB-1998	(first entry)
XX		
DE	Downstream primer for synthetic full length CAT sense RNA.	
KM	PCR primer; CAT RNA; detection; quantification; determination; ss.	
XX		
OS	Synthetic.	
PV	EP780479-A2.	
PD	25-JUN-1997.	
PF	19-DEC-1996;	96HP-00120480.
XX		
PR	23-DEC-1995;	95DE-01048680.
PA	(BOE) BOEHRINGER MANNHEIM GMBH.	
XX		
PA	(HOPE) ROCHE DIAGNOSTICS GMBH.	
PI	Leyling H, Hinzpeter M, Wiltor H, Fritton H;	
DR	WPI, 1997-322152/30.	
XX		
PT	Detection and quantitation of nucleic acid using probe with label and	
PT	binding group - and after hybridisation treatment with RNase and capture	
PT	on solid phase, particularly for RNA.	
PS	Example 2; Page 7; 13pp; German.	
XX		
CC	The present sequence is a PCR primer for synthetic full length CAT sense	
CC	RNA, which was used in a novel method for the detection and quantitative	
CC	determination of specific oligonucleotides (ON) or polynucleotides (PN).	
CC	The method comprises combining a sample containing RNA or single stranded	
CC	DNA with a lysis/hybridisation buffer, treating the homogenised solution	
CC	with 1 or more probes, which are essentially complementary to the ON or	
CC	PN and contain at least 2 different labels, one a specific binding group	
CC	and the other a detectable chemical group, hybridising under stringent	
CC	conditions, diluting the mixture and adding an agent that cleaves single	
CC	stranded nucleic acid into mononucleotides or ON, transferring the	
CC	mixture to a vessel or well, coated with a substance that binds at least	
CC	1 label, immobilising ON and PN hybrids (modified with 2 different labels	
CC	or 1 label) to the solid phase and detecting immobilised ON or PN, or the	
CC	non-immobilised labelled product, directly or via an enzyme labelled	
CC	antibody. The method can be used to detect specific mRNA in human, animal	
CC	or plant samples. The method is easy to perform and suitable for	
CC	automation, does not require preliminary RNA isolation, can be made	
CC	quantitative and has a low background. (Updated on 25-MAR-2003 to correct	
CC	PR field.) (Updated on 25-MAR-2003 to correct PA field.)	
SO	Sequence 30 BP; 2 A; 3 C; 4 G; 21 T; 0 U; 0 Other;	
QY		
DB	Query Match	0.3%; Score 20; DB 1; Length 30;
	Beat Local Similarity	100.0%; Pred. No. 4.9e+02;
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
	4464 TTTTTTTTTTTTTTTTTTTT 4483	
	1 TTTTTTTTTTTTTTTTTTTT 20	
RESULT 453		
AAVS638		
ID	AAVS6638 standard; DNA; 30 BP.	
XX		
AC	AAVS6638;	
XX		
DT	23-NOV-1998	(first entry)
XX		

```

DE      Feline FLAF CDNA primer #9.
XX      Cytokine; feline; FLAFp40; FLAPp35; heterodimer; cytotoxic; treatment;
XX      T lymphocyte cell; autoimmune disease; primer; ss.
XX      OS
XX      Synthetic.
XX      Fells catus.
XX      WO9746583-A1.
XX      PN
XX      11-DEC-1997.
XX      PD
XX      29-MAY-1997; 97WO-JP001824.
XX      PE
XX      04-JUN-1996; 96JP-00165249.
XX      PR
XX      (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX      PA
XX      Imamura T, Maeda H, Fujiyasu T, Imagawa Y, Tokiyoshi S;
XX      WI; 1998-042118/04.
XX      DR
XX      Novel feline cytokine protein - useful for treating feline autoimmune
XX      diseases, e.g. those caused by feline herpes virus or feline calicivirus.
XX      PT
XX      Example 14; Page 66; 94pp; Japanese.
XX      PS
XX      AAV56637-V56640 are primers used in the amplification of novel feline
XX      CC      cytokine proteins, FLAPp40 and FLAFp35. This protein can be used in the
XX      CC      production of a FLAPp35/FLAFp40 heterodimer which can potentiate the
XX      CC      cytotoxic activity of feline cytotoxic T lymphocyte cells. Such proteins
XX      CC      are used for treatment of feline autoimmune diseases e.g. as caused by
XX      CC      feline herpes virus or feline calicivirus
XX      CC
XX      SQ      Sequence 30 BP; 3 A; 3 C; 3 G; 21 T; 0 U; 0 Other;
Gy      4454 TGGCATGACCTTTT TTTT TTTT TTTT TTTT 4481
Db      3 TAGCTCGAGTTT TTTT TTTT TTTT TTTT 30

RESULT 454
ABLS6892
ID      ABL56892 standard; DNA; 30 BP.
XX      AC
XX      ABL56892;
XX      AC
XX      26-JUL-2002 (first entry)
XX      DT
XX      DE      Synthetic deoxyribopoligonucleotide poly e.
XX      KW      Concentration; quantification; mutation detection; polymorphic;
XX      KW      polymerase chain reaction; PCR; ss.
XX      OS
XX      Synthetic.
XX      PN      EP1046717-A2.
XX      PD      25-OCT-2000.
XX      PE      20-APR-2000; 2000EP-00108643.
XX      PR      20-APR-1999; 99JP-00111601.
XX      PA      (NIBI-) JAPAN BIOINDUSTRY ASSOC.
XX      PA      (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
XX      PA      (KANK-) KANKYO ENG CO LTD.
XX      KI      Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;

```

KW		variable region; camellised Ig heavy chain variable region.
XX		
OS	Vaccinia virus.	
OS	Escherichia coli.	
XX		
PN	US2002123057-A1.	
XX		
PD	05-SEP-2002.	
XX		
PF	14-NOV-2001; 2001US-00987456.	
PR	17-NOV-2000; 2000US-0249268P.	
PR	18-JAN-2001; 2001US-0256267P.	
PR	27-FEB-2001; 2001US-02271424P.	
PR	15-JUN-2001; 2001US-0298087P.	
XX		
PA	(UYRP) UNIV ROCHESTER.	
XX		
P1	Zauderer M., Smith ES;	
XX		
DR	WPI, 2003-066785/06.	
XX		
PT	Selecting polynucleotides which encode antigen-specific immunoglobulin molecules, by introducing the library of polynucleotides into the host cells, and recovering the polynucleotides of the library for the antigen.	
XX		
PS	Example 9; Page 49; 108pp; English.	
XX		
CC	The invention relates to selecting polynucleotides which encode antigen-specific immunoglobulins (Ig) (or fragments) comprising introducing into a population of host cells, a 1st and 2nd library of polynucleotides encoding, several 1st and 2nd Ig subunit polypeptides, permitting expression of Ig molecules (via control element e.g. an early/late promoter), contacting Ig molecules with an antigen, and recovering polynucleotides of the 1st library for the antigen. The Ig molecules are heavy and light chain constant regions and variable regions linked via peptide linkers and optionally directed via signal peptides or transmembrane domains to different cell compartments. Also included is a method of selecting polynucleotides which encode a single-domain antigen-specific Ig molecule (its anti-specific fragment), by: (a) introducing into a population of eukaryotic host cells capable of expressing the Ig molecule a library of polynucleotides encoding (through operable association with a transcriptional control region) several single-domain Ig polypeptides (each comprising a Ig heavy chain constant region, a camellised Ig heavy chain variable region, and a signal peptide capable of directing cell surface expression or secretion of Ig subunit polypeptide) (b) permitting expression of Ig molecules (or antigen-specific fragments) from the host cells; (c) contacting the Ig molecules with an antigen; and (d) recovering polynucleotides of the library from those host cells expressing Ig molecules which bind the antigens. The methods are useful for selecting polynucleotides which encode an antigen-specific Ig molecule, or its fragment. The present sequence is a PCR primer used to construct the Ig expression constructs used in the method of the invention	
SO	Sequence 29 BP; 10 A; 6 C; 4 G; 9 T; 0 U; 0 Other;	
XX		
OY	Query Match 0.3%; Score 20; DB 1; Length 29; Best Local Similarity 82.1%; Pred. No. 4.7e+02; Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0	
Dn	5438 TTGGGCATGCAAGAAATGACTT 5465 29 TTGGCGCATGCAATTAAGAATTCTT 2	
XX		
ID	ABZ22431 standard; DNA; 29 BP.	
AC	ABZ22431;	
XX		
DT	24-MAR-2003 ((first entry))	

7. 5k promoter-Gus expression vector PCR primer SEQ ID NO:134.

KX
XX

Identification; intrabody; eukaryotic cell; immunoglobulin; selection;
KX identification; diminished arrhythmia potential; cardiomyocyte; stroke;
KW cardiovascular; heart failure; arrhythmia; embolic;
KM enhanced contractile property; artery; arteriole; angina; atherosclerosis;
KW sarcolemmal calcium cycling; skin biology; keloid formation;
KM LDL metabolism; HDL metabolism; skin biology; keloid formation;
XX PCR primer; ss.
OS Vaccinia virus.
OS Homo sapiens.
XX

WO200286096-A2.

PN 31-OCT-2002.

XX

23-JAN-2002; 2002WO-US001677.

PB

23-JAN-2001; 2001US-0263225P.
PR 24-JAN-2001; 2001US-0263200P.
PR 27-FEB-2001; 2001US-0271422P.
PR 15-JUN-2001; 2001US-0298095P.
XX

(UVRP) UNIV ROCHESTER MEDICAL CENT.

PA Zauderer M, Wei C, Smith ES;
PI WPI; 2003-103408/09.
DR

Selecting polynucleotides encoding an intracellular immunoglobulin which
PT induces a modified phenotype in a eukaryotic host cell, by introducing
PT library of polynucleotides encoding immunoglobulin subunit polypeptides.
XX

Example 8; Page 149; 257pp; English.

PS

The present invention describes a method for selecting polynucleotides
XX (PNS) encoding an intracellular immunoglobulin molecule or its fragment
CC whose expression induces a modified phenotype in a eukaryotic host cell
CC (I). The method comprises introducing into (I) a first and second library
CC of PNS encoding, through operable association with a transcriptional
CC control region, first and second intracellular immunoglobulin subunit
CC polypeptides, respectively. The method is useful for selecting
CC polynucleotides which encode an intracellular immunoglobulin molecule, or
CC fragment. The method is useful e.g. for identifying polynucleotides which
CC singly or collectively encode intracellular immunoglobulin molecules, or
CC which sensitize host cells to killing by an agent. The method may also be
CC used in cardiovascular applications; for screening for diminished
CC arrhythmia potential in cardiomyocytes and for enhanced contractile
CC properties of cardiomyocytes and diminish heart failure potential; for
CC identifying intracellular immunoglobulin molecules that will regulate
CC intracellular and sarcolemmal calcium cycling in cardiomyocytes to
CC prevent arrhythmias or that will diminish embolic phenomena in arteries
CC and arterioles leading to strokes and angina; in screening for decreases
CC in atherosclerosis-producing mechanisms to find intracellular
CC immunoglobulin molecules that regulate LDL and HDL metabolism; in skin
CC biology applications; and in regulating or inhibiting keloid formation.
CC AB822379 to AB822449 and ABP56536 to AB856618 represent sequences used in
CC the exemplification of the present invention
XX

Sequence 29 BP; 10 A; 6 C; 4 G; 9 T; 0 U; 0 Other;

SQ

Query Match 0.3%; Score 20; DB 1; Length 29;
Best Local Similarity 82.1%; Pred. No. 4.7e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0.

Gy 5438 TTGGGCAATGACAGAAATAAGTTCCT 5465
DB ||||| ||||| ||||| ||||| |||||
TTTGCGCATGCATTATTAAGAATTCTT 2

RESULT_452
PAT69677

OS Synthetic.
 XX
 PN WO200172995-A2.
 XX
 XX 04-OCT-2001.
 PD
 XX 28-MAR-2001; 2001WO-US009953.
 PF
 XX 28-MAR-2000; 2000US-0192586P.
 PR 10-MAY-2000; 2000US-020343P.
 PR 23-JAN-2001; 2001US-0263226P.
 PR 27-FEB-2001; 2001US-0271426P.
 XX
 XX (UYRP) UNIV ROCHESTER.
 XX
 PI Zauderer M, Smith ES;
 XX WPI, 2001-570897/64.
 DR
 XX
 XX
 PT Selecting target polynucleotides, particularly toxic genes, involves
 PT introducing a library of insert polynucleotides into a host cell
 PT population, where the target polynucleotide promotes cell death.
 XX
 XX Example 19, Page 238; 359pp; English.
 XX
 XX The present invention relates to a method for selecting a target
 CC polynucleotide. The method comprises introducing into a host cell
 CC a population a library of insert polynucleotides, where expression of the
 CC target polynucleotide directly or indirectly promotes host cell death.
 CC The cells are cultured and the insert polynucleotides are collected from
 CC the cells which die. The method is useful for selecting target
 CC polynucleotides, particularly polynucleotides which alter cell phenotypes
 CC of induce or inhibit cell death. The method can be used to isolate toxic
 CC genes such as tumor suppressors. The present sequence is a PCR primer,
 CC which was used in an example from the present invention
 XX
 XX Sequence 29 BP; 10 A; 6 C; 4 G; 9 T; 0 U; 0 Other;
 SQ
 Query Match 0.3%; Score 20; DB 1; Length 29;
 Best Local Similarity 82.1%; Pred. No. 4.7e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 5438 TTGGGCAATGACAGAAATGAGTTCTT 5465
 DB 29 TTGGCCGATGACATTAAGGAATCTT 2
 RESULT 449
 ABS68823/c
 ID ABS68823 standard; DNA; 29 BP.
 XX
 AC ABS68823;
 XX
 DT 20-NOV-2002. (first entry)
 XX
 DE PCR primer, 7.5-gus sense, used to amplify 7.5-gus expression cassette.
 XX
 XX Regulator; transcription; cell death; phenotype; molecular scaffold;
 KM gene therapy; cancer; cardiovascular disease; arrhythmia; heart failure;
 KM ischaemia; obesity; neurodegenerative disease; Alzheimer's disease;
 KM bone pathology; dermatologic disease; psoriasis; infection; AIDS;
 KM acquired immunodeficiency syndrome; cosmetic; wound healing; primer;
 KM antibiotic transport; drug toxicity; drug resistance; immunobiology;
 KM inflammation; allergic response; human immunodeficiency virus; ss; PCR.
 XX
 OS Escherichia coli.
 OS Synthetic.
 XX
 PN WO200262822-A2.
 XX
 PD 15-AUG-2002.
 XX
 PF 04-FEB-2002; 2002WO-US002814.

XX
 PR 02-FEB-2001; 2001US-0265589P.
 PR 05-FEB-2001; 2001US-0265880P.
 PR 27-FEB-2001; 2001US-0271423P.
 XX
 XX
 PA (UYRP) UNIV ROCHESTER.
 XX
 PI Zauderer M, Smith ES;
 XX WPI, 2002-643398/69.
 DR
 XX
 XX
 PT Identifying regulator polypeptides which influence target transcriptional
 PT regulatory regions, useful for treating cancer, comprises introducing
 PT host cells expressing the polypeptide into a library of polynucleotides.
 XX
 XX Example 5; Page 115; 224pp; English.
 XX
 XX The invention discloses a method for identifying polynucleotides encoding
 CC a regulator polypeptide, whose expression induces activation of a target
 CC transcriptional regulatory region in a host cell. The method comprises
 CC providing a population of eukaryotic host cells capable of expressing the
 CC polypeptide, introducing into the host cell a library of polynucleotides
 CC encoding the polypeptides, permitting expression of the polypeptides and
 CC then recovering them from the host cells. The target transcriptional
 CC regulatory region is operably associated with a polynucleotide encoding a
 CC gene product, the expression of which results in host cell death or cause
 CC the host cells to exhibit a pre-determined modified phenotype and where
 CC the gene product is expressed upon activation of target transcriptional
 CC regulatory region. Each candidate regulator polypeptide comprises a
 CC candidate peptide and a molecular scaffold fused to the peptide so that
 CC the peptide is displayed on the surface of the candidate regulator
 CC polypeptide. The methods are useful in selecting and/or screening
 CC regulator molecules, such as polypeptides, which directly or indirectly
 CC induce or suppress the transcriptional activation of a target
 CC transcriptional regulatory region in a eukaryotic host cell. These
 CC regulator molecules may be used (e.g. in gene therapy) for preventing or
 CC treating cancers (e.g. breast or ovarian cancer), cardiovascular diseases
 CC (e.g. arrhythmia, heart failure, ischaemia), obesity, neurodegenerative
 CC diseases (e.g. Alzheimer's disease), bone pathologies, dermatologic
 CC diseases (e.g. psoriasis), infections (e.g. viral, bacterial), acquired
 CC immunodeficiency syndrome (AIDS), in cosmetic applications and in wound
 CC healing. The method is also useful in screening regulator molecules that
 CC block antibiotic transport mechanisms, in drug toxicities and drug
 CC resistance applications and in improving the performance of existing or
 CC developmental drugs. It may also be used in immunobiology, inflammation,
 CC allergic response and in biotechnology applications. The sequences
 CC presented in ABS68815-ABS68832 are the PCR primers used to amplify the
 CC reporter genes and gene regions required in the creation of vectors to
 CC express the regulator polypeptides
 XX
 XX Sequence 29 BP; 10 A; 6 C; 4 G; 9 T; 0 U; 0 Other;
 SQ
 Query Match 0.3%; Score 20; DB 1; Length 29;
 Best Local Similarity 82.1%; Pred. No. 4.7e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 5438 TTGGGCAATGACAGAAATGAGTTCTT 5465
 DB 29 TTGGCCGATGACATTAAGGAATCTT 2
 RESULT 450
 ABSX17468/c
 ID ABSX17468 standard; DNA; 29 BP.
 XX
 AC ABSX17468;
 XX
 DT 04-FEB-2003 (first entry)
 XX
 DE Vaccinia virus 7.5k promoter/GUS cassette PCR primer #1.
 XX
 XX ss; PCR; antigen-specific immunoglobulin; Ig; early/late promoter;
 KM heavy chain constant region; light chain constant region; primer;

CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
xx
SQ Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match	0.3%	Score 20;	DB 1;	Length 29;
Best Local Similarity	82.1%;	Pred. No. 4.7e+02;		
Matches 23;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;

```
OY      4458 ATGCACTTTT TTTT TTTT TTTT TTTT TG 4485
```

|||||
|||

```
Dd      28 AAGTTTTT GTTT TTTT TTTT TTTT TT 1
```

RESULT 446
AAF74921/c
ID AAF74921 standard; DNA; 29 BP.
vv

AC	AAF74921;
XX	
DT	23-MAY-2001 (first entry)
yy	

DE CD40L poly-A tract sequence SEQ ID NO:18.

KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
 KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
 KW antiinflammatory; inflammatory disease; autoimmune disease; ds.

OS Homo sapiens.

PN WO200119844-A1.

PD 22-MAR-2001

PF 13-SEP-2000; 2000WO-US024966

PR 13-SEP-1999; 99US-0153625P.
VV

PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED,
VV

PI Crow MK, Li Y;

DR WPI; 2001-244776/25.

PT New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.

PS Example 1; Fig 3; 90pp; English.

CC The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF4905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (II) has antiarthritic,
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention

SQ Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match	0.38;	Score 20;	DB 1;	Length 29;
Best Local Similarity	82.18;	Pred. No. 4.7e+02;		
Matches 23;	Conservative	0;	Mismatches 5;	Indels 0;
			Gaps	0

```
Oy      4458 ATGACCTTTTCTTTTTTTTTTTTTTTGT 4485
          ||| |||| |||||| ||||| |||
Db      28 AAGCTTTTTCCTTTTTTTTTTTTTTTT 1
```

RESULT: 447.
AAF74928/c
ID AAF74928 standard; DNA; 29 BP.

AC AAF74928;

DT 23-MAY-2001 (first entry)

DE	CD40L poly-A tract sequence SEQ ID NO:25.
----	---

KM Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis
KM diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KM antiinflammatory; inflammatory disease; autoimmune disease; ds.

OS Homo sapiens.

PN WO200119844-A1

PD 22-MAR-2001

PF 13-SEP-2000; 2000WO-US024966.

PR 13-SEP-1999; 99US-0153625P.

PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED

PI Crow MK, Li Y;

DR WPI; 2001-244776/25.

PT New altered Cpa0L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.

PS Example 1; Fig 3; 90pp; English.

CC The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF4905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (II) has antiarthritic,
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention

Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match	0.3%	Score 20;	DB 1;	Length 29;
Best Local Similarity	82.1%;	Pred. No. 4.7e+02;		
Matches 23;	Conservative	0;	Mismatches 5;	Indels 0;
				Gaps 0;

```
Oy      4458 ATGCACTTTCCTTTTCCTTTTCCTTTTCGT 4483  
         |||||  
Db      28 AAGCTTTTGTTTTTTTCCTTTTCCTTTTCCTTTTC 1
```

RESULT 448
ABA03031/c
ID ABA03031 standard; DNA; 29 BP.

AC ABA03031;

DT 04-FEB-2002 (first entry)

DE PCR primer 7.5 Gus sense.

KW PCR primer; cell death; toxic gene; tumour suppressor; ss

XX	WO200119844-A1.
PN	
XX	22-MAR-2001.
XX	
XX	13-SEP-2000; 2000WO-US024966.
PF	
XX	13-SEP-1999; 99US-0153625P.
PR	
XX	(NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
PA	
XX	Crow MK, Li Y;
PI	
XX	WPI: 2001-244776/25.
DR	
XX	
XX	New altered CD40L promoter for use in the study, diagnosis and treatment
PT	of a variety of inflammatory disorders and autoimmune diseases, such as
PT	rheumatoid arthritis.
XX	
PS	Example 1; Fig 3; 90pp; English.
XX	
XX	The present invention describes an isolated, purified nucleic acid, which
CC	is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC	residues 331-455 of the sequence comprising 455 nucleotides given in
CC	AA774905 where A in the wild type sequence at position 331 (corresponding
CC	to position -125) is replaced with C. (I) has antiarthritic,
CC	antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC	be used in gene therapy. (I) is useful in the study, diagnosis and
CC	treatment of inflammatory and autoimmune diseases, as well as diseases in
CC	which elevated expression of CD40L is a factor, e.g., rheumatoid
CC	arthritis. The present sequence represents a CD40L poly-A tract sequence
CC	which is used in an example from the present invention
XX	
XX	Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match	0.3%	Score 20	DB 1	Length 29
Best Local Similarity	82.1%	Pred. No. 4.7e+02		
Matches 23, Conservative	0	Mismatches 5	Indels 0	Gaps 0

```
Oy      4458 ATGCACTTTT TTTT TTTT TTTT TTTT GT 4485
          ||| |||| | |||| | |||| |
Db      28 AAGTTTTT TGT TTTT TTTT TTTT TTTT 1
```

RESULT 444
AAF74907/c
ID AAF74907 standard; DNA; 29 BP.
...

AC AAF74907;

DT 23-MAY-2001 (first entry)

DE CD40L poly-A tract sequence SEQ ID NO:4.

Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis; diagnosis; antiarthritis; antirheumatic; immunosuppressive; antiinflammatory; inflammatory disease; autoimmune disease; ds.

05 Homo sapiens

PN WO200119844-A1.

PD 22-MAR-2001.

PF 13-SEP-2000; 2000WO-US024966.

PR 13-SEP-1999; 99US-0153625P.

PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

PI Crow MK, LI Y;

DR WPI; 2001-244776/25.

XX New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.

PS Example 1; Fig 3; 90pp; English.

CC The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritic,
CC antineumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention

XX Sequence 29 BP, 23 A, 3 C, 0 G, 3 T, 0 U, 0 Other;

SQ Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match	0.3%	Score	20	DB	1	Length	29
Best Local Similarity	82.1%	Pred. No.	4.7e+02				
Matches	23	Conservative	0	Mismatches	5	Indels	0
						Gaps	0

Oy		4458	A T G G A C T T T T T T T T T T T T T T T T T T G T	4485
Db	28	A A G C T T T T T T G T T T T T T T T T T T T T T T T	1	

RESULT 445

ID AAF74935 standard; DNA; 29 BP.

AC AAF74935;

DT 23-MAY-2001 (first entry)

DE CD40L poly-A tract sequence SEQ ID NO:32.

KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis
 KW diagnosis; antiarthritis; antirheumatic; immunosuppressive;
 KW antiinflammatory; inflammatory disease; autoimmune disease; ds.

OS Homo sapiens.

PN WO200119844-A1.

PD 22-MAR-2001.

PF 13-SEP-2000; 2000WO-US024966.

PR 13-SEP-1999; 99US-0153625P.

PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

PI Crow MK, Li Y;

DR WPI; 2001-244776/25.

PT New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.

PS Example 1; Fig 3; 90pp; English.

CC The pressed invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter. (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antitumor, antiproliferative,
CC antineuritic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and

ID		ABK6168 standard; DNA; 24 BP.
XX		
AC		ABK6168;
XX		
DT		24-SEP-2002 (first entry)
XX		
DE	Oligo dT primer #1 used in method to study gene expression.	
XX		
KW	Oligo dT primer; gene expression analysis; primer; ss.	
OS	Synthetic.	
PN	WO200236828-A2.	
PD	10-MAY-2002.	
PF	01-NOV-2001; 2001MO-USO45401.	
XX		
PR	01-NOV-2000; 2000US-0244933P.	
PA	(GENO-) GENOMIC SOLUTIONS INC.	
PI	Kane MD, Dombkowski AA, Nagel AC;	
DR	WPI; 2002-508123/54.	
PT	Identifying and characterizing gene expression in samples, for	
PT	identifying mRNAs expressed at different levels, comprises employing an	
PT	identifier having an oligo-dT primer of a specific sequence and a	
PT	detectable marker at its 5' end.	
PS	Disclosure; Page 11; 45pp; English.	
XX		
CC	The invention relates to systems for identification and characterization	
CC	of gene expression in one or more samples, comprising an identifier having	
CC	a specific oligo-dT primer sequence, where the identifier comprises a	
CC	detectable marker at its 5' end. The system is useful for identifying any	
CC	or all genes expressed in a given in vivo or in vitro RNA sample, as well	
CC	as the relative differences in mRNA between 2 or more samples, where	
CC	desired, for supporting discovery of new genes, and for identifying mRNAs	
CC	that are expressed at different levels between 2 or more samples. The new	
CC	system or method addresses limitations of prior methods by comprising	
CC	compositions and systems that incorporate new strategies where molecular	
CC	or biochemical assay compositions and systems are linked to DNA or RNA	
CC	sequence databases for optimal resource efficiency in assaying gene	
CC	expression. The system has the following advantages over existing	
CC	methods: (a) prior sequence information or clone library construction is	
CC	not needed to enable the assay; (b) provides immediate sequence	
CC	information in addition to information concerning changes or differences	
CC	in mRNA level; (c) determines cDNA expression level and mRNA identification	
CC	in one assay; (d) generates cDNA fragments from all mRNAs present in the	
CC	sample for subsequent investigation by common molecular biology	
CC	techniques; and (e) does not require prior knowledge of the sequence of	
CC	the genome of the organism under investigation and can be employed in	
CC	organisms lacking significant genomic sequence information. The present	
CC	sequence represents an oligo dT primer used in the method of the	
CC	invention	
SO	Sequence 24 BP; 3 A; 1 C; 0 G; 20 T; 0 U; 0 Other;	
Query Match	0.3%; Score 20; DB 1; Length 24;	
Best Local Similarity	100.0%; Pred.No. 3.6e+02;	
Matches 20; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
Gy	4464 TTTTTTTTTTTTTTTTTTTTTT 4483 DB 1 TTTTTTTTTTTTTTTTTTTT 20	
RESULT 442		
AAG67205		
ID . AAG67205 standard; DNA; 29 BP.		
XX		

AC	AA067205;
XX	
DT	25-MAR-2003 (revised)
DT	13-MAR-1995 (first entry)
XX	
DE	3'-primer to PCR amplify canine growth hormone cDNA.
XX	
KW	Canine growth hormone; dGH; dog; pituitary gland; PCR;
KW	polymenase chain reaction amplification; infertility; treatment;
KW	renal insufficiency; osteoporosis; ss.
XX	
OS	Synthetic.
XX	
PN	DE3303744-A1.
XX	
PD	11-AUG-1994.
XX	
PE	09-FEB-1993; 93DE-04303744.
XX	
PR	09-FEB-1993; 93DE-04303744.
XX	
PA	(UYNNU-) UNIV NUEVO LEON AUTONOMA.
XX	
PI	Barrera-Saldana HA;
DR	WPI; 1994-250161/31.
XX	
PT	Canine growth hormone and related DNA, vectors and transformed cells -
PT	for treating infertility, renal insufficiency, etc., also improving
PT	growth, feed conversion etc., in animals.
XX	
PS	Claim 9; Page 9; 16pp; German.
XX	
CC	To amplify cDNA coding for canine growth hormone, the 5'-primer AA067203
CC	and the 3'-primer AA067204 or AA067205 are preferred. Total mRNA is
CC	extracted from the pituitary gland of a dog, converted to single-strand
CC	cDNA and the primers, which are specific for highly conserved regions of
CC	known growth hormones, are hybridised to it. The amplified sequence was
CC	isolated and sequenced (see AA067206). There is one amino acid difference
CC	between the signal sequences of canine and porcine GH but the mature
CC	polypeptides have identical sequences. The dGH can be used in veterinary
CC	medicine, esp. for dogs and pigs, to stimulate growth, improve food
CC	conversion, reduce fat content of meat and stimulate milk production. The
CC	growth hormone is also useful for treating infertility, osteoporosis,
CC	adiposity and defects of growth hormone. (Updated on 25-MAR-2003 to
CC	correct PN field.)
XX	
XX	Sequence 29 BP; 4 A; 3 C; 3 G; 19 T; 0 U; 0 Other;
XX	
SO	
XX	
Query Match	0.3%; Score 20; DB 1; Length 29;
Best Local Similarity	82.1%; Pred. No. 4.7e+02;
Matches	23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX	
Dy	4456 GCATGACCTTTTTTTTTTTTTTTTTT 4483
DB	2 GCATGCAAGCTTTTTTTTTTTTTTTT 29
XX	
RESULT 443	
AA0674918/C	
ID	AA0674918 standard; DNA; 29 BP.
XX	
AC	AA0674918;
XX	
DT	23-MAY-2001 (first entry)
XX	
DE	CD40L poly-A tract sequence SEQ ID NO:15.
XX	
KW	Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW	diagnosis; antiarthritis; antirheumatic; immunosuppressive;
KW	antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX	
OS	Homo sapiens.

XX	(ROBB/) ROBBINS D.
PA	(LING/) LIN-GOERKE J L.
PA	(LING/) LING J C.
PI	Robbins D, Lin-Goerke JL, Ling JC;
DR	WPI; 2002-105577/14.
PT	New variants of the human MLH1 and MSH2 genes for diagnosing or determining a predisposition for hereditary non-polyposis colorectal cancer.
PS	Disclosure; Page 4; 38pp; English.
XX	The present invention describes a variant human MLH1 or MSH2 gene. Also
CC	described are: (1) a method for diagnosing or predicting susceptibility
CC	to hereditary non-polyposis colorectal cancer (HNPC), comprising
CC	screening a DNA sample for the variant MLH1 or MSH2 gene where presence
CC	of the variant indicates presence of, or susceptibility to HNPC; (2) a
CC	method of identifying mutants in splice donor or acceptor sites of a
CC	human MLH1 gene, comprising sequencing splice donor or acceptor sites of
CC	the gene with intronic primers for the human MLH1 gene and analysing the
CC	sequence to identify any mutants; (3) a method of identifying mutants in
CC	splice donor or acceptor sites of a human MSH2 gene, comprising
CC	sequencing splice donor or acceptor sites of the gene with intronic
CC	primers for the human MSH2 gene and analysing the sequence to identify
CC	any mutants; and (4) a transgenic model system for colorectal cancer
CC	comprising cells expressing the variant MLH1 or MSH2 gene. The hMLH1 and
CC	hMSH2 variants are used to diagnose or determine a patients
CC	susceptibility to hereditary non-polyposis colorectal cancer. ABL01648 to
CC	ABL01745 and ABL01746 to ABL01831 represent hMLH1 and hMSH2 gene
CC	fragments from the present invention. ABL01832 to ABL01839 represent
CC	mutagenic primers used in the exemplification of the present invention
SQ	Sequence 23 BP; 21 A; 0 C; 1 G; 1 T; 0 U; 0 Other;
OY	Query Match 0.3%; Score 20; DB 1; Length 23; Best Local Similarity 100.0%; Pred.No. 3.4e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
DG	4464 TTTT TTTTTTTTTTTTTTTTTT 4483 Dg 23 TTTT TTTTTTTTTTTTTTTT 4
RESULT 337	
AAZ00877	standard; DNA; 24 BP.
AAZ00877;	
DT	27-SEP-1999 (first entry)
PCR primer PGRT32 for PGI coding sequence.	
PGI gene; biallelic marker; PCR primer; PGI-related biallelic marker;	
cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;	
PSA; human; ss.	
Synthetic.	
Homo sapiens.	
WO932644-A2.	
01-JUL-1999.	
98WO-IB002133.	
97US-00996306.	
98US-0099658E.	
GENSET) GENSET.	

```

XX Cohen D, Blumenfeld M, Chumakov I, Bougueleret L;
XX 373
XX MPI; 1999-405178/34.
DR
XX
XX Use of a prostate cancer associated gene and biallelic markers derived
XX from it.
XX
XX Example 6; Page 42, 385pp; English.
XX
XX The invention relates to a mammalian PGI gene and protein, and a set of
XX PGI biallelic markers. The PGI polymucleotide and biallelic markers are
XX used in a hybridisation assay, a sequencing assay, or in an allele-
XX specific amplification assay for determining the identity of a nucleotide
XX at a PGI-related biallelic marker. The methods can be used to detect and
XX to assess the risk of developing cancer or prostate cancer. Early-stage
XX diagnosis of prostate cancer relies on prostate specific antigen (PSA)
XX dosage. However, the effectiveness of this is limited due to its
XX inability to discriminate between malignant and non-malignant affections
XX of the organ. A need exists for both a reliable diagnostic procedure
XX which would enable early-stage diagnosis, and for preventative and
XX curative treatments of the disease. The PGI gene can be used for
XX detection of prostate cancer, and the risk of developing it in the
XX future, and can also be used to determine therapies for the disease
XX
XX Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.3%; Score 20; DB 1; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4465 TTTTTTTTTTTTTTTTTTTG 4484
XX |||||
XX 1 TTTTTTTTTTTTTTTTTTGG 20
XX
XX RESULT 438
XX AA16361
XX ID AA16361 standard; DNA; 24 BP.
XX
XX AA16361;
XX AC
XX AT
XX 23-JAN-2002 (first entry)
XX
XX Human phosphatidylinositol-3 kinase 35 cDNA PCR primer #2.
XX
XX DE
XX
XX Human; phosphatidylinositol-3 kinase 35; PTDINS3 kinase 35; cancer;
XX haemopathy; development disorder; HIV infection; immunological disease;
XX inflammation; gene therapy; PCR primer; ss.
XX
XX
XX Homo sapiens.
XX
XX OS
XX
XX WO200175014-A2.
XX
XX PN
XX
XX 11-OCT-2001.
XX
XX PD
XX
XX 16-MAR-2001; 2001WO-CN000328.
XX
XX PF
XX
XX 17-MAR-2000; 2000CN-00114973.
XX
XX PR
XX
XX (BIOW- ) BIOWINDOW GENE DEV INC SHANGHAI.
XX
XX PA
XX
XX Mao Y, Xie Y;
XX
XX PI
XX
XX WPI; 2002-025836/03.
XX
XX DR
XX
XX New human phosphatidylinositol-3 (PTDINS3) kinase 35 for diagnosis and
XX treating malignant tumor, hemopathy, human immunodeficiency virus
XX infection, immunological diseases and various inflammations.
XX
XX PT
XX
XX Example 2; Page 12; 34pp; Chinese.
XX
XX PS
XX
XX The present invention provides the protein and coding sequences of human
XX

```

Seq	Sequence	21 BP	0 A	0 C	0 G	21 T	0 U	0 Other
SC	Query Match	0.3%	Score 20	DB 1	Length 21			
	Best Local Similarity	100.0%	Pred. No. 2.9e+02					
	Matches 20	Conservative 0	Mismatches 0	Indels 0	Gaps 0			
OY	4464	TTTTTTTTTTTTTTTTTTTTTT	4483					
DB	1	TTTTTTTTTTTTTTTTTTTTTT	20					
	RESULT 434							
	ACH03246							
ID	ACH03246	standard; DNA; 21 BP.						
XX	ACH03246							
XX	25-SEP-2003	(first entry)						
DE	Immunostimulatory nucleic acid #881.							
XX	Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;							
KW	antuleter; gene therapy; vaccine; non-allergic inflammatory disease;							
KW	psoriasis; eczema; allergic contact dermatitis; latex dermatitis;							
KW	inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.							
XX	Synthetic.							
OS	US2003050268-A1.							
XX	13-MAR-2003.							
PD	29-MAR-2002; 2002US-00112653.							
XX	29-MAR-2001; 2001US-0279642P.							
PR	(KRIE/) KRIEG A M.							
PA	(BERG/) BERG D J.							
XX	Krieg AM, Berg DJ;							
PI	WPI; 2003-521815/49.							
XX	Treating non-allergic inflammatory diseases, such as psoriasis, eczema,							
XX	allergic contact dermatitis, latex dermatitis or inflammatory bowel							
PT	disease by administering an immunostimulatory nucleic acid.							
PS	Disclosure; Page 33; 229pp; English.							
CC	The invention describes a method of treating non-allergic inflammatory							
CC	disease comprising administering to a subject having or at risk of							
CC	developing a non-allergic inflammatory disease an immunostimulatory							
CC	nucleic acid for prevention or treatment of the disease. The method is							
CC	useful for treating non-allergic inflammatory diseases, such as							
CC	psoriasis, eczema, allergic contact dermatitis, latex dermatitis or							
CC	inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.							
CC	This sequence represents an immunostimulatory nucleic acid							
XX	Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;							
SQ	Query Match	0.3%	Score 20	DB 1	Length 21			
	Best Local Similarity	100.0%	Pred. No. 2.9e+02					
	Matches 20	Conservative 0	Mismatches 0	Indels 0	Gaps 0			
OY	4464	TTTTTTTTTTTTTTTTTTTTTT	4483					
DB	1	TTTTTTTTTTTTTTTTTTTTTT	20					
	RESULT 435							
	ADB37209							
ID	ADB37209	standard; DNA; 21 BP.						

XX	AD537209;
AC	
XX	04-DEC-2003 (first entry)
DT	
XX	
XX	Immunostimulatory nucleic acid #823.
DE	
XX	ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW	hypo-responsive subject; immunostimulatory.
KW	
XX	Synthetic.
OS	
XX	US2003087848-A1.
PN	
XX	08-MAY-2003.
PD	
XX	
XX	02-FEB-2001; 2001US-00776479.
PF	
XX	03-FEB-2000; 2000US-0179991P.
PR	
XX	(BRAT/) BRATZLER R L.
XX	(PETE/) PETERSEN D M.
PA	(FOUR/) FOURON Y.
PA	
XX	
XX	Bratzler RL, Petersen DM, Fouron Y;
PI	
XX	WPI; 2003-657977/62.
DR	
XX	Treating and/or preventing allergy or asthma using an immunostimulatory
XX	nucleic acid alone or in combination with an asthma/allergy medicament.
PT	
XX	
XX	Disclosure; Page 17; 221pp; English.
PS	
XX	
XX	The invention relates to a method of treating or preventing allergy or
CC	asthma which comprises administering to a subject a poly-G nucleic acid
CC	in an aerosol formulation. The methods and compositions of the present
CC	invention are useful for diagnosing and/or treating asthma and allergy
CC	especially in a hypo-responsive subject. The present sequence represents
CC	an immunostimulatory nucleic acid of the invention.
CC	
XX	
XX	Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
SQ	
XX	
XX	Query Match 0.3%; Score 20; DB 1; Length 21;
XX	Best Local Similarity 100.0%; Pred. No. 2.9e+02;
XX	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps
XX	
Oy	4464 TTTTTTTTTTTTTTTTTT 4483
XX	
DB	1 TTTTTTTTTTTTTTTTTT 20
XX	
XX	RESULT 436
XX	ABL01773/c
ID	ABL01773 standard; DNA; 23 BP.
ID	
AC	ABL01773;
XX	
XX	18-MAR-2002 (first entry)
DT	
XX	
XX	Human MSH2 (hMSH2) intronic sequence SEQ ID NO:126.
DE	
XX	Human; MLH1; MSH2; hMLH1; hMSH2; variant gene; diagnosis; HNPCC;
KW	hereditary non-polyposis colorectal cancer; ds.
KW	
XX	Homo sapiens.
OS	
XX	US2001044936-A1.
PN	
XX	22-NOV-2001.
PD	
XX	22-OCT-1999; 99US-00426548.
PF	
XX	22-OCT-1998; 98US-0105180P.
XX	
XX	

CC	included is a kit comprising a first container housing the antiangiogenic
CC	nucleic acids; and instructions for administering them to a subject
CC	having a condition characterised by unwanted angiogenesis. The method is
CC	useful for inhibiting angiogenesis associated with solid tumour growth.
CC	tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC	diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC	corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC	rubeosis, Osler-Weber Syndrome, myocardial angiogenesis, plaque
CC	neovasculatisation, telangiectasia, haemophilic joints, angiodroma,
CC	wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC	hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC	acid of the invention
SQ	Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
XX	
Query Match	0.3%; Score 20; DB 1; Length 21;
Best Local Similarity	100.0%; Pred. No. 2.9e+02;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Cy	4464 TTTT TTTTTTTTTTTTTTTTTT 4483 1 TTTT TTTTTTTTTTTTTTTTTT 20
Db	
RESULT 432	
ABL39404	
ID	ABL39404 standard; DNA; 21 BP.
XX	
AC	ABL39404;
XX	
DT	16-APR-2002 (first entry)
DE	
XX	Immunostimulatory nucleic acid SEQ ID NO: 840.
KM	Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KX	angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	modified_base 1..21
FT	/*tag= a
FT	/mod_base= OTHER
PT	/note= "phosphorothioate backbone"
PV	
XX	WO200197843-A2.
XX	
PD	27-DEC-2001.
PF	
XX	22-JUN-2001; 2001WO-US020154.
XX	
PR	22-JUN-2000; 2000US-0213346P.
XX	
PA	(IOWA) UNIV IOWA RES FOUND.
PI	
XX	Weiner G, Hartmann G;
DR	WPI, 2002-154611/20.
XX	
PT	Treating or preventing cancer, such as basal cell carcinoma, comprises
PT	administering immunostimulatory nucleic acids that induce expression of
PT	cell surface antigens and antibodies to a subject having or at risk of
PT	developing cancer.
XX	
PS	Disclosure: Page 309, 312pp; English.
XX	
CC	The present invention relates to methods for treating or preventing
CC	cancer, involving administering to a subject having or at risk of
CC	developing cancer immunostimulatory nucleic acids that induce expression
CC	of cell surface antigens and antibodies. The methods are useful for
CC	treating or preventing cancer such as basal cell carcinoma, bladder
CC	cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC	breast cancer, cervical cancer, colon and rectum cancer, connective

CC tissue cancer, cesophagseal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention

XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

XX Query March 0.3%; Score 20; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Oy 4464 TTTTTTTTTTTTTTTTTTTT 4483
|||
|||
Db 1 TTTTTTTTTTTTTTTTTTTT 20

RESULT 433
ID AAD51323
AC AAD51323 standard; DNA; 21 BP.
XX AAD51323;
XX DT 16-APR-2003 (first entry)
XX DE Regular oligo dt primer used to illustrate the method of the invention.
XX
XX Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis;
XX gastritis; gastric ulcer; respiratory ailment; fracture; joint disease;
XX musculoskeletal damage; ss.
XX
XX Unidentified.
XX
XX WO200290579-A1.
XX
XX 14-NOV-2002.
XX
XX 03-MAY-2002; 2002MO-AU000553.
XX
XX 04-MAY-2001; 2001AU-00004809.
XX PR 29-JUN-2001; 2001US-00896941.
XX
XX (GENO-) GENOMICS RES PARTNERS PTY LTD.
XX
XX Brandon RB;
XX
XX WPI; 2003-120558/11.
XX
XX
XX Assessing condition e.g. athletic ability, stage of disease, presence of
XX drugs, response to exercise, response to vaccines, therapies, nutritional
XX states, of performance animal involves analyzing nucleic acid expression.
XX
XX Disclosure; Page 46; 87bp; English.
XX
XX
XX The invention relates to a method for assessing a condition of a
XX performance animal. The method involves determining in sample abundance
XX of expressed target nucleic acid; transmitting digital sample signal to
XX remote diagnostic server; processing digital sample signal at remotely
XX located database to correlate digital signal with digital information and
XX returning report of particular condition of animal. The method is useful
XX for assessing a condition of a performance animal preferably human, dog
XX or camel. The condition can be an athletic ability and a condition that
XX enhances, hinders, impedes or does not change an expected ability of the
XX performance animal; and also normal, pre-clinical, overt progress and/or
XX stage of disease, undiagnosed of unclassified conditions, presence of
XX drugs, response to exercise, response to vaccines, therapies, nutritional
XX states, and response to environmental conditions. Diseases assessed by the
XX invention include laminitis, lameness, viral or bacterial disease,
XX gastritis, gastric ulcers, respiratory ailments, fractures, epistaxis,
XX musculoskeletal damage or disorders and joint diseases. The present
XX sequence is a primer used to illustrate the method of the invention

XX	Krieg AM, Schetter C, Vollmer J;
PI	WPI; 2001-273485/28.
XX	Vaccinating against tumors, infectious diseases, allergies and asthma
PT	using immunostimulatory Py-rich and TG nucleic acids.
XX	Claim 101; Page 56; 338pp; English.
PS	
CC	The present invention relates to a method for stimulating an immune
CC	response. The method comprises administering an immunostimulatory nucleic
CC	acid to a non-rodent subject in sufficient quantity to stimulate an
CC	immune response. The present sequence is one such immunostimulatory
CC	nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC	(py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC	against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC	and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC	haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC	staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC	also useful for preventing cancer, asthma, infectious disease, allergy or
CC	immune deficiency. The present sequence can also be used to redirect a
CC	T _H 2 to a T _H 1 immune response and to activate immune cells. Note: the
CC	present sequence may have a phosphorothioate backbone
SO	
Sequence	21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
Query Match	0.3%; Score 20; DB 1; Length 21;
Best Local Similarity	100.0%; Pred. No. 2.9e+02;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	4464 TTTTTTTTTTTTTTTTTTTT 4483 1 TTTTTTTTTTTTTTTTTTTT 20
Db	
RESULT 430	
ID	AAH42480 standard; DNA; 21 BP.
AC	AAH42480;
XX	
DT	01-OCT-2001 (first entry)
XX	
DE	Oligonucleotide used to produce branched chain compounds.
XX	
Branched chain compound; nucleic acid synthesis; primer extension;	
KW	reverse transcription; nucleic acid hybridization;
KW	nucleic acid amplification; ss.
OS	Synthetic.
XX	
FH	Key
FT	modified_base
FT	1
FT	/tag= a
FT	/note= "NH2-C6 attached"
FT	4
FT	modified_base
FT	/tag= b
FT	/note= "NH2-C6 attached"
FT	6..7
FT	misc_feature
FT	/tag= c
FT	/note= "branch present"
XX	
EP1111068-A1.	
PN	
PD	27-JUN-2001.
PF	
21-DEC-1999;	99BP-00125484.
BR	
21-DEC-1999;	99BP-00125484.
XX	
(LION-) LION BIOSCIENCE AG.	
(VBCG-) VBC GENOMICS GMBH.	

XX	Schmidt W, Hiller R, Huber M, Mueller M;
PI	WPI; 2001-466959/51.
XX	
DR	Branched compounds useful in e.g. nucleic acid synthesis reaction
XX	comprises nucleic acid moieties optionally extended by a polymerase.
PT	
XX	Example 1; Page 10; 31pp; English.
PS	
XX	
CC	The specification describes branched compounds containing nucleic acid
CC	moieties optionally extended by a polymerase. The branched chain
CC	compounds of the invention are used in nucleic acid synthesis reaction,
CC	primer extension reaction, reverse transcription reaction of RNA into
CC	DNA, nucleic acid hybridization experiment (for identifying sequence of a
CC	nucleic acid), and nucleic acid amplification experiment (for analysing
CC	the expression pattern of genes). The compounds are also used in solid-
CC	phase enzymatic reactions. The present sequence was used in the course of
CC	the invention to produce branched chain compounds
XX	
SQ	Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
XX	
Query Match	0.3%; Score 20; DB 1; Length 21;
Best Local Similarity	100.0%; Pred. No. 2.9e+02;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	4464 TTTTTTTTTTTTTTTTTTTT 4483
Db	1 TTTTTTTTTTTTTTTTTTTT 20
XX	
RESULT 431	
AB578428	
ID	AB578428 standard; DNA; 21 BP.
XX	
AC	AB578428;
XX	
DT	13-DEC-2002 (first entry)
XX	
DE	Angiogenesis inhibitory oligonucleotide #912.
XX	
KW	Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW	tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW	diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW	corneal rejection; neovascular glaucoma; retrolental fibroplasia;
KW	rubeosis; Osler-Weber Syndrome; myocardial angiogenesis;
KW	plaque neovascularisation; telangiectasia; haemophilic joint;
KW	angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW	scleroderma; hypertrophic scar.
XX	
OS	Synthetic.
XX	
PN	WO200253141-A2.
XX	
DD	11-JUL-2002.
XX	
XX	14-DEC-2001; 2001WO-US048458.
PF	
XX	14-DEC-2000; 2000US-0255534P.
PR	
PA	(COLE-) COLEY PHARM GROUP INC.
XX	
PI	Bratzler RL;
XX	
DR	WPI; 2002-566690/60.
XX	
PT	Inhibiting angiogenesis in a subject, involves administering at least one
XX	antiangiogenic nucleic acid molecule to the subject.
XX	
XX	Claim 2; Page 35; 276p; English.
XX	
CC	The invention relates to inhibiting angiogenesis in a subject, comprising
CC	administering at least one antiangiogenic nucleic acid molecule. Also

CC permeable to a molecule capable of insulating or binding to the
CC electrode. The attachment layer is capable of attaching a macromolecule.
CC The ED is used for genetic typing and comprises a number of
CC electronically addressable locations each comprising an electrode, and a
CC binding entity, such as one of these probes, attached to each of the
CC locations capable of detecting the presence of a genetic sequence
SQ Sequence 21 BP, 20 A, 0 C, 0 G, 0 T, 1 U, 0 Other;

Query Match	0.3%	Score	20;	DB	1;	Length	21;
Best Local Similarity	100.0%	Pred. No.	2.9e+02;				
Matches	20;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;

Qy	4464	TTTTTTTTTTTTTTTTTTTTTTTTTTT	4483
Dd	20	TTTTTTTTTTTTTTTTTTTTTTTTTTT	1

RESULT 425
AAV35395/c
ID AAV35395 standard; DNA; 21 BP

AC	AAV35395;
XX	
DT	13-OCT-1998 (first entry)
xx	

HIV-1 gag protein DNA primer #8.

KM Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;
 KM vaccines; infection; protection; primer; ss.

OS Synthetic.

PN WO9822596-A1

PD 28-MAY-1998.

PF 19-NOV-1997; 97WO-JP004216.

PR 19-NOV-1996; 96JP-00323412.

PA (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.

XX	:	3
	:	3
	:	0
	:	1
	:	2
	:	3
	:	0
	:	2
	:	0
	:	3

XX
E1 KOJ IIND A, NUTALD I, IASUUA A,
XX

XX
DN
WFI; 1998-312401/2/.

P1 recombinant vaccinia virus containing HIV gag gene - production in host cells of gag protein for use as vaccine

Example 1: Page 66: TTTTTTTT

CC ANV355188-V35414 are primers used in a method which results in a
CC recombinant vaccinia virus comprising of a gag gene from a retrovirus
CC such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope
CC region (30-300 bases in length) of a retroviral gene other than the gag
CC gene. The gag gene may be altered so as to produce a gag protein modified
CC from the natural sequence by the addition, deletion or substitution of a
CC least 1 amino acid residue. The fusion gene is inserted into a region of
CC a vaccinia virus not essential to its propagation, to give a recombinant
CC vaccinia virus vector which is used to transform a host cell (such as
CC HeLa, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon
CC culturing the host cell produces particulate structures containing the
CC fusion gag protein. The recombinant vaccinia virus or the fusion gag
CC protein particles may be used in the production of vaccines for
CC protecting against infection with retroviruses such as HIV

SQ Sequence 21 BP; 19 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	4465	TTTTTTTTTTTTTTTTTTG	4484
Db	21	TTTTTTTTTTTTTTTTTTG	2

```

RESULT 426
AAx81302/c
ID    AAx81302 standard; DNA; 21 BP.

```

AC AAX81302;

DT 20-AUG-1999 (first entry)

DE 3' ribonucleoside oligonucleotide probe CP-1.

KM Microelectronic device; multi-step reaction; microscopic format;
KM ion-permeable permeation layer; electrode; electrical control; transport
KM attachment; binding; DNA/RNA hybrid; probe; ss.

OS Synthetic.

FH	Key	Location/Qualifiers

FT / *tag= a

PN WO9929711-A1

17-JUN-1999

01-DEC-1998: 98WO-US025475-

XX 05-DEC-1997. 97TIS-009A6065
PB

XX
PA (NANO-) NANOCEN INC

XX
XX
PC
Butler
F. E.
Neighborhood
MT
Holt
MT
Elliott
CE

XX 1000 205557/22

XX

PT and multiplex molecular biological reactions in microscopic format.

PS Example 1; Page 89; 179pp; English.

The specification describes a self-addressable, self-assembling microelectronic device which is designed to actively carry out and control multi-step and multiplex molecular biological reactions in microscopic formats. A key aspect of this invention is played by the ion-permeable permeation layer which overlies the electrode. This permeation layer allows attachment of nucleic acids to permit immobilization but also separates the attached oligonucleotides and hybridized target DNA sequences from the highly reactive electrochemical environment generated immediately at the electrode surface. The microelectronic device is designed and fabricated to actively carry out and control reactions such as nucleic acid hybridizations, antibody/antigen reactions, sample preparation, diagnostics and biopolymer synthesis. The device can electronically control the transport and attachment of specific binding entities, such as nucleic acids and polypeptides, to specific micro-locations. The device can subsequently control the transport and reaction of analytes or reactants at the addressed specific micro-locations. The device is able to concentrate analytes and reactants, remove non-specifically bound molecules, provide stringency control for DNA hybridization reactions and improve the detection of analytes. The present sequence represents a probe used to exemplify the invention

SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

Query March	0.3%	Score 20;	DB 1;	Length 21;
Best Local Similarity	100.0%;	Pred. No. 2,	9e+02;	
Matches 20;	Conservative 0;	Mismatches 0;	Gaps 0;	
OY	4464	TTTTTTTTTTTTTTTTTTT	4483	

```

XX      JP0630397-A.
XX
XX      01-NOV-1994.
XX
XX      16-APR-1993;      93JP-00112515.
XX
XX      16-APR-1993;      93JP-00112515.
XX
XX      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX      WPI; 1995-018287/03.
XX
XX      Analysis of cDNA and gene expression - by amplification of mRNA followed
XX      by digestion with restriction enzymes.
XX
XX      Disclosure; Page 6; 11pp; Japanese.
XX
XX      A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX      labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
XX      and using the aggregate of mRNAs as the template for each reverse
XX      transcription primer; (b) digesting each of the prepared aggregates of
XX      the double-stranded cDNAs with restriction enzyme and; (c)
XX      electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX      method can be used to analyse gene expression rapidly and easily
XX
XX      Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
XX
XX      Query Match      0.3%; Score 20; DB 1; Length 21;
XX      Best Local Similarity 100.0%; Pred. No. 2.9e+02;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      Oy      4467 TTTT TTTT TTTT TTTT TTTT GTC 4486
XX      Db      1 TTTT TTTT TTTT TTTT TTTT GTC 20
XX
XX      RESULT 423
XX      ID      AAQ90391/c
XX      AAQ90391 standard; DNA; 21 BP.
XX
XX      AC      AAQ90391;
XX      DT      08-JAN-1996 (first entry)
XX
XX      CP-1 (synthetic DNA probe with 3'ribonucleoside terminal #2).
XX
XX      CP-1; HLA; dQa; 3' ribonucleoside; self-addressable electronic device;
XX      SAEb; hybridisation; ss.
XX
XX      OS      Synthetic.
XX
XX      FH      Key      Location/Qualifiers
XX      FT      misc_feature      21
XX      FT      /*tag=      a
XX      FT      /note= "3' ribonucleoside terminal"
XX
XX      PN      WO9512808-A1.
XX
XX      PD      11-MAY-1995.
XX
XX      PF      26-OCT-1994;      94MO-US012270.
XX
XX      PR      01-NOV-1993;      93US-00146504.
XX
XX      PA      (MANO-) NANOGEN INC.
XX
XX      PI      Heller MJ, Tu E;
XX
XX      DR      WPI; 1995-185870/24.
XX
XX      New self-addressable electronic devices - used for multi-step and

```

PT	multiplex reactions such as DNA hybridisation(s), clinical diagnostics									
PT	and bio-polymer synthesis.									
XX	Example 1; Page 40; 86pp; English.									
XX	The sequences represented by, AAQ90390-90401 are synthetic DNA probes									
CC	containing 3' ribonucleoside termini. The sequences shown in AAQ90402-15									
CC	are synthetic DNA probes with 5' amino termini. These sequences were									
CC	specific for the polymorphisms of HLA gene dqa. The sequences were used									
CC	in the device of the invention. This is a self-addressable electronic									
CC	device (SMEED) that can be used to carry out multi-step and multiplex									
CC	reactions, such as nucleic acid hybridisations. The advantages of this									
CC	method are that these reactions can be carried out with complete and									
CC	precise electronic control, and that the rate, specificity and									
CC	sensitivity of these reactions are greatly improved at micro-locations									
XX	SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;									
QY	4464	TTTTTTTTTTTTTTTTTT	4483							
Db	20	TTTTTTTTTTTTTTTTTT	1							
RESULT 424										
ID	AA110743/C									
XX	AA110743	standard; RNA; 21 BP.								
AC	AA110743;									
XX	09-SEP-1996	(first entry)								
DT	XX									
DE	XX	Oligonucleotide probe, CP-1.								
XX	XX									
KW	XX	Electronically self-addressable device; ED; electrode; current source;								
KW	XX	attachment layer; permeable; counterion; genetic typing; probe;								
KW	XX	detection; ss.								
OS	XX	Synthetic.								
XX	XX									
FH	XX	Key	Location/Qualifiers							
FT	XX	modified_base	21							
FT	XX	/*tag= a								
FT	XX	/note= "3'-ribonucleoside terminus"								
XX	XX									
XX	XX	WO9601836-A1.								
XX	XX	25-JAN-1996.								
XX	XX	05-JUL-1995;	95WO-US008570.							
XX	XX	07-JUL-1994;	94US-00271882.							
XX	XX									
PA	XX	(NANO-) NANOCEN INC.								
PI	XX									
PI	XX	Heller MJ, Tu E, Evans GA, Sosnowski RG;								
XX	XX									
DR	XX	WPI; 1996-097582/10.								
PT	XX	Electronically self-addressable device - used for electronic control of,								
PT	XX	e.g. nucleic acid hybridisation.								
XX	XX									
PS	XX	Example 1; Page 60; 155pp; English.								
CC	XX	The sequences given in AA110742-67 are synthetic oligonucleotides which								
CC	XX	are used in the construction of the electronically self-addressable								
CC	XX	device (ED) of the invention. The ED comprises a substrate, an electrode								
CC	XX	or opt. a number of electrodes supported by the substrate, a current								
CC	XX	source operatively connected to the electrode and an attachment layer								
CC	XX	adjacent to the electrode which is permeable to a counterion but not								

DR WPI; 1991-310529/42.
 XX
 PT New oligo:nucleotide- transport agent di:ulphide conjugate(s) - for
 PT inhibiting nucleotide expression in therapy and diagnosis of endogenous
 PT nucleotide sequences in cells.
 XX
 XX Example; Page 37; 67pp; English.
 XX
 CC The oligonucleotide has a disulphide linker incorporated into the probe
 CC which acts as a hybridisation-triggered crosslinking agent. This will
 CC permit novel diagnostic assay modifications such as the use of
 CC crosslinker to increase probe discrimination and incorporation of a
 CC denaturing wash step to reduce background. Also carrying out
 CC hybridisation and crosslinking at or near the melting temperature of the
 CC hybrid DNA will reduce secondary structure in the target DNA and increase
 CC probe specificity. See also AAQ14195
 XX
 SQ Sequence 21 BP; 6 A; 7 C; 7 G; 0 T; 0 U; 1 Other;
 XX
 Query Match 0.3%; Score 20; DB 1; Length 21;
 Best Local Similarity 95.2%; Pred. No. 2.9e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7413 CAGCAGCAGCAGCAGCAGCAG 7433
 DB 1 CAGCAGCAGCAGCAGCAGCAG 21
 XX
 RESULT 420
 AAQ75651
 ID AAQ75651 standard; DNA; 21 BP.
 XX
 AC AAQ75651;
 XX
 DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 6; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
 XX
 Query Match 0.3%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4467 TTTT
 DB 1 TTTT

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4467 TTTT
 DB 1 TTTT
 XX
 RESULT 421
 AAQ75652
 ID AAQ75652 standard; DNA; 21 BP.
 XX
 AC AAQ75652;
 XX
 DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 6; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
 XX
 Query Match 0.3%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4467 TTTT
 DB 1 TTTT
 XX
 RESULT 422
 AAQ75654
 ID AAQ75654 standard; DNA; 21 BP.
 XX
 AC AAQ75654;
 XX
 DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.

```

PI      Ward DT, Matt AT;
XX
XX      WPI; 2003-449448/42.
DR
XX      New compound, having a sequence targeted to a nucleic acid encoding human
PT      collapsin response mediator protein 2, useful for preparing a composition
PT      for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX      cancer.
XX
XX      Claim 3; Page 76; 120pp; English.
PS
XX      This invention relates to novel antisense oligonucleotides that modulate
CC      the expression of human eukaryotic translation initiation factor 2C 1
CC      (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC      Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC      intracellular membrane associated protein thought to be involved in
CC      cellular differentiation, such that altered expression of EIF2C1 can
CC      affect cell growth, morphology and tumorigenicity. Accordingly,
CC      antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC      or tissues can be used in gene therapy to treat various conditions
CC      including hyperproliferative disorders, familial hypercholesterolaemia
CC      and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC      progeroid syndrome. As such, the oligos of the present invention can be
CC      described as having cytostatic and antiproliferative activities. This
CC      oligonucleotide sequence is an antisense oligo used to inhibit expression
CC      of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC      of the invention.
XX
SQ      Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
XX
Query Match      0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2891 GAGGAGTGTAGGATGCTTG 2910
DB      20 GAGGAGTGTAGGATGCTTG 1
XX
RESULT 418
ADB81530/C
ID      ADB81530 standard; DNA; 20 BP.
XX
AC      ADB81530;
XX
DT      04-DEC-2003 (first entry)
XX
DB      Antisense oligo. (SeqID 47) used to inhibit human EIF2C1 DNA.
XX
KM      antisense; ss; human; eukaryotic translation initiation factor 2C 1;
KM      EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP95; Q99;
KW      gene therapy; hyperproliferative disorder;
KW      familial hypercholesterolaemia; cancer; polycystic kidney disease;
KW      cystic fibrosis; progeroid syndrome; cytostatic; antiproliferative.
XX
OS      Homo sapiens.
XX
XX      Key      Location/Qualifiers
FH      modified_base      1..20
FT      /tag= a
FT      /mod_base= OTHER
FT      /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT      16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT      5-methylcytidines"
XX
XX      WO2003040321-A2.
XX
XX      15-MAY-2003.
XX
XX      04-NOV-2002; 2002WO-US035324.
XX
XX      08-NOV-2001; 2001US-0007078.
XX

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```

PA      (ISIS-) ISIS PHARM INC.
XX
XX      Ward DT, Matt AT;
XX
XX      WPI; 2003-449448/42.
DR
XX      New compound, having a sequence targeted to a nucleic acid encoding human
PT      collapsin response mediator protein 2, useful for preparing a composition
PT      for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX      cancer.
XX
XX      Claim 3; Page 76; 120pp; English.
PS
XX      This invention relates to novel antisense oligonucleotides that modulate
CC      the expression of human eukaryotic translation initiation factor 2C 1
CC      (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC      Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC      intracellular membrane associated protein thought to be involved in
CC      cellular differentiation, such that altered expression of EIF2C1 can
CC      affect cell growth, morphology and tumorigenicity. Accordingly,
CC      antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC      or tissues can be used in gene therapy to treat various conditions
CC      including hyperproliferative disorders, familial hypercholesterolaemia
CC      and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC      progeroid syndrome. As such, the oligos of the present invention can be
CC      described as having cytostatic and antiproliferative activities. This
CC      oligonucleotide sequence is an antisense oligo used to inhibit expression
CC      of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC      of the invention.
XX
SQ      Sequence 20 BP; 8 A; 1 C; 9 G; 2 T; 0 U; 0 Other;
XX
Query Match      0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      3412 CCCTATTCCCTCTGTGCA 3431
DB      20 CCCTATTCTCTGTGCA 1
XX
RESULT 419
AAQ14196
ID      AAQ14196 standard; DNA; 21 BP.
XX
AC      AAQ14196;
XX
DT      02-JAN-1992 (first entry)
XX
DB      Oligonucleotide probe incorporating disulphide linker.
XX
KM      ss.
KW      Synthetic.
OS
XX
XX      Key      Location/Qualifiers
FH      misc_feature      8
FT      /tag= a
FT      /note= "n = 02-P-O-CH2-CH2-O-CH2-CH2-S-S-CH2-CH2-O-
FT      CH2-O-P-O3"
XX
XX      WO9114696-A.
XX
XX      03-OCT-1991.
XX
XX      29-MAR-1990; 90US-00502361.
XX
XX      29-MAR-1990; 90US-00502361.
XX
XX      (GILE-) GILEAD SCI INC.
XX
XX      Latham JA, Lin KY, Matteucci M;
XX

```

PT New compound, having a sequence targeted to a nucleic acid encoding human
PT collapse response mediator protein 2, useful for preparing a composition
PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX cancer.
XX
PS Claim 3; Page 76; 120pp; English.
XX
CC This invention relates to novel antisense oligonucleotides that modulate
CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP5 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
CC affect cell growth, morphology and tumorigenicity. Accordingly,
CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC or tissues can be used in gene therapy to treat various conditions
CC including hyperproliferative disorders, familial hypercholesterolemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC progeroid syndrome. As such, the oligos of the present invention can be
CC described as having cytosstatic and antiproliferative activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC of the invention.
XX
SQ Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1602 GGTCCTCAGAGACTTCACAG 1621
DB 20 GGTCCTCAGAGACTTCACAG 1
XX
RESULT 416
ADB81523/c
ID ADB81523 standard; DNA; 20 BP.
XX
AC ADB81523;
XX
DT 04-DEC-2003 (first entry)
XX
DE Antisense oligo (SeqID 40) used to inhibit human EIF2C1 DNA.
XX
KW antisense; sg; human; eukaryotic translation initiation factor 2C 1;
KW EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP5; Q99;
KW gene therapy; hyperproliferative disorder;
KW familial hypercholesterolemia; cancer; polycystic kidney disease;
KW cystic fibrosis; progeroid syndrome; cytosstatic; antiproliferative.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
XX PN WO2003040321-A2.
XX
XX PD 15-MAY-2003.
XX
XX PF 04-NOV-2002; 2002WO-US035324.
XX
XX PR 08-NOV-2001; 2001US-00007078.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Ward DT, Watt AT;
XX

DR WPI; 2003-449448/42.
XX
XX New compound, having a sequence targeted to a nucleic acid encoding human
XX collapse response mediator protein 2, useful for preparing a composition
XX for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
XX cancer.
XX
PS Claim 3; Page 76; 120pp; English.
XX
CC This invention relates to novel antisense oligonucleotides that modulate
CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP5 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
CC affect cell growth, morphology and tumorigenicity. Accordingly,
CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC or tissues can be used in gene therapy to treat various conditions
CC including hyperproliferative disorders, familial hypercholesterolemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC progeroid syndrome. As such, the oligos of the present invention can be
CC described as having cytosstatic and antiproliferative activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC of the invention.
XX
SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2739 AGCGGTGACAGTTCCACAG 2758
DB 20 AGCGGTGACAGTTCCACAG 1
XX
RESULT 417
ADB81525/c
ID ADB81525 standard; DNA; 20 BP.
XX
AC ADB81525;
XX
DT 04-DEC-2003 (first entry)
XX
DE Antisense oligo (SeqID 42) used to inhibit human EIF2C1 DNA.
XX
KW antisense; sg; human; eukaryotic translation initiation factor 2C 1;
KW EIF2C1; Co-EIF2C; EIF2C; Golgi ER protein 95kDa; GERP5; Q99;
KW gene therapy; hyperproliferative disorder;
KW familial hypercholesterolemia; cancer; polycystic kidney disease;
KW cystic fibrosis; progeroid syndrome; cytosstatic; antiproliferative.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
XX PN WO2003040321-A2.
XX
XX PD 15-MAY-2003.
XX
XX PF 04-NOV-2002; 2002WO-US035324.
XX
XX PR 08-NOV-2001; 2001US-00007078.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX

XX Claim 3, Page 76; 120pp; English.

PS This invention relates to novel antisense oligonucleotides that modulate

XX the expression of human eukaryotic translation initiation factor 2C 1

CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as

CC Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an

CC intracellular membrane associated protein thought to be involved in

CC cellular differentiation, such that altered expression of EIF2C1 can

CC affect cell growth, morphology and tumorigenicity. Accordingly,

CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells

CC or tissues can be used in gene therapy to treat various conditions

CC including hyperproliferative disorders, familial hypercholesterolaemia

CC and cancer, as well as polycystic kidney disease, cystic fibrosis and

CC progeroid syndrome. As such, the oligos of the present invention can be

CC described as having cytostatic and antiproliferative activities. This

CC oligonucleotide sequence is an antisense oligo used to inhibit expression

CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA

CC of the invention.

XX

SQ Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

XX

Query Match 0.3%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5245 GTCATTGACCAAGCATTGCA 5264

DB 20 GTCATTGACCAAGCATTGCA 1

RESULT 414

ADB81560/c

ID ADB81560 standard; DNA; 20 BP.

XX

AC ADB81560;

XX

DT 04-DEC-2003 (first entry)

XX

DE Antisense oligo (SeqID 77) used to inhibit human EIF2C1 DNA.

XX

XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;

KW EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;

KW gene therapy; hyperproliferative disorder;

KW familial hypercholesterolaemia; cancer; polycystic kidney disease;

KW cystic fibrosis; progeroid syndrome; cytostatic; antiproliferative.

XX

OS Homo sapiens.

XX

XX

XX Key Location/Qualifiers

FT modified_base 1..20

FT /tag= a

FT /mod_base= OTHER

FT /note= "OTHER= phosphorothioate backbone, where 1-5 and

FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are

FT 5-methylcytidines"

XX

XX WO2003040321-A2.

XX

XX

XX 15-MAY-2003.

XX

XX PD 04-NOV-2002; 2002WO-US035324.

XX

XX PF 08-NOV-2001; 2001US-00007078.

XX

XX PR (ISIS-) ISIS PHARM INC.

XX

XX PA

XX PI Ward DT, Watt AT;

XX

XX DR WPI; 2003-449448/42.

XX

XX New compound, having a sequence targeted to a nucleic acid encoding human

PT collapsein response mediator protein 2, useful for preparing a composition

PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,

PT cancer.

XX

PS Claim 3; Page 77; 120pp; English.

XX

XX This invention relates to novel antisense oligonucleotides that modulate

CC the expression of human eukaryotic translation initiation factor 2C 1

CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as

CC Co-EIF2C, EIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an

CC intracellular membrane associated protein thought to be involved in

CC cellular differentiation, such that altered expression of EIF2C1 can

CC affect cell growth, morphology and tumorigenicity. Accordingly,

CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells

CC or tissues can be used in gene therapy to treat various conditions

CC including hyperproliferative disorders, familial hypercholesterolaemia

CC and cancer, as well as polycystic kidney disease, cystic fibrosis and

CC progeroid syndrome. As such, the oligos of the present invention can be

CC described as having cytostatic and antiproliferative activities. This

CC oligonucleotide sequence is an antisense oligo used to inhibit expression

CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA

CC of the invention.

XX

SQ Sequence 20 BP; 4 A; 3 C; 6 G; 7 T; 0 U; 0 Other;

XX

Query Match 0.3%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7394 CTTCTGAGCAAGCAACATC 7413

DB 20 CTTCTGAGCAAGCAACATC 1

RESULT 415

ADB81514/c

ID ADB81514 standard; DNA; 20 BP.

XX

AC ADB81514;

XX

DT 04-DEC-2003 (first entry)

XX

DE Antisense oligo (SeqID 31) used to inhibit human EIF2C1 DNA.

XX

XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;

KW EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;

KW gene therapy; hyperproliferative disorder;

KW familial hypercholesterolaemia; cancer; polycystic kidney disease;

KW cystic fibrosis; progeroid syndrome; cytostatic; antiproliferative.

XX

OS Homo sapiens.

XX

XX

XX Key Location/Qualifiers

FT modified_base 1..20

FT /tag= a

FT /mod_base= OTHER

FT /note= "OTHER= phosphorothioate backbone, where 1-5 and

FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are

FT 5-methylcytidines"

XX

XX WO2003040321-A2.

XX

XX

XX 15-MAY-2003.

XX

XX PD 04-NOV-2002; 2002WO-US035324.

XX

XX PF 08-NOV-2001; 2001US-00007078.

XX

XX PR (ISIS-) ISIS PHARM INC.

XX

XX PA

XX PI Ward DT, Watt AT;

XX

XX DR WPI; 2003-449448/42.

XX

CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
CC affect cell growth, morphology and tumorigenicity. Accordingly,
CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC or tissues can be used in gene therapy to treat various conditions
CC including hyperproliferative disorders, familial hypercholesterolemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC progeria syndrome. As such, the oligos of the present invention can be
CC described as having cytosolic and antipneumatic activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX

SQ Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7124 TTCTGTGCACACAGTCCAG 7143
DB 20 TTCTGTGCACACAGTCCAG 1

RESULT 412
ADB81516/c
ID ADB81516 standard; DNA; 20 BP.
XX
AC ADB81516;
XX
DT 04-DEC-2003 (first entry)
XX
DE Antisense oligo (SeqID 33) used to inhibit human EIF2C1 DNA.
XX
KM antisense; sg; human; eukaryotic translation initiation factor 2C 1;
KM EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
KM gene therapy; hyperproliferative disorder;
KM familial hypercholesterolemia; cancer; polycystic kidney disease;
KM cystic fibrosis; progeria syndrome; cytosolic; antipneumatic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
PN WO2003040321-A2.
XX
PD 15-MAY-2003.
XX
PF 04-NOV-2002; 2002MO-US035324.
XX
PR 08-NOV-2001; 2001US-00007078.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ward DT, Walt AT;
XX
PI WPI; 2003-449448/42.
XX
PT New compound, having a sequence targeted to a nucleic acid encoding human
PT collapsin response mediator protein 2, useful for preparing a composition
PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT cancer.
PS Claim 3; Page 76; 120pp; English.

XX This invention relates to novel antisense oligonucleotides that modulate
CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
CC affect cell growth, morphology and tumorigenicity. Accordingly,
CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC or tissues can be used in gene therapy to treat various conditions
CC including hyperproliferative disorders, familial hypercholesterolemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC progeria syndrome. As such, the oligos of the present invention can be
CC described as having cytosolic and antipneumatic activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
XX

SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1746 AGGCGTCGACGTCATTATTG 1765
DB 20 AGGCGTCGACGTCATTATTG 1

RESULT 413
ADB81542/c
ID ADB81542 standard; DNA; 20 BP.
XX
AC ADB81542;
XX
DT 04-DEC-2003 (first entry)
XX
DE Antisense oligo (SeqID 59) used to inhibit human EIF2C1 DNA.
XX
KM antisense; sg; human; eukaryotic translation initiation factor 2C 1;
KM EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
KM gene therapy; hyperproliferative disorder;
KM familial hypercholesterolemia; cancer; polycystic kidney disease;
KM cystic fibrosis; progeria syndrome; cytosolic; antipneumatic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
PN WO2003040321-A2.
XX
PD 15-MAY-2003.
XX
PF 04-NOV-2002; 2002MO-US035324.
XX
PR 08-NOV-2001; 2001US-00007078.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ward DT, Walt AT;
XX
PI WPI; 2003-449448/42.
XX
PT New compound, having a sequence targeted to a nucleic acid encoding human
PT collapsin response mediator protein 2, useful for preparing a composition
PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT cancer.

CC cellular differentiation, such that altered expression of EIF2C1 can
 CC affect cell growth, morphology and tumorigenicity. Accordingly,
 CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
 CC or tissues can be used in gene therapy to treat various conditions
 CC including hyperproliferative disorders, familial hypercholesterolaemia
 CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
 CC progeroid syndrome. As such, the oligos of the present invention can be
 CC described as having cytostatic and antiproliferative activities. This
 CC oligonucleotide sequence is an antisense oligo used to inhibit expression
 CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
 CC of the invention.

SO Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3118 GCTTGACAGCTGTGTAAGGT 3137
 DB 20 GCTTGACAGCTGTGTAAGGT 1

RESULT 410
 ADB81548/c
 ID ADB81548 standard; DNA; 20 BP.

AC ADB81548;
 DT 04-DEC-2003 (first entry)

DE Antisense oligo (SeqID 65) used to inhibit human EIF2C1 DNA.

XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;
 KW EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
 KM gene therapy; hyperproliferative disorder;
 KW familial hypercholesterolaemia; cancer; polycystic kidney disease;
 XX cystic fibrosis; progeroid syndrome; cytostatic; antiproliferative;
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 FT 5-methylcytidines"

XX MO2003040321-A2.

XX 15-MAY-2003.

XX 04-NOV-2002; 2002WO-US035324.

XX 08-NOV-2001; 2001US-00007078.

XX (ISIS-) ISIS PHARM INC.

XX Ward DT, Watt AT;

XX WPI; 2003-449448/42.

XX New compound, having a sequence targeted to a nucleic acid encoding human
 XX collapsin response mediator protein 2, useful for preparing a composition
 XX for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
 XX cancer.

XX Claim 3; Page 77; 120pp; English.

XX This invention relates to novel antisense oligonucleotides that modulate
 CC the expression of human eukaryotic translation initiation factor 2C 1
 CC (EIF2C1). EIF2C1 is located on chromosome 1p4-35, and is also known as

CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
 CC intracellular membrane associated protein thought to be involved in
 CC cellular differentiation, such that altered expression of EIF2C1 can
 CC affect cell growth, morphology and tumorigenicity. Accordingly,
 CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
 CC or tissues can be used in gene therapy to treat various conditions
 CC including hyperproliferative disorders, familial hypercholesterolaemia
 CC and cancer, as well as polycystic kidney disease, cystic fibrosis and
 CC progeroid syndrome. As such, the oligos of the present invention can be
 CC described as having cytostatic and antiproliferative activities. This
 CC oligonucleotide sequence is an antisense oligo used to inhibit expression
 CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
 CC of the invention.

SO Sequence 20 BP; 5 A; 3 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6397 TATGCCACCTGCTAGATA 6416
 DB 20 TATGCCACCTGCTAGATA 1

RESULT 411
 ADB81557/c
 ID ADB81557 standard; DNA; 20 BP.

AC ADB81557;

DT 04-DEC-2003 (first entry)

DE Antisense oligo (SeqID 74) used to inhibit human EIF2C1 DNA.

XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;
 KW EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
 KM gene therapy; hyperproliferative disorder;
 KW familial hypercholesterolaemia; cancer; polycystic kidney disease;
 XX cystic fibrosis; progeroid syndrome; cytostatic; antiproliferative;
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 FT 5-methylcytidines"

XX MO2003040321-A2.

XX 15-MAY-2003.

XX 04-NOV-2002; 2002WO-US035324.

XX 08-NOV-2001; 2001US-00007078.

XX (ISIS-) ISIS PHARM INC.

XX Ward DT, Watt AT;

XX WPI; 2003-449448/42.

XX New compound, having a sequence targeted to a nucleic acid encoding human
 XX collapsin response mediator protein 2, useful for preparing a composition
 XX for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
 XX cancer.

XX Claim 3; Page 77; 120pp; English.

XX This invention relates to novel antisense oligonucleotides that modulate

CC	including hyperproliferative disorders, familial hypercholesterolaemia
CC	and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC	progeroid syndrome. As such, the oligos of the present invention can be
CC	described as having cytosstatic and antiproliferative activities. This
CC	oligonucleotide sequence is an antisense oligo used to inhibit expression
CC	of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC	of the invention.
XX	
SQ	Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
	Query Match 0.3%; Score 20; DB 1; Length 20;
	Best Local Similarity 100.0%; Pred. No. 2.7e+02;
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	2450 TCTATCTGTGAGCCACGCCA 2469 .
DB	20 TCTATCTGTGAGCCACGCCA 1
RESULT 408	
ID	ADB81522/C
XX	ADB81522 standard; DNA; 20 BP.
AC	
XX	ADB81522;
XX	
DT	04-DEC-2003 (first entry)
XX	
DE	Antisense oligo (SeqID 39) used to inhibit human EIF2C1 DNA.
XX	
KM	antisense; ss; human; eukaryotic translation initiation factor 2C 1;
KW	EIF2C1. Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GRP95; Q99;
KM	gene therapy; hyperproliferative disorder;
KW	familial hypercholesterolaemia; cancer; polycystic kidney disease;
KM	cystic fibrosis; progeroid syndrome; cytostatic; antiproliferative.
OS	Homo sapiens.
XX	
FT	Key Location/Qualifiers
FT	modified_base 1..20
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "OTHER= phosphorothioate backbone, where 1-5 and
FT	16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT	5-methylcytidines"
XX	
PN	WO2003040321-A2.
XX	
PD	15-MAY-2003.
XX	
PF	04-NOV-2002; 2002MO-US035324.
XX	
PR	08-NOV-2001; 2001US-00007078.
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
PI	Ward DT, Watt AT;
DR	WPI; 2003-449448/42.
PT	
PT	New compound, having a sequence targeted to a nucleic acid encoding human
PT	collapse response mediator protein 2, useful for preparing a composition
PT	for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT	cancer.
PS	
PS	Claim 3; Page 76; 120pp; English.
XX	
XX	This invention relates to novel antisense oligonucleotides that modulate
CC	the expression of human eukaryotic translation initiation factor 2C 1
CC	(EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC	Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GRP95 and Q99. It is an
CC	intracellular membrane associated protein thought to be involved in
CC	cellular differentiation, such that altered expression of EIF2C1 can
CC	affect cell growth, morphology and tumourigenicity. Accordingly,

CC	antlense oligonucleotides that inhibit the expression of EIF2C1 in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disorders, familial hypercholesterolaemia and cancer, as well as polycystic kidney disease, cystic fibrosis and progeroid syndrome. As such, the oligos of the present invention can be described as having cytosostatic and antiproliferative activities. This CC
CC	oligonucleotide sequence is an antlense oligo used to inhibit expression of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA CC
XX	Sequence 20 BP; 2 A; 6 C; 5 G; 7 T; 0 U; 0 Other;
SQ	
Query Match	0.3%; Score 20; DB 1; Length 20;
Best Local Similarity	100.0%; Pred.No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	2692 CACATATCGGGCAGAGCA 2711
Dd	20 CACATATCGGGCAGAGCA 1
RESULT 409	
ADB81528/c	
ID	ADB81528 standard; DNA; 20 BP.
AC	
XX	ADB81528;
XX	
DT	04-DEC-2003 (first entry)
XX	
DE	Antlense oligo (SeqID 45) used to inhibit human EIF2C1 DNA.
XX	
KM	antlense; ss; human; eukaryotic translation initiation factor 2C 1;
KW	EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
KX	gene therapy; hyperproliferative disorder;
KM	familial hypercholesterolaemia; cancer; polycystic kidney disease;
KW	cystic fibrosis; progeroid syndrome; cytosostatic; antiproliferative.
XX	
OS	Homo sapiens.
FH	
FT	Key Location/Qualifiers
FT	modified_base 1..20
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "OTHER= phosphorothioate backbone, where 1-5 and 15-20 are 2' methoxyethyl nucleotides. All cytidines are 5-methylcytidines"
XX	
PN	WO2003040321-A2.
XX	
PD	15-MAY-2003.
XX	
Pf	04-NOV-2002; 2002WC-US035324.
PR	08-NOV-2001; 2001US-00007078.
PA	(ISIS-) ISIS PHARM INC.
XX	
Pt	Ward DT, Watt AT;
XX	
XX	WPI; 2003-449448/42.
XX	
PT	New compound, having a sequence targeted to a nucleic acid encoding human collagen response mediator protein 2, useful for preparing a composition for treating hypercholesterolemia or hyperproliferative disorder, e.g., cancer.
XX	
PS	Claim 3; Page 76; 120pp; English.
CC	This invention relates to novel antlense oligonucleotides that modulate the expression of human eukaryotic translation initiation factor 2C 1 (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an intracellular membrane associated protein thought to be involved in

CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC of the invention.

XX Sequence 20 BP; 7 A; 3 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7442 TGTGTTTATTAAGACACCA 7461

Db 20 TGTGTTTATTAAGACACCA 1

RESULT 406

ADB81502/c

ID ADB81502 standard; DNA; 20 BP.

XX ADB81502;

XX 04-DEC-2003 (first entry)

XX Antisense oligo (SeqID 19) used to inhibit human EIF2C1 DNA.

XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;

KW EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;

KM gene therapy; hyperproliferative disorder;

KW familial hypercholesterolaemia; cancer; polycystic kidney disease;

KM cystic fibrosis; progeroid syndrome; cytostatic; antilipemic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /tag= a

FT /mod_base= OTHER

FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
16-20 are 2' methoxyethyl nucleotides. All cytidines are
5-methylcytidines"

FT MO2003040321-A2.

XX 15-MAY-2003.

XX 04-NOV-2002; 2002WO-US035324.

XX 08-NOV-2001; 2001US-00007078.

XX (ISIS-) ISIS PHARM INC.

XX Ward DT, Watt AT;

XX WPI; 2003-449448/42.

XX New compound, having a sequence targeted to a nucleic acid encoding human
PT collapsin response mediator protein 2, useful for preparing a composition
PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT cancer.

PS Claim 3; Page 76; 120pp; English.

XX This invention relates to novel antisense oligonucleotides that modulate
CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
CC affect cell growth, morphology and tumorigenicity. Accordingly,
CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC or tissues can be used in gene therapy to treat various conditions
CC including hyperproliferative disorders, familial hypercholesterolaemia
CC and cancer, as well as polycystic kidney disease, cystic fibrosis and

CC progeroid syndrome. As such, the oligos of the present invention can be
CC described as having cytostatic and antilipemic activities. This
CC oligonucleotide sequence is an antisense oligo used to inhibit expression
CC of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA
CC of the invention.

XX Sequence 20 BP; 5 A; 6 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 818 AGCTGTGGGCGCCCTGCATG 837

Db 20 AGCTGTGGGCGCCCTGCATG 1

RESULT 407

ADB81520/c

ID ADB81520 standard; DNA; 20 BP.

XX ADB81520;

XX 04-DEC-2003 (first entry)

XX Antisense oligo (SeqID 37) used to inhibit human EIF2C1 DNA.

XX antisense; ss; human; eukaryotic translation initiation factor 2C 1;

KW EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;

KM gene therapy; hyperproliferative disorder;

KW familial hypercholesterolaemia; cancer; polycystic kidney disease;

KM cystic fibrosis; progeroid syndrome; cytostatic; antilipemic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /tag= a

FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
16-20 are 2' methoxyethyl nucleotides. All cytidines are
5-methylcytidines"

FT MO2003040321-A2.

XX 15-MAY-2003.

XX 04-NOV-2002; 2002WO-US035324.

XX 08-NOV-2001; 2001US-00007078.

XX (ISIS-) ISIS PHARM INC.

XX Ward DT, Watt AT;

XX WPI; 2003-449448/42.

XX New compound, having a sequence targeted to a nucleic acid encoding human
PT collapsin response mediator protein 2, useful for preparing a composition
PT for treating hypercholesterolemia or hyperproliferative disorder, e.g.,
PT cancer.

PS Claim 3; Page 76; 120pp; English.

XX This invention relates to novel antisense oligonucleotides that modulate
CC the expression of human eukaryotic translation initiation factor 2C 1
CC (EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
CC Co-eIF2C, eIF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an
CC intracellular membrane associated protein thought to be involved in
CC cellular differentiation, such that altered expression of EIF2C1 can
CC affect cell growth, morphology and tumorigenicity. Accordingly,
CC antisense oligonucleotides that inhibit the expression of EIF2C1 in cells
CC or tissues can be used in gene therapy to treat various conditions

Seq	Sequence	20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
Query Match	0.3%;	Score 20; DB 1; Length 20;
Best Local Similarity	100.0%;	Pred. No. 2.7e+02;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
Cy	3794 AACATGACACGCTCGAGC 3813	
DB	20 AACATGACACGCTCGAGC 1	
RESULT 404		
ADB81537/C		
ID	ADB81537 standard; DNA; 20 BP.	
AC	ADB81537;	
XX		
DT	04-DEC-2003 (first entry)	
XX		
DE	Antisense oligo (SeqID 54) used to inhibit human EIF2C1 DNA.	
XX		
KW	antisense; ss; human; eukaryotic translation initiation factor 2C 1;	
KW	EIF2C1; Co-eiF2C; eiF2C; Golgi ER protein 95kDa; GERP95; Q99;	
KW	gene therapy; hyperproliferative disorder;	
KW	familial hypercholesterolaemia; cancer; polycystic kidney disease;	
KW	cystic fibrosis; progeria syndrome; cytostatic; antilipemic.	
XX		
OS	Homo sapiens.	
XX		
Key	Location/Qualifiers	
FT	modified_base 1..20	
FT	/tag= a	
FT	/mod_base= OTHER	
FT	/note= "OTHER= phosphorothioate backbone, where 1-5 and 16-20 are 2' methoxyethyl nucleotides. All cytidines are 5-methylcytidines"	
FT		
XX		
PN	WO2003040321-A2.	
XX		
PD	15-MAY-2003.	
XX		
PE	04-NOV-2002; 2002MO-US05324.	
XX		
PR	08-NOV-2001; 2001US-00007078.	
XX		
PA	(ISIS-) ISIS PHARM INC.	
XX		
PI	Ward DT, Watt AT;	
XX		
DR	WPI; 2003-449448/42.	
XX		
PT	New compound, having a sequence targeted to a nucleic acid encoding human	
PT	collapse response mediator protein 2, useful for preparing a composition	
PT	for treating hypercholesterolemia or hyperproliferative disorder, e.g.,	
PT	cancer.	
XX		
PS	Example 15; Page 76; 120p; English.	
XX		
CC	This invention relates to novel antisense oligonucleotides that modulate	
CC	the expression of human eukaryotic translation initiation factor 2C 1	
CC	(EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as	
CC	Co-eiF2C, eiF2C, Golgi ER protein 95kDa, GERP95 and Q99. It is an	
CC	intracellular membrane associated protein thought to be involved in	
CC	cellular differentiation, such that altered expression of EIF2C1 can	
CC	affect cell growth, morphology and tumorigenicity. Accordingly,	
CC	antisense oligonucleotides that inhibit the expression of EIF2C1 in cells	
CC	or tissues can be used in gene therapy to treat various conditions	
CC	including hyperproliferative disorders, familial hypercholesterolaemia	
CC	and cancer, as well as polycystic kidney disease, cystic fibrosis and	
CC	progeria syndrome. As such, the oligos of the present invention can be	
CC	described as having cytostatic and antilipemic activities. This	
CC	oligonucleotide sequence is an antisense oligo used to inhibit expression	
CC	of the human eukaryotic translation initiation factor 2C 1 (EIF2C1) DNA	
CC		

CC	of the invention.
XX	
SQ	Sequence 20 BP; 2 A; 2 C; 7 G; 9 T; 0 U; 0 Other;
	Query Match 0.3%; Score 20; DB 1; Length 20;
	Best Local Similarity 100.0%; Pred. No. 2.7e+02;
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	4879 CAACTCACAAAAGTAGCAC 4898
DB	20 CAACTCACAAAAGTAGCACC 1
RESULT 405	
ADB81561/C	
ID	ADB81561 standard; DNA; 20 BP.
XX	
AC	ADB81561;
XX	
DT	04-DEC-2003 (first entry)
DE	
XX	Antisense oligo (SeqID 78) used to inhibit human EIF2C1 DNA.
XX	
KM	antisense; ss; human; eukaryotic translation initiation factor 2C 1;
KM	EIF2C1; Co-eIF2C; eIF2C; Golgi ER protein 95kDa; GERP95; Q99;
KM	gene therapy; hyperproliferative disorder;
KM	familial hypercholesterolemia; cancer; polycystic kidney disease;
XX	cyclic fibrosis; progeroid syndrome; cyostatic; antilipaeamic.
OS	Homo sapiens.
XX	
FH	Key
FT	modified_base
FT	Location/Qualifiers
FT	1..20
FT	/*tag= A
FT	/note= "OTHER= phosphorothioate backbone, where 1-5 and
FT	16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT	5-methylcytidines"
PN	
XX	WO2003040321-A2.
PD	
XX	15-MAY-2003.
PF	
XX	04-NOV-2002; 2002WO-US035324.
PR	
XX	08-NOV-2001; 2001US-00007078.
PA	(ISIS-) ISIS PHARM INC.
PI	
XX	Ward DT, Watt AT;
DR	
XX	WPI; 2003-449448/42.
PT	
XX	New compound, having a sequence targeted to a nucleic acid encoding human
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PT	cancer.
PS	
XX	Claim 3; Page 77; 120p; English.
XX	
CC	This invention relates to novel antisense oligonucleotides that modulate
CC	the expression of human eukaryotic translation initiation factor 2C 1
CC	(EIF2C1). EIF2C1 is located on chromosome 1p34-35, and is also known as
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CC	and cancer, as well as polycystic kidney disease, cystic fibrosis and
CC	progeroid syndrome. As such, the oligos of the present invention can be
CC	described as having cytostatic and antilipaeamic activities. This